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(22) International Filing Date: 23 February 1995 (23.02.95)		(72) Inventors: STINCHCOMB, Dan, T.; 7203 Old Post Road, Boulder, CO 80301 (US). CHOWRIRA, Bharat; 3250 O'Neal Circle, B-25, Boulder, CO 80301 (US). DIRENZO, Anthony; 1197 Ravenwood Road, Boulder, CO 80303 (US). DRAPER, Kenneth, G.; 4619 Cloud Ct., Boulder, CO 80301 (US). DUDYCZ, Lech, W.; 24 A Gates Road, Worcester, MA 01603 (US). GRIMM, Susan; 6968 1/2 S. Boulder Road, Boulder, CO 80303 (US). KARPEISKY, Alexander; 5121 Williams Fork Trail #209, Boulder, CO 80301 (US). KISICH, Kevin; 2451 Jonquil Circle, Lafayette, CO 80026 (US). MATULIC-ADAMIC, Jasenka; 760 South 42nd Street, Boulder, CO 80303 (US). McSWIGGEN, James, A.; 4866 Franklin Drive, Boulder, CO 80301 (US). MODAK, Anil; 3855 Hauptman Court, Boulder, CO 80301 (US). PAVCO, Pamela; 705 Barbary Circle, Lafayette, CO 80026 (US). BEIGELMAN, Leonid; 5530 Colt Drive, Longmont, CO 80503 (US). SULLIVAN, Sean, M.; 850 Marina Village Parkway, Alameda, CA 94501 (US). SWEEDLER, David; 956 St. Andrews Lane, Louisville, CO 80027 (US). THOMPSON, James, D.; 2925 Glenwood Drive #301, Boulder, CO 80301 (US). TRACZ, Danuta; 6200 Habitat #3029, Boulder, CO 80301 (US). USMAN, Nassim; 2954 Kalmia #37, Boulder, CO 80304 (US). WINCOTT, Francine, E.; 7920 N. 95th Street, Longmont, CO 80501 (US). WOOLF, Tod; 18 Fairview Avenue, Watertown, MA 02172 (US).																																																																															
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(57) Abstract

Enzymatic RNA molecules which cleave ICAM-1 mRNA, IL-5 mRNA, *ret A* mRNA, TNF- α mRNA, RSV mRNA or RSV genomic RNA, or CML associated mRNA, and use of these molecules for the treatment of pathological conditions related to those mRNA-levels; ribonucleosides or nucleotides modified in 2', 3' or 5', methods for their synthesis, purification and deprotection; vectors containing multiple enzymatic nucleic acids, optionally in chimeric form with tRNAs; method for introducing enzymatic nucleic acids into cells by forming a complex with a second nucleic acid, where the complex is capable of taking an R-loop base-paired structure; method for altering a mutant nucleic acid *in vivo* by hybridization with an oligonucleotide capable of activating dsRNA deaminase, comprising an enzymatic activity or a chemical mutagen. Further are disclosed trans-cleaving or -ligating hairpin ribozymes lacking a substrate RNA moiety, as well as hammerhead ribozymes having an interconnecting loop between base pairs in stem II.

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METHOD AND REAGENT FOR INHIBITING THE EXPRESSION
OF DISEASE RELATED GENESBackground of the Invention

This invention relates to reagents useful as inhibitors of gene expression relating to diseases such as inflammatory or autoimmune disorders, chronic myelogenous leukemia, or respiratory tract illness.

5

Summary of the Invention

The invention features novel enzymatic RNA molecules, or ribozymes, and methods for their use for inhibiting the expression of disease related genes, e.g., ICAM-1, IL-5, relA, TNF- α , p210 bcr-abl, and respiratory syncytial virus genes. Such ribozymes can be used in a method for
10 treatment of diseases caused by the expression of these genes in man and other animals, including other primates.

Ribozymes are RNA molecules having an enzymatic activity which is able to repeatedly cleave other separate RNA molecules in a nucleotide base sequence specific manner. Such enzymatic RNA molecules can be
15 targeted to virtually any RNA transcript, and efficient cleavage has been achieved *in vitro*. Kim et al., 84 Proc. Natl. Acad. Sci. USA 8788, 1987; Haseloff and Gerlach, 334 Nature 585, 1988; Cech, 260 JAMA 3030, 1988; and Jefferies et al., 17 Nucleic Acids Research 1371, 1989.

Six basic varieties of naturally-occurring enzymatic RNAs are known
20 presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds in trans (and thus can cleave other RNA molecules) under physiological conditions. Table 1 summarizes some of the characteristics of these ribozymes.

Ribozymes act by first binding to a target RNA. Such binding occurs
25 through the target RNA binding portion of a ribozyme which is held in close proximity to an enzymatic portion of the RNA which acts to cleave the target RNA. Thus, the ribozyme first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a
30 target RNA will destroy its ability to direct synthesis of an encoded protein. After a ribozyme has bound and cleaved its RNA target it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over other technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the effective concentration of ribozyme necessary to effect a therapeutic treatment is lower than that of an antisense oligonucleotide. The advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding, but also on the mechanism by which the molecule inhibits the expression of the RNA to which it binds. That is, the inhibition is caused by cleavage of the RNA target and so specificity is defined as the ration of the rate of cleavage of the targeted RNA over the rate of cleavage of non-targeted RNA. This cleavage mechanism is dependent upon factors additional to those involved in base pairing. Thus, it is thought that the specificity of action of a ribozyme is greater than that of antisense oligonucleotide binding the same RNA site. With their catalytic activity and increased site specificity, ribozymes represent more potent and safe therapeutic molecules than antisense oligonucleotides.

Thus, in a first aspect, this invention relates to ribozymes, or enzymatic RNA molecules, directed to cleave RNA species encoding ICAM-1, IL-5, relA, TNF- α , p210^{bcr-abl}, or RSV proteins. In particular, applicant describes the selection and function of ribozymes capable of cleaving these RNAs and their use to reduce levels of ICAM-1, IL-5, relA, TNF- α , p210 bor-abl or RSV proteins in various tissues to treat the diseases discussed herein. Such ribozymes are also useful for diagnostic uses.

Applicant indicates that these ribozymes are able to inhibit expression of ICAM-1, IL-5, rel A, TNF- α , p210^{bcr-abl}, or RSV genes and that the catalytic activity of the ribozymes is required for their inhibitory effect. Those of ordinary skill in the art, will find that it is clear from the examples described that other ribozymes that cleave target ICAM-1, IL-5, rel A, TNF- α , p210^{bcr-abl}, or RSV encoding mRNAs may be readily designed and are within the invention.

These chemically or enzymatically synthesized RNA molecules contain substrate binding domains that bind to accessible regions of their target mRNAs. The RNA molecules also contain domains that catalyze the

cleavage of RNA. Upon binding, the ribozymes cleave the target encoding mRNAs, preventing translation and protein accumulation. In the absence of the expression of the target gene, a therapeutic effect may be observed.

By "gene" is meant to refer to either the protein coding regions of the cognate mRNA, or any regulatory regions in the RNA which regulate synthesis of the protein or stability of the mRNA; the term also refers to those regions of an mRNA which encode the ORF of a cognate polypeptide product, and the proviral genome.

By "enzymatic RNA molecule" it is meant an RNA molecule which has complementarity in a substrate binding region to a specified gene target, and also has an enzymatic activity which is active to specifically cleave RNA in that target. That is, the enzymatic RNA molecule is able to intermolecularly cleave RNA and thereby inactivate a target RNA molecule. This complementarity functions to allow sufficient hybridization of the enzymatic RNA molecule to the target RNA to allow the cleavage to occur. One hundred percent complementarity is preferred, but complementarity as low as 50-75% may also be useful in this invention. By "equivalent" RNA to a virus is meant to include those naturally occurring viral encoded RNA molecules associated with viral caused diseases in various animals, including humans, cats, simians, and other primates. These viral or viral-encoded RNAs have similar structures and equivalent genes to each other.

By "complementarity" it is meant a nucleic acid that can form hydrogen bond(s) with other RNA sequence by either traditional Watson-Crick or other non-traditional types (for example, Hoogsteen type) of base-paired interactions.

In preferred embodiments of this invention, the enzymatic nucleic acid molecule is formed in a hammerhead or hairpin motif, but may also be formed in the motif of a hepatitis delta virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or *Neurospora* VS RNA. Examples of such hammerhead motifs are described by Rossi *et al.*, 1992, Aids Research and Human Retroviruses, 8,183, of hairpin motifs by Hampel and Tritz, 1989 Biochemistry, 28, 4929, EP 0360257 and Hampel *et al.*, 1990, Nucleic Acids Res. 18,299 and an example of the hepatitis delta virus motif is described by Perotta and Been, 1992 Biochemistry, 31 16 of the RNaseP motif by Guerrier-Takada *et al.*, 1983 Cell, 35 849,

Neurospora VS RNA ribozyme motif is described by Collins (Seville and Collins, 1990 Cell 61, 685-696; Saville and Collins, 1991 Proc. Natl. Acad. Sci. USA 88, 8826-8830; Collins and Olive, 1993 Biochemistry 32, 2795-2799 Guo and Collins, 1995 EMBO J., 14, 368) and of the Group I intron by Cech et al., U.S. Patent 4,987,071. These specific motifs are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it has nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule.

The invention provides a method for producing a class of enzymatic cleaving agents which exhibit a high degree of specificity for the RNA of a desired target. The enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of a target (i.e., I CAM-1, IL-5, reLA, TNF- α , p210 bcr-abl or RSV proteins) encoding mRNA such that specific treatment of a disease or condition can be provided with either one or several enzymatic nucleic acids. Such enzymatic nucleic acid molecules can be delivered exogenously to specific cells as required. Alternatively, the ribozymes can be expressed from vectors that are delivered to specific cells. By "vectors" is meant any nucleic acid and/or viral-based technique used to deliver a desired nucleic acid.

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention small enzymatic nucleic acid motifs (e.g., of the hammerhead or the hairpin structure) are used for exogenous delivery. The simple structure of these molecules increases the ability of the enzymatic nucleic acid to invade targeted regions of the mRNA structure. However, these catalytic RNA molecules can also be expressed within cells from eukaryotic promoters (e.g. Scanion, K.J. et al., 1991, Proc. Natl. Acad. Sci. USA, 88, 10591-5; Kashani-Sabet, M., et al., 1992, Antisense Res. Dev., 2, 3-15; Dropoulic, B., et al., 1992, J. Virol, 66, 1432-41; Weerasinghe, M., et al., 1991, J. Virol, 65, 5531-4; Ojwang, J.O., et al., 1992, Proc. Natl. Acad. Sci. USA, 89 10802-6; Chen C.J., et al., 1992, Nucleic Acids Res., 20, 4581-9; Sarver, H., et al., 1990 Science, 247, 1222-1225). Those skilled in the art would realize that any ribozyme can be

expressed in eukaryotic cells from the appropriate DNA or RNA vector. The activity of such ribozymes can be augmented by their release from the primary transcript by a second ribozyme (Draper et al., PCT WO93/23569, and Sullivan et al., PCT WO94/02595, both hereby incorporated in their totality by reference herein; Ohkawa, J., et al., 1992, Nucleic Acids Symp. Ser. 27, 15-6; Taira, K. et al., Nucleic Acids Res., 19, 5125-30; Ventura, M., et al., 1993, Nucleic Acids Res., 21, 3249-55, Chowrira et al., 1994 J. Biol. Chem., 269, 25856).

By "inhibit" is meant that the activity or level of ICAM-1, Rel A, IL-5, TNF- α , p210^{bcr-abl} or RSV encoding mRNA is reduced below that observed in the absence of the ribozyme, and preferably is below that level observed in the presence of an inactive RNA molecule able to bind to the same site on the mRNA, but unable to cleave that RNA.

Such ribozymes are useful for the prevention of the diseases and conditions discussed above, and any other diseases or conditions that are related to the level of ICAM-1, IL-5, Rel A, TNF- α , p210^{bcr-abl} or RSV protein or activity in a cell or tissue. By "related" is meant that the inhibition of ICAM-1, IL-5, Rel A, TNF- α , p210^{bcr-abl} or RSV mRNA translation, and thus reduction in the level of, ICAM-1, IL-5, Rel A, TNF- α , p210^{bcr-abl} or RSV proteins will relieve to some extent the symptoms of the disease or condition.

Ribozymes are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells. The RNA or RNA complexes can be locally administered to relevant tissues through the use of a catheter, infusion pump or stent, with or without their incorporation in biopolymers. In preferred embodiments, the ribozymes have binding arms which are complementary to the sequences in Tables 2,3,6-9, 11, 13, 15-23, 27, 28, 31, 33, 34, 36 and 37.

Examples of such ribozymes are shown in Tables 4-8, 10, 12, 14-16, 19-22, 24, 26-28, 30, 32, 34 and 36-38. Examples of such ribozymes consist essentially of sequences defined in these Tables. By "consists essentially of" is meant that the active ribozyme contains an enzymatic center equivalent to those in the examples, and binding arms able to bind mRNA such that cleavage at the target site occurs. Other sequences may be present which do not interfere with such cleavage.

Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. For example, stem-loop II sequence of hammerhead ribozymes listed in the above identified Tables can be altered (substitution, deletion, and/or insertion) to contain any sequences provided a minimum of two base-paired stem structure can form. Similarly, stem-loop IV sequence of hairpin ribozymes listed in the above identified Tables can be altered (substitution, deletion, and/or insertion) to contain any sequence, provided a minimum of two base-paired stem structure can form. The sequence listed in the above identified Tables may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the ribozymes described specifically in the Tables.

In another aspect of the invention, ribozymes that cleave target molecules and inhibit ICAM-1, IL-5, Rel A, TNF- α , p210^{bcr-abl} or RSV gene expression are expressed from transcription units inserted into DNA, RNA, or viral vectors. Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA or RNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990 *Proc. Natl. Acad. Sci. USA*, 87, 6743-7; Gao and Huang 1993 *Nucleic Acids Res.*, 21 2867-72; Lieber et al., 1993 *Methods Enzymol.*, 217, 47-66; Zhou et al., 1990 *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet et al., 1992 *Antisense Res. Dev.*, 2, 3-15; Ojwang et al., 1992 *Proc. Natl. Acad. Sci. USA*, 90, 6340-4; L'Huillier et al., 1992 *EMBO J.* 11, 4411-8; Lisiewicz et al., 1993 *Proc. Natl. Acad. Sci. U.S.A.*, 90 8000-4). The above ribozyme transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors

(such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors).

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from
5 the claims.

Description Of The Preferred Embodiments

The drawings will first briefly be described.

Drawings:

Figure 1 is a diagrammatic representation of the hammerhead
10 ribozyme domain known in the art. Stem II can be ≥ 2 base-pair long.

Figure 2(a) is a diagrammatic representation of the hammerhead
ribozyme domain known in the art; Figure 2(b) is a diagrammatic
representation of the hammerhead ribozyme as divided by Uhlenbeck
(1987, *Nature*, 327, 596-600) into a substrate and enzyme portion; Figure
15 2(c) is a similar diagram showing the hammerhead divided by Haseloff and
Gerlach (1988, *Nature*, 334, 585-591) into two portions; and Figure 2(d) is
a similar diagram showing the hammerhead divided by Jeffries and
Symons (1989, *Nucl. Acids. Res.*, 17, 1371-1371) into two portions.

Figure 3 is a diagrammatic representation of the general structure of a
20 hairpin ribozyme. Helix 2 (H2) is provided with a least 4 base pairs (*i.e.*, n
is 1,2,3 or 4) and helix 5 can be optionally provided of length 2 or more
bases (preferably 3-20 bases, *i.e.*, m is from 1-20 or more). Helix 2 and
helix 5 may be covalently linked by one or more bases (*i.e.*, r is ≥ 1 base).
25 Helix 1, 4 or 5 may also be extended by 2 or more base pairs (*e.g.*, 4-20
base pairs) to stabilize the ribozyme structure, and preferably is a protein
binding site. In each instance, each N and N' independently is any normal
or modified base and each dash represents a potential base-pairing
interaction. These nucleotides may be modified at the sugar, base or
phosphate. Complete base-pairing is not required in the helices, but is
30 preferred. Helix 1 and 4 can be of any size (*i.e.*, o and p is each
independently from 0 to any number, *e.g.* 20) as long as some base-pairing
is maintained. Essential bases are shown as specific bases in the
structure, but those in the art will recognize that one or more may be

modified chemically (abasic, base, sugar and/or phosphate modifications) or replaced with another base without significant effect. Helix 4 can be formed from two separate molecules, *i.e.*, without a connecting loop. The connecting loop when present may be a ribonucleotide with or without
5 modifications to its base, sugar or phosphate. "q" is ≥ 2 bases. The connecting loop can also be replaced with a non-nucleotide linker molecule. H refers to bases A, U, or C. Y refers to pyrimidine bases. "____" refers to a covalent bond.

10 Figure 4 is a representation of the general structure of the hepatitis delta virus ribozyme domain known in the art.

Figure 5 is a representation of the general structure of the self-cleaving VS RNA ribozyme domain.

Figure 6 is a diagrammatic representation of the genetic map of RSV strain A2.

15 Figure 7 is a diagrammatic representation of the solid-phase synthesis of RNA.

Figure 8 is a diagrammatic representation of exocyclic amino protecting groups for nucleic acid synthesis.

Figure 9 is a diagrammatic representation of the deprotection of RNA.

20 Figure 10 is a graphical representation of the cleavage of an RNA substrate by ribozymes synthesized, deprotected and purified using the improved methods described herein.

Figure 11 is a schematic representation of a two pot deprotection protocol. Base deprotection is carried out with aqueous methyl amine at 65
25 °C for 10 min. The sample is dried in a speed-vac for 2-24 hours depending on the scale of RNA synthesis. Silyl protecting group at the 2'-hydroxyl position is removed by treating the sample with 1.4 M anhydrous HF at 65°C for 1.5 hours.

30 Figure 12 is a schematic representation of a one pot deprotection of RNA synthesized using RNA phosphoramidite chemistry. Anhydrous methyl amine is used to deprotect bases at 65°C for 15 min. The sample is allowed to cool for 10 min before adding TEA•3HF reagent, to the same

pot, to remove protecting groups at the 2'-hydroxyl position. The deprotection is carried out for 1.5 hours.

5 Figs. 13a - b is a HPLC profile of a 36 nt long ribozyme, targeted to site B. The RNA is deprotected using either the two pot or the one pot deprotection protocol. The peaks corresponding to full-length RNA is indicated. The sequence for site B is CCUGGGCCAGGGAUUA AUGGAGAUGCCCACU.

Figure 14 is a graph comparing RNA cleavage activity of ribozymes deprotected by two pot vs one pot deprotection protocols.

10 Figure 15 is a schematic representation of an improved method of synthesizing RNA containing phosphorothioate linkages.

Figure 16 shows RNA cleavage reaction catalyzed by ribozymes containing phosphorothioate linkages. Hammerhead ribozyme targeted to site C is synthesized such that 4 nts at the 5' end contain phosphorothioate linkages. P=O refers to ribozyme without phosphorothioate linkages. P=S
15 refers to ribozyme with phosphorothioate linkages. The sequence for site C is UCAUUUUGGCCAUCUC UCCCUUCAGGCGUGG.

Figure 17 is a schematic representation of synthesis of 2'-N-phtalimido-nucleoside phosphoramidite.

20 Figure 18 is a diagrammatic representation of a prior art method for the solid-phase synthesis of RNA using silyl ethers, and the method of this invention using SEM as a 2'-protecting group.

Figure 19 is a diagrammatic representation of the synthesis of 2'-SEM-protected nucleosides and phosphoramidites useful for the synthesis
25 of RNA. B is any nucleotide base as exemplified in the Figure, P is purine and I is inosine. Standard abbreviations are used throughout this application, well known to those in the art.

Figure 20 is a diagrammatic representation of a prior art method for deprotection of RNA using TBDMS protection of the 2'-hydroxyl group.

30 Figure 21 is a diagrammatic representation of the deprotection of RNA having SEM protection of the 2'-hydroxyl group.

Figure 22 is a representation of an HPLC chromatogram of a fully deprotected 10-mer of uridylic acid.

Figs. 23 - 25 are diagrammatic representations of hammerhead, hairpin or hepatitis delta virus ribozyme containing self-processing RNA transcript. Solid arrows indicate self-processing sites. Boxes indicate the sites of nucleotide substitution. Solid lines are drawn to show the binding sites of primers used in a primer-extension assay. Lower case letters indicate vector sequence present in the RNA when transcribed from a *HindIII*-linearized plasmid. (23) HH Cassette, transcript containing the hammerhead trans-acting ribozyme linked to a 3' cis-acting hammerhead ribozyme. The structure of the hammerhead ribozyme is based on phylogenetic and mutational analysis (reviewed by Symons, 1992 *supra*). The trans ribozyme domain extends from nucleotide 1 through 49. After 3'-end processing, the trans-ribozyme contains 2 non-ribozyme nucleotides (UC at positions 50 and 51) at its 3' end. The 3' processing ribozyme is comprised of nucleotides 44 through 96. Roman numerals I, II and III, indicate the three helices that contribute to the structure of the 3' cis-acting hammerhead ribozyme (Hertel et al., 1992 *Nucleic Acids Res.* 20, 3252). Substitution of G70 and A71 to U and G respectively, inactivates the hammerhead ribozyme (Ruffner et al., 1990 *Biochemistry* 29, 10695) and generates the HH(mutant) construct. (24) HP Cassette, transcript containing the hammerhead trans-acting ribozyme linked to a 3' cis-acting hairpin ribozyme. The structure of the hairpin ribozyme is based on phylogenetic and mutational analysis (Berzal-Herranz et al., 1993 *EMBO. J.* 12, 2567). The trans-ribozyme domain extends from nucleotide 1 through 49. After 3'-end processing, the trans-ribozyme contains 5 non-ribozyme nucleotides (UGGCA at positions 50 to 54) at its 3' end. The 3' cis-acting ribozyme is comprised of nucleotides 50 through 115. The transcript named HP(GU) was constructed with a potential wobble base pair between G52 and U77; HP(GC) has a Watson-Crick base pair between G52 and C77. A shortened helix 1 (5 base pairs) and a stable tetraloop (GAAA) at the end of helix 1 was used to connect the substrate with the catalytic domain of the hairpin ribozyme (Feldstein & Bruening, 1993 *Nucleic Acids Res.* 21, 1991; Altschuler et al., 1992 *supra*). (25) HDV Cassette, transcript containing the trans-acting hammerhead ribozyme linked to a 3' cis-acting hepatitis delta virus (HDV) ribozyme. The secondary structure of the HDV ribozyme is as proposed by Been and

coworkers (Been et al., 1992 Biochemistry 31, 11843). The trans-ribozyme domain extends from nucleotides 1 through 48. After 3'-end processing, the trans-ribozyme contains 2 non-ribozyme nucleotides (AA at positions 49 to 50) at its 3' end. The 3' cis-acting HDV ribozyme is comprised of
5 nucleotides 50 through 114. Roman numerals I, II, III & IV, indicate the location of four helices within the 3' cis-acting HDV ribozyme (Perrota & Been, 1991 Nature 350, 434). The Δ HDV transcript contains a 31 nucleotide deletion in the HDV portion of the transcript (nucleotides 84 through 115 deleted).

10 Fig. 26 is a schematic representation of a plasmid containing the insert encoding self-processing cassette. The figure is not drawn to scale.

Fig. 27 demonstrates the effect of 3' flanking sequences on RNA self-processing *in vitro*. H, Plasmid templates linearized with *Hind*III restriction enzyme. Transcripts from H templates contain four non-ribozyme
15 nucleotides at the 3' end. N, Plasmid templates linearized with *Nde*I restriction enzyme. Transcripts from N templates contain 220 non-ribozyme nucleotides at the 3' end. R, Plasmid templates linearized with *Rca*I restriction enzyme. Transcripts from R templates contain 450 non-ribozyme nucleotides at the 3' end.

20 Fig. 28 shows the effect of 3' flanking sequences on the trans-cleavage reaction catalyzed by a hammerhead ribozyme. A 622 nt internally-labeled RNA (<10 nM) was incubated with ribozyme (1000 nM) under single turn-over conditions (Herschlag and Cech, 1990 Biochemistry 29, 10159). HH+2, HH+37, and HH+52 are trans-acting ribozymes
25 produced by transcription from the HH, Δ HDV, and HH(mutant) constructs, respectively, and that contain 2, 37 and 52 extra nucleotides on the 3' end. The plot of the fraction of uncleaved substrate versus time was fit to a double exponential curve using the KaleidaGraph graphing program (Synergy Software, Reading, PA). A double exponential curve fit was used
30 because the data points did not fall on a single exponential curve, presumably due to varying conformers of ribozyme and/or substrate RNA.

Fig. 29 shows RNA self-processing in OST7-1 cells. *In vitro* lanes contain full-length, unprocessed transcripts that were added to cellular
lysates prior to RNA extraction. These RNAs were either pre-incubated
35 with MgCl₂ (+) or with DEPC-treated water (-) prior to being hybridized

with 5' end-labeled primers. Cellular lanes contain total cellular RNA from cells transfected with one of the four self-processing constructs. Cellular RNA are probed for ribozyme expression using a sequence specific primer-extension assay. Solid arrows indicate the location of primer extension bands corresponding to Full-Length RNA and 3' Cleavage Products.

Figs. 30,31 are diagrammatic representations of self-processing cassettes that will release trans-acting ribozymes with defined, stable stem-loop structures at the 5' and the 3' end following self-processing. 30, shows various permutations of a hammerhead self-processing cassette. 31, shows various permutations of a hairpin self-processing cassette.

Figs. 32a-b Schematic representation of RNA polymerase III promoter structure. Arrow indicates the transcription start site and the direction of coding region. A, B and C, refer to consensus A, B and C box promoter sequences. I, refers to intermediate cis-acting promoter sequence. PSE, refers to proximal sequence element. DSE, refers to distal sequence element. ATF, refers to activating transcription factor binding element. ?, refers to cis-acting sequence element that has not been fully characterized. EBER, Epstein-Barr-virus-encoded-RNA. TATA is a box well known in the art.

Figs. 33a-e Sequence of the primary tRNAⁱ_{met} and Δ3-5 transcripts. The A and B box are internal promoter regions necessary for pol III transcription. Arrows indicate the sites of endogenous tRNA processing. The Δ3-5 transcript is a truncated version of tRNA wherein the sequence 3' of B box has been deleted (Adeniyi-Jones et al., 1984 *supra*). This modification renders the Δ 3-5 RNA resistant to endogenous tRNA processing.

Figure 34. Schematic representation of RNA structural motifs inserted into the Δ3-5 RNA. Δ3-5/HHI- a hammerhead (HHI) ribozyme was cloned at the 3' region of Δ3-5 RNA; S3- a stable stem-loop structure was incorporated at the 3' end of the Δ3-5/HHI chimera; S5- stable stem-loop structures were incorporated at the 5' and the 3' ends of Δ3-5/HHI ribozyme chimera; S35- sequence at the 3' end of the Δ3-5/HHI ribozyme chimera was altered to enable duplex formation between the 5' end and a complementary 3' region of the same RNA; S35Plus- in addition to structural alterations of S35, sequences were altered to facilitate additional

duplex formation within the non-ribozyme sequence of the $\Delta 3$ -5/HHI chimera.

Figures 35 and 36. Northern analysis to quantitate ribozyme expression in T cell lines transduced with $\Delta 3$ -5 vectors. 35) $\Delta 3$ -5/HHI and its variants were cloned individually into the DC retroviral vector (Sullenger et al., 1990 *supra*). Northern analysis of ribozyme chimeras expressed in MT-2 cells was performed. Total RNA was isolated from cells (Chomczynski & Sacchi, 1987 *Analytical Biochemistry* 162, 156-159), and transduced with various constructs described in Fig. 34. Northern analysis was carried out using standard protocols (*Curr. Protocols Mol. Biol.* 1992, ed. Ausubel et al., Wiley & Sons, NY). Nomenclature is same as in Figure 34. This assay measures the level of expression from the type 2 pol III promoter. 36) Expression of S35 constructs in MT2 cells. S35 (+ribozyme), S35 construct containing HHI ribozyme. S35 (-ribozyme), S35 construct containing no ribozyme.

Figure 37. Ribozyme activity in total RNA extracted from transduced MT-2 cells. Total RNA was isolated from cells transduced with $\Delta 3$ -5 constructs described in Figs. 35 and 36. In a standard ribozyme cleavage reaction, 5 μ g total RNA and trace amounts of 5' terminus-labeled ribozyme target RNA were denatured separately by heating to 90°C for 2 min in the presence of 50 mM Tris-HCl, pH 7.5 and 10 mM MgCl₂. RNAs were renatured by cooling the reaction mixture to 37°C for 10-15 min. Cleavage reaction was initiated by mixing the labeled substrate RNA and total cellular RNA at 37°C. The reaction was allowed to proceed for ~ 18h, following which the samples were resolved on a 20 % urea-polyacrylamide gel. Bands were visualized by autoradiography.

Figures 38 and 39. Ribozyme expression and activity levels in S35-transduced clonal CEM cell lines. 38) Northern analysis of S35-transduced clonal CEM cell lines. Standard curve was generated by spiking known concentrations of in vitro transcribed S5 RNA into total cellular RNA isolated from non-transduced CEM cells. Pool, contains RNA from pooled cells transduced with S35 construct. Pool (-G418 for 3 Mo), contains RNA from pooled cells that were initially selected for resistance to G418 and then grown in the absence of G418 for 3 months. Lanes A through N contain RNA from individual clones that were generated from the pooled cells transduced with S35 construct. tRNA_{met}, refers to the

endogenous tRNA. S35, refers to the position of the ribozyme band. M, marker lane. 39) Activity levels in S35-transduced clonal CEM cell lines. RNA isolation and cleavage reactions were as described in Fig.37. Nomenclature is same as in Figs. 35 and 36 except, S, 5' terminus-labeled substrate RNA. P, 8 nt 5' terminus-labeled ribozyme-mediated RNA cleavage product.

Figures 40 and 41 are proposed secondary structures of S35 and S35 containing a desired RNA (HHI), respectively. The position of HHI ribozyme is indicated in figure 41. Intramolecular stem refers to the stem structure formed due to an intramolecular base-paired interaction between the 3' sequence and the complementary 5' terminus. The length of the stem ranges from 15-16 base-pairs. Location of the A and the B boxes are shown.

Figures 42 and 43 are proposed secondary structures of S35 plus and S35 plus containing HHI ribozyme.

Figures 44, 45, 46 and 47 are the nucleotide base sequences of S35, HHIS35, S35 Plus, and HHIS35 Plus respectively.

Figs. 48a-b is a general formula for pol III RNA of this invention.

Figure 49 is a digrammatic representation of 5T construct. In this construct the desired RNA is located 3' of the intramolecular stem.

Figures 50 and 51 contain proposed secondary structures of 5T construct alone and 5T construct containing a desired RNA (HHI ribozyme) respectively.

Figure 52 is a diagrammatic representation of TRZ-tRNA chimeras. The site of desired RNA insertion is indicated.

Figure 53 shows the general structure of HHITRZ-A ribozyme chimera. A hammerhead ribozyme targeted to site I is inserted into the stem II region of TRZ-tRNA chimera.

Figure 54 shows the general structure of HPITRZ-A ribozyme chimera. A hairpin ribozyme targeted to site I is cloned into the indicated region of TRZ-tRNA chimera.

Figure 55 shows a comparison of RNA cleavage activity of HHITRZ-A, HHITRZ-B and a chemically synthesized HHI hammerhead ribozymes.

Figure 56 shows expression of ribozymes in T cell lines that are stably transduced with viral vectors. M, markers; lane 1, non-transduced CEM cells; lanes 2 and 3, MT2 and CEM cells transduced with retroviral vectors; lanes 4 and 5, MT2 and CEM cells transduced with AAV vectors.

Figs. 57a-b Schematic diagram of adeno-associated virus and adenoviruses vectors for ribozyme delivery. Both vectors utilize one or more ribozyme encoding transcription units (RZ) based on RNA polymerase II or RNA polymerase III promoters. A. Diagram of an AAV-based vector containing minimal AAV sequences comprising the inverted terminal repeats (ITR) at each end of the vector genome, an optional selectable marker (Neo) driven by an exogenous promoter (Pro), a ribozyme transcription unit, and sufficient additional sequences (stuffer) to maintain a vector length suitable for efficient packaging. B. Diagram of ribozyme expressing adenovirus vectors containing deletions of one or more wild type adenovirus coding regions (cross-hatched boxes marked as E1, pIX, E3, and E4), and insertion of the ribozyme transcription unit at any or several of those regions of deletions.

Fig. 58 is a graph showing the effect of arm length variation on the activity of ligated hammerhead (HH) ribozymes. Nomenclature 5/5, 6/6, 7/7, 8/8 and so on refers to the number of base-pairs being formed between the ribozyme and the target. For example, 5/8 means that the HH ribozyme forms 5 bp on the 5' side and 8 bp on the 3' side of the cleavage site for a total of 13 bp. $-\Delta G$ refers to the free energy of binding calculated for base-paired interactions between the ribozyme and the substrate RNA (Turner and Sugimoto, 1988 Ann. Rev. Biophys. Chem. 17, 167). RPI A is a HH ribozyme with 6/6 binding arms.

Figs. 59 and 60 and 61 show cleavage of long substrate (622 nt) by ligated HH ribozymes.

Fig. 62 is a diagrammatic representation of a hammerhead ribozyme (HH-H) targeted against a site termed H. Variants of HH-H are also shown that contain either a 2 base-paired stem II (HH-H1 and HH-H2) or a 3 base-paired stem II (HH-H3 and HH-H4).

Figs. 63 and 64 show RNA cleavage activity of HH-I and its variants (see Fig.62). 63) cleavage of matched substrate RNA (15 nt). 64) cleavage of long substrate RNA (613 nt).

5 Figs. 65a-b is a schematic representation of a method of this invention to synthesize a full length hairpin ribozyme. No splint strand is required for ligation but rather the two fragments hybridize together at helix 4 prior to ligation. The only prerequisite is that the 3' fragment is phosphorylated at its 5' end and that the 3' end of the 5' fragment have a hydroxyl group. The hairpin ribozyme is targeted against site J. H1 and H2 are intermolecular
10 helices formed between the ribozyme and the substrate. H3 and H4 are intramolecular helices formed within the hairpin ribozyme motif. Arrow indicates the cleavage site.

Fig. 66 shows RNA cleavage activity of ligated hairpin ribozymes targeted against site J.

15 Figs. 67a-b is a diagrammatic representation of a Site K Hairpin Ribozyme (HP-K) showing the proposed secondary structure of the hairpin ribozyme-substrate complex as described in the art (Berzal-Herranz *et al.*, 1993 *EMBO. J.*12, 2567). The ribozyme has been assembled from two fragments (bimolecular ribozyme; Chowrira and Burke, 1992 *Nucleic Acids*
20 *Res.* 20, 2835); #H1 and H2 represent intermolecular helix formation between the ribozyme and the substrate. H3 and H4 represent intramolecular helix formation within the ribozyme (intermolecular helix in the case of bimolecular ribozyme). Left panel (HP-K1) indicates 4 base-paired helix 2 and the right panel (HP-K2) indicates 6 base-paired helix 2.
25 Arrow indicates the site of RNA cleavage. All the ribozymes discussed herein were chemically synthesized by solid phase synthesis using RNA phosphoramidite chemistry, unless otherwise indicated. Those skilled in the art will recognize that these ribozymes could also be made transcriptionally *in vitro* and *in vivo*.

30 Figure 68 is a graph showing RNA cleavage by hairpin ribozymes targeted to site K. A plot of fraction of the target RNA uncleaved (fraction uncleaved) as a function of time is shown. HP-K2 (6 bp helix 2) cleaves a 422 target RNA to a greater extent than the HP-K1 (4 bp helix 2).

To make internally-labeled substrate RNA for trans-ribozyme cleavage reactions, a 422 nt region (containing hairpin site A) was synthesized by PCR using primers that place the T7 RNA promoter upstream of the amplified sequence. Target RNA was transcribed in a standard transcription buffer in the presence of [α - 32 P]CTP (Chowrira & Burke, 1991 *supra*). The reaction mixture was treated with 15 units of ribonuclease-free DNaseI, extracted with phenol followed chloroform:isoamyl alcohol (25:1), precipitated with isopropanol and washed with 70% ethanol. The dried pellet was resuspended in 20 μ l DEPC-treated water and stored at -20°C.

Unlabeled ribozyme (1 μ M) and internally labeled 422 nt substrate RNA (<10 nM) were denatured and renatured separately in a standard cleavage buffer (containing 50 mM Tris-HCl pH 7.5 and 10 mM MgCl₂) by heating to 90°C for 2 min. and slow cooling to 37°C for 10 min. The reaction was initiated by mixing the ribozyme and substrate mixtures and incubating at 37°C. Aliquots of 5 μ l were taken at regular time intervals, quenched by adding an equal volume of 2X formamide gel loading buffer and frozen on dry ice. The samples were resolved on 5% polyacrylamide sequencing gel and results were quantitatively analyzed by radioanalytic imaging of gels with a PhosphorImager (Molecular Dynamics, Sunnyvale, CA).

Figs. 69a-b is the Site L Hairpin Ribozyme (HP-L) showing proposed secondary structure of the hairpin ribozyme-substrate complex. The ribozyme was assembled from two fragments as described above. The nomenclature is the same as above.

Figure 70 shows RNA cleavage by hairpin ribozymes targeted to site L. A. plot of fraction of the target RNA uncleaved (fraction uncleaved) as a function of time is shown. HP-L2 (6 bp helix 2) cleaves a 2 KB target RNA to a greater extent than the HP-L1 (4 bp helix 2). To make internally-labeled substrate RNA for *trans*-ribozyme cleavage reactions, a 2 kB region (containing hairpin site L) was synthesized by PCR using primers that place the T7 RNA promoter upstream of the amplified sequence. The cleavage reactions were carried out as described above.

Figs. 71a-b shows a Site M Hairpin Ribozyme (HP-M) with the proposed secondary structure of the hairpin ribozyme-substrate complex. The ribozyme was assembled from two fragments as described above.

Figure 72 is a graph showing RNA cleavage by hairpin ribozymes targeted to site M. The ribozymes were tested at both 20°C and at 26°C. To make internally-labeled substrate RNA for trans-ribozyme cleavage reactions, a 1.9 KB region (containing hairpin site M) was synthesized by PCR using primers that place the T7 RNA promoter upstream of the amplified sequence. Cleavage reactions were carried out as described above except that 20°C and at 26°C temperatures were used.

Figs. 73a-d shows various structural modifications of the present invention. A) Hairpin ribozyme lacking helix 5. Nomenclature is same as described under figure 3. B) Hairpin ribozyme lacking helix 4 and helix 5. Helix 4 is replaced by a nucleotide loop wherein $q \geq 2$ bases. Nomenclature is same as described under figure 3. C) Hairpin ribozyme lacking helix 5. Helix 4 loop is replaced by a linker 103"L", wherein L is a non-nucleotide linker molecule (Benseler *et al.*, 1993 *J. Am. Chem. Soc.* 115, 8483; Jennings *et al.*, WO 94/13688). Nomenclature is same as described under figure 3. D) Hairpin ribozyme lacking helix 4 and helix 5. Helix 4 is replaced by non-nucleotide linker molecule "L" (Benseler *et al.*, 1993 *supra*; Jennings *et al.*, *supra*). Nomenclature is same as described under figure 3.

Figs. 74a-b shows Hairpin ribozymes containing nucleotide spacer region "s" at the indicated location, wherein $s \geq 1$ base. Hairpin ribozymes containing spacer region, can be synthesized as one fragment or can be assembled from multiple fragments. Nomenclature is same as described under figure 3.

Figs. 75a-e shows the structures of the 5'-C-alkyl-modified nucleotides. R_1 is as defined above. R is OH, H, O-protecting group, NH, or any group described by the publications discussed above, and those described below. B is as defined in the Figure or any other equivalent nucleotide base. CE is cyanoethyl, DMT is a standard blocking group. Other abbreviations are standard in the art.

Figure 76 is a diagrammatic representation of the synthesis of 5'-C-alkyl-D-allose nucleosides and their phosphoramidites.

Figure 77 is a diagrammatic representation of the synthesis of 5'-C-alkyl-L-talose nucleosides and their phosphoramidites.

- 5 Figure 78 is a diagrammatic representation of hammerhead ribozymes targeted to site O containing 5'-C-methyl-L-talo modifications at various positions.

Figure 79 shows RNA cleavage activity of HH-O ribozymes. Fraction of target RNA uncleaved as a function of time is shown.

- 10 Figure 80 is a diagrammatic representation of a position numbered hammerhead ribozyme (according to Hertel *et al. Nucleic Acids Res.* 1992, 20, 3252) showing specific substitutions.

- 15 Figs. 81a-j shows the structures of various 2'-alkyl modified nucleotides which exemplify those of this invention. R groups are alkyl groups, Z is a protecting group.

Figure 82 is a diagrammatic representation of the synthesis of 2'-C-allyl uridine and cytidine.

Figure 83 is a diagrammatic representation of the synthesis of 2'-C-methylene and 2'-C-difluoromethylene uridine.

- 20 Figure 84 is a diagrammatic representation of the synthesis of 2'-C-methylene and 2'-C-difluoromethylene cytidine.

Figure 85 is a diagrammatic representation of the synthesis of 2'-C-methylene and 2'-C-difluoromethylene adenosine.

- 25 Figure 86 is a diagrammatic representation of the synthesis of 2'-C-carboxymethylidene uridine, 2'-C-methoxycarboxymethylidene uridine and derivatized amidites thereof. X is CH₃ or alkyl as discussed above, or another substituent.

Figure 87 is a diagrammatic representation of a synthesis of nucleoside 5'-deoxy-5'-difluoromethylphosphonates.

Figure 88 is a diagrammatic representation of the synthesis of nucleoside 5'-deoxy-5'-difluoromethylphosphonate 3'-phosphoramidites, dimers and solid supported dimers.

Figure 89 is a diagrammatic representation of the synthesis of
5 nucleoside 5'-deoxy-5'-difluoromethylene triphosphates.

Figures 90 and 91 are diagrammatic representations of the synthesis of 3'-deoxy-3'-difluoromethylphosphonates and dimers.

Figure 92 is a schematic representation of synthesizing RNA phosphoramidite of a nucleotide containing a 2'-hydroxyl group
10 modification of the present invention.

Figs. 93a-b describes a method for deprotection of oligonucleotides containing a 2'-hydroxyl group modification of the present invention.

Figure 94 is a diagrammatic representation of a hammerhead ribozyme targeted to site N. Positions of 2'-hydroxyl group substitution is
15 indicated.

Figure 95 shows RNA cleavage activity of ribozymes containing a 2'-hydroxyl group modification of the present invention. All RNA, represents hammerhead ribozyme (HHN) with no 2'-hydroxyl group modifications. U7-ala, represents HHN ribozyme containing 2'-NH-alanine modification at the
20 U7 position. U4/U7-ala, represents HHA containing 2'-NH-alanine modifications at U4 and U7 positions. U4 lys, represents HHA containing 2'-NH-lysine modification at U4 position. U7 lys, represents HHA containing 2'-NH-lysine modification at U7 position. U4/U7-lys, represents HHN containing 2'-NH-lysine modification at U4 and U7 positions.

25 Figures 96 and 97 are schematic representations of synthesizing (solid-phase synthesis) 3' ends of RNA with modification of the present invention. B, refers to either a base, modified base or an H.

Figure 98 and 99 are schematic representations of synthesizing (solid-phase synthesis) 5' ends of RNA with modification of the present
30 invention. B, refers to either a base, modified base or an H.

Figures 100 and 101 are general schematic representations of the invention.

Fig. 102a-d is a schematic representation of a method of the invention.

Fig. 103 is a graph of the results of the experiment diagrammed in figure 104.

Figure 104 is a diagrammatic representation of a fusion mRNA used
5 in the experiment diagrammed in Fig. 102.

Figure 105 is a diagrammatic representation of a method for selection of useful ribozymes of this invention.

Figure 106 generally shows R-loop formation, and an R-loop complex. In addition, it indicates the location at which ligands can be
10 provided to target the R-loop complex to cells using at least three different procedures, such as ligand receptor interaction, lipid or calcium phosphate mediated delivery, or electroporation.

Figure 107 shows a method for use of self-processing ribozymes to generate therapeutic ribozymes of unit length. This method is essentially
15 described by Draper et al., PCT WO 93/23509.

Figure 108 shows a method of linking ligands like folate, carbohydrate or peptides to R-loop forming RNA.

Ribozymes of this invention block to some extent ICAM-1, IL-5, rel A, TNF- α , p210^{bcr-abl}, or RSV genes expression and can be used to treat
20 diseases or diagnose such diseases. Ribozymes will be delivered to cells in culture and to tissues in animal models. Ribozyme cleavage of ICAM-1, IL-5, rel A, TNF- α , p210^{bcr-abl}, or RSV mRNA in these systems may prevent or alleviate disease symptoms or conditions.

I. Target sites

25 Targets for useful ribozymes can be determined as disclosed in Draper et al PCT WO93/23509, Sullivan et al., PCT WO94/02595 as well as by Draper et al., PCT/US94/13129 and hereby incorporated by reference herein in totality. Rather than repeat the guidance provided in those documents here, below are provided specific examples of such
30 methods, not limiting to those in the art. Ribozymes to such targets are designed as described in those applications and synthesized to be tested *in vitro* and *in vivo*, as also described. Such ribozymes can also be

optimized and delivered as described therein. While specific examples to animal and human RNA are provided, those in the art will recognize that the equivalent human RNA targets described can be used as described below. Thus, the same target may be used, but binding arms suitable for
5 targeting human RNA sequences are present in the ribozyme. Such targets may also be selected as described below.

It must be established that the sites predicted by the computer-based RNA folding algorithm correspond to potential cleavage sites. Hammerhead or hairpin ribozymes are designed that could bind and are
10 individually analyzed by computer folding (Jaeger et al., 1989 Proc. Natl. Acad. Sci., USA, 86 7706-7710) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm
15 lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

mRNA is screened for accessible cleavage sites by the method described generally in Draper et al., PCT WO93/23569 hereby incorporated by reference herein. Briefly, DNA oligonucleotides
20 representing potential hammerhead or hairpin ribozyme cleavage sites are synthesized. A polymerase chain reaction is used to generate a substrate for T7 RNA polymerase transcription from cDNA clones. Labeled RNA transcripts are synthesized *in vitro* from DNA templates. The oligonucleotides and the labeled transcripts are annealed, RNaseH is
25 added and the mixtures are incubated for the designated times at 37°C. Reactions are stopped and RNA separated on sequencing polyacrylamide gels. The percentage of the substrate cleaved is determined by autoradiographic quantitation using a phosphor imaging system. From these data, hammerhead or hairpin ribozyme sites are chosen as the
30 most accessible.

Ribozymes of the hammerhead or hairpin motif are designed to anneal to various sites in the mRNA message. The binding arms are complementary to the target site sequences described above. The ribozymes are chemically synthesized. The method of synthesis used
35 follows the procedure for normal RNA synthesis as described in Usman et al., 1987 *J. Am. Chem. Soc.*, 109, 7845 and in Scaringe et al., 1990

Nucleic Acids Res., 18, 5433 and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, phosphoramidites at the 3'-end. The average stepwise coupling yields are >98%. Inactive ribozymes are synthesized by substituting a U for G₅ and a U for A₁₄ (numbering from Hertel et al., 1992 *Nucleic Acids Res.*, 20, 3252). Hairpin ribozymes are synthesized in two parts and annealed to reconstruct the active ribozyme (Chowrira and Burke, 1992 *Nucleic Acids Res.*, 20, 2835-2840). Ribozymes are also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbach, 1989, *Methods Enzymol*, 180, 51). All ribozymes are modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992 *TIBS* 17,34). Ribozymes are purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography and are resuspended in water.

Example 1: ICAM-1

Ribozymes that cleave ICAM-1 mRNA represent a novel therapeutic approach to inflammatory or autoimmune disorders. ICAM-1 function can be blocked therapeutically using monoclonal antibodies. Ribozymes have the advantage of being generally immunologically inert, whereas significant neutralizing anti-IgG responses can be observed with some monoclonal antibody treatments.

The following is a brief description of the physiological role of ICAM-1. The discussion is not meant to be complete and is provided only for understanding of the invention that follows. This summary is not an admission that any of the work described below is prior art to the claimed invention.

Intercellular adhesion molecule-1 (ICAM-1) is a cell surface protein whose expression is induced by inflammatory mediators. ICAM-1 is required for adhesion of leukocytes to endothelial cells and for several immunological functions including antigen presentation, immunoglobulin production and cytotoxic cell activity. Blocking ICAM-1 function prevents immune cell recognition and activity during transplant rejection and in animal models of rheumatoid arthritis, asthma and reperfusion injury.

- Cell-cell adhesion plays a pivotal role in inflammatory and immune responses (Springer et al., 1987 *Ann. Rev. Immunol.* 5, 223-252). Cell adhesion is required for leukocytes to bind to and migrate through vascular endothelial cells. In addition, cell-cell adhesion is required for antigen presentation to T cells, for B cell induction by T cells, as well as for the cytotoxicity activity of T cells, NK cells, monocytes or granulocytes. Intercellular adhesion molecule-1 (ICAM-1) is a 110 kilodalton member of the immunoglobulin superfamily that is involved in all of these cell-cell interactions (Simmons et al., 1988 *Nature (London)* 331, 624-627).
- 10 ICAM-1 is expressed on only a limited number of cells and at low levels in the absence of stimulation (Dustin et al., 1986 *J. Immunol.* 137, 245-254). Upon treatment with a number of inflammatory mediators (lipopolysaccharide, γ -interferon, tumor necrosis factor- α , or interleukin-1), a variety of cell types (endothelial, epithelial, fibroblastic and hematopoietic cells) in a variety of tissues express high levels of ICAM-1 on their surface (Springer et al. *supra*; Dustin et al., *supra*; and Rothlein et al., 1988 *J. Immunol.* 141, 1665-1669). Induction occurs via increased transcription of ICAM-1 mRNA (Simmons et al., *supra*). Elevated expression is detectable after 4 hours and peaks after 16 - 24 hours of induction.
- 20 ICAM-1 induction is critical for a number of inflammatory and immune responses. *In vitro*, antibodies to ICAM-1 block adhesion of leukocytes to cytokine-activated endothelial cells (Boyd, 1988 *Proc. Natl. Acad. Sci. USA* 85, 3095-3099; Dustin and Springer, 1988 *J. Cell Biol.* 107, 321-331). Thus, ICAM-1 expression may be required for the extravasation of immune cells to sites of inflammation. Antibodies to ICAM-1 also block T cell killing, mixed lymphocyte reactions, and T cell-mediated B cell differentiation, suggesting that ICAM-1 is required for these cognate cell interactions (Boyd et al., *supra*). The importance of ICAM-1 in antigen presentation is underscored by the inability of ICAM-1 defective murine B cell mutants to stimulate antigen-dependent T cell proliferation (Dang et al., 1990 *J. Immunol.* 144, 4082-4091). Conversely, murine L cells require transfection with human ICAM-1 in addition to HLA-DR in order to present antigen to human T cells (Altmann et al., 1989 *Nature (London)* 338, 512-514). In summary, evidence *in vitro* indicates that ICAM-1 is required for cell-cell interactions critical to inflammatory responses, cellular immune responses, and humoral antibody responses.

By engineering ribozyme motifs we have designed several ribozymes directed against ICAM-1 mRNA sequences. These have been synthesized with modifications that improve their nuclease resistance. These ribozymes cleave ICAM-1 target sequences *in vitro*.

- 5 The sequence of human, rat and mouse ICAM-1 mRNA can be screened for accessible sites using a computer folding algorithm. Regions of the mRNA that did not form secondary folding structures and that contain potential hammerhead or hairpin ribozyme cleavage sites can be identified. These sites are shown in Tables 2, 3, and 6-9. (All sequences
10 are 5' to 3' in the tables) While rat, mouse and human sequences can be screened and ribozymes thereafter designed, the human targeted sequences are of most utility.

- 15 The sequences of the chemically synthesized ribozymes useful in this study are shown in Tables 4 - 8 and 10. Those in the art will recognize that these sequences are representative only of many more such sequences
15 where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity and may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the ribozymes described specifically in the Tables.

- 20 The ribozymes will be tested for function *in vivo* by exogenous delivery to human umbilical vein endothelial cells (HUVEC). Ribozymes will be delivered by incorporation into liposomes, by complexing with cationic lipids, by microinjection, or by expression from DNA or RNA
25 vectors described above. Cytokine-induced ICAM-1 expression will be monitored by ELISA, by indirect immunofluoresence, and/or by FACS analysis. ICAM-1 mRNA levels will be assessed by Northern, by RNase protection, by primer extension or by quantitative RT-PCR analysis. Ribozymes that block the induction of ICAM-1 protein and mRNA by more than 90% will be identified.

- 30 As disclosed by Sullivan et al., PCT WO94/02595, incorporated by reference herein, ribozymes and/or genes encoding them will be locally delivered to transplant tissue *ex vivo* in animal models. Expression of the ribozyme will be monitored by its ability to block *ex vivo* induction of ICAM-1 mRNA and protein. The effect of the anti-ICAM-1 ribozymes on graft
35 rejection will then be assessed. Similarly, ribozymes will be introduced

into joints of mice with collagen-induced arthritis or rabbits with *Streptococcal* cell wall-induced arthritis. Liposome delivery, cationic lipid delivery, or adeno-associated virus vector delivery can be used. One dose (or a few infrequent doses) of a stable anti-ICAM-1 ribozyme or a gene
5 construct that constitutively expresses the ribozyme may abrogate inflammatory and immune responses in these diseases.

Uses

ICAM-1 plays a central role in immune cell recognition and function. Ribozyme inhibition of ICAM-1 expression can reduce transplant rejection
10 and alleviate symptoms in patients with rheumatoid arthritis, asthma or other acute and chronic inflammatory disorders. We have engineered several ribozymes that cleave ICAM-1 mRNA. Ribozymes that efficiently inhibit ICAM-1 expression in cells can be readily found and their activity measured with regard to their ability to block transplant rejection and
15 arthritis symptoms in animal models. These anti-ICAM-1 ribozymes represent a novel therapeutic for the treatment of immunological or inflammatory disorders.

The therapeutic utility of reduction of activity of ICAM-1 function is evident in the following disease targets. The noted references indicate the
20 role of ICAM-1 and the therapeutic potential of ribozymes described herein. Thus, these targets can be therapeutically treated with agents that reduce ICAM-1 expression or function. These diseases and the studies that support a critical role for ICAM-1 in their pathology are listed below. This list is not meant to be complete and those in the art will recognize further
25 conditions and diseases that can be effectively treated using ribozymes of the present invention.

- Transplant rejection

ICAM-1 is expressed on venules and capillaries of human cardiac biopsies with histological evidence of graft rejection (Briscoe et al., 1991 *Transplantation*
30 51, 537-539).

Antibody to ICAM-1 blocks renal (Cosimi et al., 1990 *J. Immunol.* 144, 4604-4612) and cardiac (Flavin et al., 1991 *Transplant. Proc.* 23, 533-534) graft rejection in primates.

A Phase I clinical trial of a monoclonal anti-ICAM-1 antibody showed significant reduction in rejection and a significant increase in graft function in human kidney transplant patients (Haug, et al., 1993 *Transplantation* 55, 766-72).

- Rheumatoid arthritis

- 5 ICAM-1 overexpression is seen on synovial fibroblasts, endothelial cells, macrophages, and some lymphocytes (Chin et al., 1990 *Arthritis Rheum* 33, 1776-86; Koch et al., 1991 *Lab Invest* 64, 313-20).

Soluble ICAM-1 levels correlate with disease severity (Mason et al., 1993 *Arthritis Rheum* 36, 519-27).

- 10 Anti-ICAM antibody inhibits collagen-induced arthritis in mice (Kakimoto et al., 1992 *Cell Immunol* 142, 326-37).

Anti-ICAM antibody inhibits adjuvant-induced arthritis in rats (Iigo et al., 1991 *J Immunol* 147, 4167-71).

- Myocardial ischemia, stroke, and reperfusion injury

- 15 Anti-ICAM-1 antibody blocks adherence of neutrophils to anoxic endothelial cells (Yoshida et al., 1992 *Am J Physiol* 262, H1891-8).

Anti-ICAM-1 antibody reduces neurological damage in a rabbit model of cerebral stroke (Bowes et al., 1993 *Exp Neurol* 119, 215-9).

- 20 Anti-ICAM-1 antibody protects against reperfusion injury in a cat model of myocardial ischemia (Ma et al., 1992 *Circulation* 86, 937-46).

- Asthma

Antibody to ICAM-1 partially blocks eosinophil adhesion to endothelial cells and is overexpressed on inflamed airway endothelium and epithelium *in vivo* (Wegner et al., 1990 *Science* 247, 456-9).

- 25 In a primate model of asthma, anti-ICAM-1 antibody blocks airway eosinophilia (Wegner et al., *supra*) and prevents the resurgence of airway inflammation and hyper-responsiveness after dexamethosone treatment (Gundel et al., 1992 *Clin Exp Allergy* 22, 569-75).

- Psoriasis

Surface ICAM-1 and a clipped, soluble version of ICAM-1 is expressed in psoriatic lesions and expression correlates with inflammation (Kellner et al., 1991 *Br J Dermatol* 125, 211-6; Griffiths 1989 *J Am Acad Dermatol* 20, 617-29; Schopf et al., 1993 *Br J Dermatol* 128, 34-7).

- 5 Anti-ICAM antibody blocks keratinocyte antigen presentation to T cells (Nickoloff et al., 1993 *J Immunol* 150, 2148-59).

- Kawasaki disease

Surface ICAM-1 expression correlates with the disease and is reduced by effective immunoglobulin treatment (Leung, et al., 1989 *Lancet* 2, 1298-302).

- 10 Soluble ICAM levels are elevated in Kawasaki disease patients; particularly high levels are observed in patients with coronary artery lesions (Furukawa et al., 1992 *Arthritis Rheum* 35, 672-7; Tsuji, 1992 *Arerugi* 41, 1507-14).

- 15 Circulating LFA-1⁺ T cells are depleted (presumably due to ICAM-1 mediated extravasation) in Kawasaki disease patients (Furukawa et al., 1993 *Scand J Immunol* 37, 377-80).

Example 2: IL-5

- 20 Ribozymes that cleave IL-5 mRNA represent a novel therapeutic approach to inflammatory disorders like asthma. The invention features use of ribozymes to treat chronic asthma, e.g., by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of eosinophils.

- 25 A number of cytokines besides IL-5 may also be involved in the activation of inflammation in asthmatic patients, including platelet activating factor, IL-1, IL-3, IL-4, GM-CSF, TNF- α , gamma interferon, VCAM, ILAM-1, ELAM-1 and NF- κ B. In addition to these molecules, it is appreciated that any cellular receptors which mediate the activities of the cytokines are also good targets for intervention in inflammatory diseases. These targets include, but are not limited to, the IL-1R and TNF- α R on keratinocytes, epithelial and endothelial cells in airways. Recent data suggest that certain
- 30 neuropeptides may play a role in asthmatic symptoms. These peptides include substance P, neurokinin A and calcitonin-gene-related peptides. These target genes may have more general roles in inflammatory diseases, but are currently assumed to have a role only in asthma.

Ribozymes of this invention block to some extent IL-5 expression and can be used to treat disease or diagnose such disease. Ribozymes will be delivered to cells in culture and to cells or tissues in animal models of asthma (Clutterbuck et al., 1989 supra; Garssen et al., 1991 Am. Rev. Respir. Dis. 144, 931-938; Larsen et al., 1992 J. Clin. Invest. 89, 747-752; Mauser et al., 1993 supra). Ribozyme cleavage of IL-5 mRNA in these systems may prevent inflammatory cell function and alleviate disease symptoms.

The sequence of human and mouse IL-5 mRNA were screened for accessible sites using a computer folding algorithm. Potential hammerhead or hairpin ribozyme cleavage sites were identified. These sites are shown in Tables 11, 13, and 14, 15. (All sequences are 5' to 3' in the tables.) While mouse and human sequences can be screened and ribozymes thereafter designed, the human targeted sequences are of most utility. However, mouse targeted ribozymes are useful to test efficacy of action of the ribozyme prior to testing in humans. The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of ribozyme. (In Table 12, lower case letters indicate positions that are not conserved between the Human and the Mouse IL-5 sequences.)

The sequences of the chemically synthesized ribozymes useful in this study are shown in Tables 12, 14 - 16. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. For example, stem loop II sequence of hammerhead ribozymes listed in Tables 12 and 14 (5'-GGCCGAAAGGCC-3') can be altered (substitution, deletion and/or insertion) to contain any sequence provided, a minimum of two base-paired stem structure can form. Similarly, stem-loop IV sequence of hairpin ribozymes listed in Tables 15 and 16 (5'-CACGUUGUG-3') can be altered (substitution, deletion and/or insertion) to contain any sequence provided, a minimum of two base-paired stem structure can form. The sequences listed in Tables 12, 14 - 16 may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the ribozymes described specifically in the Tables.

By engineering ribozyme motifs we have designed several ribozymes directed against IL-5 mRNA sequences. These ribozymes are synthesized

with modifications that improve their nuclease resistance. The ability of ribozymes to cleave IL-5 target sequences *in vitro* is evaluated.

The ribozymes will be tested for function *in vivo* by analyzing IL-5 expression levels. Ribozymes will be delivered to cells by incorporation
5 into liposomes, by complexing with cationic lipids, by microinjection, or by expression from DNA or RNA vectors. IL-5 expression will be monitored by biological assays, ELISA, by indirect immunofluorescence, and/or by FACS analysis. IL-5 mRNA levels will be assessed by Northern analysis, RNase protection or primer extension analysis or quantitative RT-PCR.
10 Ribozymes that block the induction of IL-5 activity and/or IL-5 mRNA by more than 90% will be identified.

Uses

Interleukin 5 (IL-5), a cytokine produced by CD4+ T helper cells and mast cells, was originally termed B cell growth factor II (reviewed by
15 Takatsu et al., 1988 Immunol. Rev. 102, 107). It stimulates proliferation of activated B cells and induces production of IgM and IgA. IL-5 plays a major role in eosinophil function by promoting differentiation (Clutterbuck et al., 1989 Blood 73, 1504-12), vascular adhesion (Walsh et al., 1990 Immunology 71, 258-65) and *in vitro* survival of eosinophils (Lopez et al.,
20 1988 J. Exp. Med. 167, 219-24). This cytokine also enhances histamine release from basophils (Hirai et al., 1990 J. Exp. Med. 172, 1525-8). The following summaries of clinical results support the selection of IL-5 as a primary target for the treatment of asthma:

Several studies have shown a direct correlation between the number
25 of activated T cells and the number of eosinophils from asthmatic patients vs. normal patients (Oehling et al., 1992 J. Investig. Allergol. Clin. Immunol. 2, 295-9). Patients with either allergic asthma or intrinsic asthma were treated with corticosteroids. The bronchoalveolar lavage was monitored for eosinophils, activated T helper cells and recovery of pulmonary function
30 over a 28 to 30 day period. The number of eosinophils and activated T helper cells decreased progressively with subsequent improvement in pulmonary function compared to intrinsic asthma patients with no corticosteroid treatment.

Bronchoalveolar lavage cells were screened for production of
35 cytokines using *in situ* hybridization for mRNA. *In situ* hybridization signals

were detected for IL-2, IL-3, IL-4, IL-5 and GM-CSF. Upregulation of mRNA was observed for IL-4, IL-5 and GM-CSF (Robinson et al., 1993 J. Allergy Clin. Immunol. 92, 313-24). Another study showed that upregulation of IL-5 transcripts from allergen challenged vs. saline challenged asthmatic patients (Krishnaswamy et al., 1993 Am. J. Respir. Cell. Mol. Biol. 9, 279-86).

An 18 patient study was performed to determine a mechanism of action for corticosteroid improvement of asthma symptoms. Improvement was monitored by methacholine responsiveness. A correlation was observed between the methacholine responsiveness, a reduction in the number of eosinophils, a reduction in the number of cells expressing IL-4 and IL-5 mRNA and an increase in number of cells expressing interferon-gamma.

Bronchial biopsies from 15 patients were analyzed 24 hours after allergen challenge (Bentley et al., 1993 Am. J. Respir. Cell. Mol. Biol. 8, 35-42). Increased numbers of eosinophils and IL-2 receptor positive cells were found in the biopsies. No differences in the numbers of total leukocytes, T lymphocytes, elastase-positive neutrophils, macrophages or mast cell subtypes were observed. The number of cells expressing IL-5 and GM-CSF mRNA significantly increased.

In another patient study, the eosinophil phenotype was the same for asthmatic patients and normal individuals. However, eosinophils from asthmatic patients had greater leukotriene C4 producing capacity and migration capacity. There were elevated levels of IL-3, IL-5 and GM-CSF in the circulation of asthmatics but not in normal individuals (Bruijnzeel et al., 1992 Schweiz. Med. Wochenschr. 122, 298-301).

Efficacy of antibody to IL-5 was assessed in a guinea pig asthma model. The animals were challenged with ovalbumin and assayed for eosinophilia and the responsiveness to the bronchioconstriction substance P. A 30 mg/kg dose of antibody administered i.p. blocked ovalbumin-induced increased sensitivity to substance P and blocked increases in bronchoalveolar and lung tissue accumulation of eosinophils (Mausser et al., 1993 Am. Rev. Respir. Dis. 148, 1623-7). In a separate study guinea pigs challenged for eight days with ovalbumin were treated with monoclonal antibody to IL-5. Treatment produced a reduction in the

number of eosinophils in bronchoalveolar lavage. No reduction was observed for unchallenged guinea pigs and guinea pigs treated with a control antibody. Antibody treatment completely inhibited the development of hyperreactivity to histamine and arecoline after ovalbumin challenge
5 (van Oosterhout et al., 1993 Am. Rev. Respir. Dis. 147, 548-52)

Results obtained from human clinical analysis and animal studies indicate the role of activated T helper cells, cytokines and eosinophils in asthma. The role of IL-5 in eosinophil development and function makes IL-5 a good candidate for target selection. The antibody studies neutralized
10 IL-5 in the circulation thus preventing eosinophilia. Inhibition of the production of IL-5 will achieve the same goal.

Asthma – a prominent feature of asthma is the infiltration of eosinophils and deposition of toxic eosinophil proteins (e.g. major basic protein, eosinophil-derived neurotoxin) in the lung. A number of T-cell-
15 derived factors like IL-5 are responsible for the activation and maintenance of eosinophils (Kay, 1991 J. Allergy Clin. Immun. 87, 893). Inhibition of IL-5 expression in the lungs can decrease the activation of eosinophils and will help alleviate the symptoms of asthma.

Atopy – is characterized by the development of type I hypersensitive
20 reactions associated with exposure to certain environmental antigens. One of the common clinical manifestations of atopy is eosinophilia (accumulation of abnormally high levels of eosinophils in the blood). Antibodies against IL-5 have been shown to lower the levels of eosinophils in mice (Cook et al., 1993 in Immunopharmacol. Eosinophils ed. Smith and
25 Cook, pp. 193-216, Academic, London, UK)

Parasitic infection-related eosinophilia– infections with parasites like helminths, can lead to severe eosinophilia (Cook et al., 1993 supra). Animal models for eosinophilia suggest that infection of mice, for example, can lead to blood, peritoneal and/or tissue eosinophilia, all of
30 which seem to be lowered to varying degrees by antibodies directed against IL-5.

Pulmonary infiltration eosinophilia– is characterised by accumulation of high levels of eosinophils in pulmonary parenchyma (Gleich, 1990 J. Allergy Clin. Immunol. 85, 422).

L-Tryptophan-associated eosinophilia-myalgia syndrome (EMS)— The EMS disease is closely linked to the consumption of L-tryptophan, an essential aminoacid used to treat conditions like insomnia (for review see Varga et al., 1993 J Invest. Dermatol. 100, 97s). Pathologic and histologic studies have demonstrated high levels of eosinophils and mononuclear inflammatory cells in patients with EMS. It appears that IL-5 and transforming growth factor play a significant role in the development of EMS (Varga et al., 1993 supra) by activating eosinophils and other inflammatory cells.

Thus, ribozymes of the present invention that cleave IL-5 mRNA and thereby IL-5 activity have many potential therapeutic uses, and there are reasonable modes of delivering the ribozymes in a number of the possible indications. Development of an effective ribozyme that inhibits IL-5 function is described above; available cellular and activity assays are numerous, reproducible, and accurate. Animal models for IL-5 function and for each of the suggested disease targets exist (Cook et al., 1993 supra) and can be used to optimize activity.

Example 3: NF- κ B

Ribozymes that cleave *rel A* mRNA represent a novel therapeutic approach to inflammatory or autoimmune disorders. Inflammatory mediators such as lipopolysaccharide (LPS), interleukin-1 (IL-1) or tumor necrosis factor- α (TNF- α) act on cells by inducing transcription of a number of secondary mediators, including other cytokines and adhesion molecules. In many cases, this gene activation is known to be mediated by the transcriptional regulator, NF- κ B. One subunit of NF- κ B, the *rel A* gene product (termed RelA or p65) is implicated specifically in the induction of inflammatory responses. Ribozyme therapy, due to its exquisite specificity, is particularly well-suited to target intracellular factors that contribute to disease pathology. Thus, ribozymes that cleave mRNA encoded by *rel A* or TNF- α may represent novel therapeutics for the treatment of inflammatory and autoimmune disorders.

The nuclear DNA-binding activity, NF- κ B, was first identified as a factor that binds and activates the immunoglobulin κ light chain enhancer in B cells. NF- κ B now is known to activate transcription of a variety of other cellular genes (*e.g.*, cytokines, adhesion proteins, oncogenes and viral

proteins) in response to a variety of stimuli (e.g., phorbol esters, mitogens, cytokines and oxidative stress). In addition, molecular and biochemical characterization of NF- κ B has shown that the activity is due to a homodimer or heterodimer of a family of DNA binding subunits. Each subunit bears a stretch of 300 amino acids that is homologous to the oncogene, *v-rel*. The activity first described as NF- κ B is a heterodimer of p49 or p50 with p65. The p49 and p50 subunits of NF- κ B (encoded by the *nf- κ B2* or *nf- κ B1* genes, respectively) are generated from the precursors NF- κ B1 (p105) or NF- κ B2 (p100). The p65 subunit of NF- κ B (now termed Rel A) is encoded by the *rel A* locus.

The roles of each specific transcription-activating complex now are being elucidated in cells (N.D. Perkins, et al., 1992 Proc. Natl Acad. Sci USA 89, 1529-1533). For instance, the heterodimer of NF- κ B1 and Rel A (p50/p65) activates transcription of the promoter for the adhesion molecule, VCAM-1, while NF- κ B2/RelA heterodimers (p49/p65) actually inhibit transcription (H.B. Shu, et al., Mol. Cell. Biol. 13, 6283-6289 (1993)). Conversely, heterodimers of NF- κ B2/RelA (p49/p65) act with Tat-I to activate transcription of the HIV genome, while NF- κ B1/RelA (p50/p65) heterodimers have little effect (J. Liu, N.D. Perkins, R.M. Schmid, G.J. Nabel, J. Virol. 1992 66, 3883-3887). Similarly, blocking *rel A* gene expression with antisense oligonucleotides specifically blocks embryonic stem cell adhesion; blocking NF- κ B1 gene expression with antisense oligonucleotides had no effect on cellular adhesion (Narayanan et al., 1993 Mol. Cell. Biol. 13, 3802-3810). Thus, the promiscuous role initially assigned to NF- κ B in transcriptional activation (M.J. Lenardo, D. Baltimore, 1989 Cell 58, 227-229) represents the sum of the activities of the *rel* family of DNA-binding proteins. This conclusion is supported by recent transgenic "knock-out" mice of individual members of the *rel* family. Such "knock-outs" show few developmental defects, suggesting that essential transcriptional activation functions can be performed by more than one member of the *rel* family.

A number of specific inhibitors of NF- κ B function in cells exist, including treatment with phosphorothioate antisense oligonucleotide, treatment with double-stranded NF- κ B binding sites, and over expression of the natural inhibitor MAD-3 (an I κ B family member). These agents have

been used to show that NF- κ B is required for induction of a number of molecules involved in inflammation, as described below.

- NF- κ B is required for phorbol ester-mediated induction of IL-6 (I. Kitajima, et al., Science 258, 1792-5 (1992)) and IL-8 (Kunsch and Rosen, 1993 Mol. Cell. Biol. 13, 6137-46).

•NF- κ B is required for induction of the adhesion molecules ICAM-1 (Eck, et al., 1993 Mol. Cell. Biol. 13, 6530-6536), VCAM-1 (Shu et al., *supra*), and E-selectin (Read, et al., 1994 J. Exp. Med. 179, 503-512) on endothelial cells.

- NF- κ B is involved in the induction of the integrin subunit, CD18, and other adhesive properties of leukocytes (Eck et al., 1993 *supra*).

The above studies suggest that NF- κ B is integrally involved in the induction of cytokines and adhesion molecules by inflammatory mediators. Two recent papers point to another connection between NF- κ B and inflammation: glucocorticoids may exert their anti-inflammatory effects by inhibiting NF- κ B. The glucocorticoid receptor and p65 both act at NF- κ B binding sites in the ICAM-1 promoter (van de Stolpe, et al., 1994 J. Biol. Chem. 269, 6185-6192). Glucocorticoid receptor inhibits NF- κ B-mediated induction of IL-6 (Ray and Prefontaine, 1994 Proc. Natl Acad. Sci USA 91, 752-756). Conversely, overexpression of p65 inhibits glucocorticoid induction of the mouse mammary tumor virus promoter. Finally, protein cross-linking and co-immunoprecipitation experiments demonstrated direct physical interaction between p65 and the glucocorticoid receptor (*Id.*).

Ribozymes of this invention block to some extent NF- κ B expression and can be used to treat disease or diagnose such disease. Ribozymes will be delivered to cells in culture and to cells or tissues in animal models of restenosis, transplant rejection and rheumatoid arthritis. Ribozyme cleavage of *relA* mRNA in these systems may prevent inflammatory cell function and alleviate disease symptoms.

The sequence of human and mouse *relA* mRNA can be screened for accessible sites using a computer folding algorithm. Potential hammerhead or hairpin ribozyme cleavage sites were identified. These sites are shown in Tables 17, 18 and 21-22. (All sequences are 5' to 3' in the tables.) While mouse and human sequences can be screened and

ribozymes thereafter designed, the human targetted sequences are of most utility.

5 The sequences of the chemically synthesized ribozymes useful in this study are shown in Tables 19 - 22. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity and may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the ribozymes described specifically in the Tables.

10 By engineering ribozyme motifs we have designed several ribozymes directed against *rel A* mRNA sequences. These ribozymes are synthesized with modifications that improve their nuclease resistance. The ability of ribozymes to cleave *rel A* target sequences *in vitro* is evaluated.

15 The ribozymes will be tested for function *in vivo* by analyzing cytokine-induced VCAM-1, ICAM-1, IL-6 and IL-8 expression levels. Ribozymes will be delivered to cells by incorporation into liposomes, by complexing with cationic lipids, by microinjection, or by expression from DNA and RNA vectors. Cytokine-induced VCAM-1, ICAM-1, IL-6 and IL-8 expression will be monitored by ELISA, by indirect immunofluoresence, and/or by FACS
20 analysis. *Rel A* mRNA levels will be assessed by Northern analysis, RNase protection or primer extension analysis or quantitative RT-PCR. Activity of NF- κ B will be monitored by gel-retardation assays. Ribozymes that block the induction of NF- κ B activity and/or *rel A* mRNA by more than 50% will be identified.

25 RNA ribozymes and/or genes encoding them will be locally delivered to transplant tissue *ex vivo* in animal models. Expression of the ribozyme will be monitored by its ability to block *ex vivo* induction of VCAM-1, ICAM-1, IL-6 and IL-8 mRNA and protein. The effect of the anti-*rel A* ribozymes on graft rejection will then be assessed. Similarly, ribozymes will be
30 introduced into joints of mice with collagen-induced arthritis or rabbits with *Streptococcal* cell wall-induced arthritis. Liposome delivery, cationic lipid delivery, or adeno-associated virus vector delivery can be used. One dose (or a few infrequent doses) of a stable anti-*rel A* ribozyme or a gene construct that constitutively expresses the ribozyme may abrogate
35 inflammatory and immune responses in these diseases.

Uses

A therapeutic agent that inhibits cytokine gene expression, inhibits adhesion molecule expression, and mimics the anti-inflammatory effects of glucocorticoids (without inducing steroid-responsive genes) is ideal for the treatment of inflammatory and autoimmune disorders. Disease targets for such a drug are numerous. Target indications and the delivery options each entails are summarized below. In all cases, because of the potential immunosuppressive properties of a ribozyme that cleaves *rel A* mRNA, uses are limited to local delivery, acute indications, or *ex vivo* treatment.

10 •Rheumatoid arthritis (RA).

Due to the chronic nature of RA, a gene therapy approach is logical. Delivery of a ribozyme to inflamed joints is mediated by adenovirus, retrovirus, or adeno-associated virus vectors. For instance, the appropriate adenovirus vector can be administered by direct injection into the synovium: high efficiency of gene transfer and expression for several months would be expected (B.J. Roessler, E.D. Allen, J.M. Wilson, J.W. Hartman, B. L. Davidson, J. Clin. Invest. 92, 1085-1092 (1993)). It is unlikely that the course of the disease could be reversed by the transient, local administration of an anti-inflammatory agent. Multiple administrations may be necessary. Retrovirus and adeno-associated virus vectors would lead to permanent gene transfer and expression in the joint. However, permanent expression of a potent anti-inflammatory agent may lead to local immune deficiency.

•Restenosis.

25 Expression of NF- κ B in the vessel wall of pigs causes a narrowing of the luminal space due to excessive deposition of extracellular matrix components. This phenotype is similar to matrix deposition that occurs subsequent to coronary angioplasty. In addition, NF- κ B is required for the expression of the oncogene c-myc (F.A. La Rosa, J.W. Pierce, G.E. Sonenshein, Mol. Cell. Biol. 14, 1039-44 (1994)). Thus NF- κ B induces smooth muscle proliferation and the expression of excess matrix components: both processes are thought to contribute to reocclusion of vessels after coronary angioplasty.

•Transplantation.

NF- κ B is required for the induction of adhesion molecules (Eck et al., *supra*, K. O'Brien, et al., J. Clin. Invest. 92, 945-951 (1993)) that function in immune recognition and inflammatory responses. At least two potential modes of treatment are possible. In the first, transplanted organs are treated *ex vivo* with ribozymes or ribozyme expression vectors. Transient inhibition of NF- κ B in the transplanted endothelium may be sufficient to prevent transplant-associated vasculitis and may significantly modulate graft rejection. In the second, donor B cells are treated *ex vivo* with ribozymes or ribozyme expression vectors. Recipients would receive the treatment prior to transplant. Treatment of a recipient with B cells that do not express T cell co-stimulatory molecules (such as ICAM-1, VCAM-1, and/or B7 and B7-2) can induce antigen-specific anergy. Tolerance to the donor's histocompatibility antigens could result; potentially, any donor could be used for any transplantation procedure.

•Asthma.

Granulocyte macrophage colony stimulating factor (GM-CSF) is thought to play a major role in recruitment of eosinophils and other inflammatory cells during the late phase reaction to asthmatic trauma. Again, blocking the local induction of GM-CSF and other inflammatory mediators is likely to reduce the persistent inflammation observed in chronic asthmatics. Aerosol delivery of ribozymes or adenovirus ribozyme expression vectors is a feasible treatment.

•Gene Therapy.

Immune responses limit the efficacy of many gene transfer techniques. Cells transfected with retrovirus vectors have short lifetimes in immune competent individuals. The length of expression of adenovirus vectors in terminally differentiated cells is longer in neonatal or immune-compromised animals. Insertion of a small ribozyme expression cassette that modulates inflammatory and immune responses into existing adenovirus or retrovirus constructs will greatly enhance their potential.

Thus, ribozymes of the present invention that cleave *rel A* mRNA and thereby NF- κ B activity have many potential therapeutic uses, and there are reasonable modes of delivering the ribozymes in a number of the possible indications. Development of an effective ribozyme that inhibits NF- κ B

function is described above; available cellular and activity assays are number, reproducible, and accurate. Animal models for NF- κ B function (Kitajima, et al., *supra*) and for each of the suggested disease targets exist and can be used to optimize activity.

5 **Example 4: TNF- α**

Ribozymes that cleave the specific sites in TNF- α mRNA represent a novel therapeutic approach to inflammatory or autoimmune disorders.

10 Tumor necrosis factor- α (TNF- α) is a protein, secreted by activated leukocytes, that is a potent mediator of inflammatory reactions. Injection of TNF- α into experimental animals can simulate the symptoms of systemic and local inflammatory diseases such as septic shock or rheumatoid arthritis.

15 TNF- α was initially described as a factor secreted by activated macrophages which mediates the destruction of solid tumors in mice (Old, 1985 Science 230, 4225-4231). TNF- α subsequently was found to be identical to cachectin, an agent responsible for the weight loss and wasting syndrome associated with tumors and chronic infections (Beutler, et al., 1985 Nature 316, 552-554). The cDNA and the genomic locus for TNF- α have been cloned and found to be related to TNF- β (Shakhov et al., 1990 J. Exp. Med. 171, 35-47). Both TNF- α and TNF- β bind to the same receptors and have nearly identical biological activities. The two TNF receptors have been found on most cell types examined (Smith, et al., 20 1990 Science 248, 1019-1023). TNF- α secretion has been detected from monocytes/macrophages, CD4+ and CD8+ T-cells, B-cells, lymphokine activated killer cells, neutrophils, astrocytes, endothelial cells, smooth muscle cells, as well as various non-hematopoietic tumor cell lines (for a review see Turetskaya et al., 1991 in Tumor Necrosis Factor: Structure, Function, and Mechanism of Action B. B. Aggarwal, J. Vilcek, Eds. Marcel Dekker, Inc., pp. 35-60). TNF- α is regulated transcriptionally and translationally, and requires proteolytic processing at the plasma membrane in order to be secreted (Kriegler et al., 1988 Cell 53, 45-53). 25 Once secreted, the serum half life of TNF- α is approximately 30 minutes. The tight regulation of TNF- α is important due to the extreme toxicity of this cytokine. Increasing evidence indicates that overproduction of TNF- α

during infections can lead to severe systemic toxicity and death (Tracey & Cerami, 1992 Am. J. Trop. Med. Hyg. 47, 2-7).

Antisense RNA and Hammerhead ribozymes have been used in an attempt to lower the expression level of TNF- α by targeting specified cleavage sites [Sioud et al., 1992 J. Mol. Biol. 223; 831; Sioud WO 94/10301; Kisich and co-workers, 1990 abstract (FASEB J. 4, A1860; 1991 slide presentation (J. Leukocyte Biol. sup. 2, 70); December, 1992 poster presentation at Anti-HIV Therapeutics Conference in San Diego, CA; and "Development of anti-TNF- α ribozymes for the control of TNF- α gene expression"- Kisich, Doctoral Dissertation, 1993 University of California, Davis] listing various TNF α targeted ribozymes.

Ribozymes of this invention block to some extent TNF- α expression and can be used to treat disease or diagnose such disease. Ribozymes will be delivered to cells in culture and to cells or tissues in animal models of septic shock and rheumatoid arthritis. Ribozyme cleavage of TNF- α mRNA in these systems may prevent inflammatory cell function and alleviate disease symptoms.

The sequence of human and mouse TNF- α mRNA can be screened for accessible sites using a computer folding algorithm. Hammerhead or hairpin ribozyme cleavage sites were identified. These sites are shown in Tables 23, 25, and 27 - 28. (All sequences are 5' to 3' in the tables.) While mouse and human sequences can be screened and ribozymes thereafter designed, the human targeted sequences are of most utility. However, mouse targeted ribozymes are useful to test efficacy of action of the ribozyme prior to testing in humans. The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of ribozyme. (In Table 24, lower case letters indicate positions that are not conserved between the human and the mouse TNF- α sequences.)

The sequences of the chemically synthesized ribozymes useful in this study are shown in Tables 24, 26 - 28. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. For example, stem-loop II sequence of hammerhead ribozymes listed in Tables 24 and 26 (5'-GGCCGAAAGGCC-3') can be altered (substitution, deletion, and/or insertion) to contain any

sequences provided a minimum of two base-paired stem structure can form. Similarly, stem-loop IV sequence of hairpin ribozymes listed in Tables 27 and 28 (5'-CACGUUGUG-3') can be altered (substitution, deletion, and/or insertion) to contain any sequence, provided a minimum of two base-paired stem structure can form. The sequences listed in Tables 24, 26 - 28 may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the ribozymes described specifically in the Tables or AAV.

In a preferred embodiment of the invention, a transcription unit expressing a ribozyme that cleaves TNF- α RNA is inserted into a plasmid DNA vector or an adenovirus DNA viral vector or AAV or alpha virus or retrovirus vectors. Viral vectors have been used to transfer genes to the intact vasculature or to joints of live animals (Willard et al., 1992 Circulation, 86, 1-473.; Nabel et al., 1990 Science, 249, 1285-1288) and both vectors lead to transient gene expression. The adenovirus vector is delivered as recombinant adenoviral particles. DNA may be delivered alone or complexed with vehicles (as described for RNA above). The DNA, DNA/vehicle complexes, or the recombinant adenovirus particles are locally administered to the site of treatment, e.g., through the use of an injection catheter, stent or infusion pump or are directly added to cells or tissues *ex vivo*.

In another preferred embodiment of the invention, a transcription unit expressing a ribozyme that cleaves TNF- α RNA is inserted into a retrovirus vector for sustained expression of ribozyme(s).

By engineering ribozyme motifs we have designed several ribozymes directed against TNF- α mRNA sequences. These ribozymes are synthesized with modifications that improve their nuclease resistance. The ability of ribozymes to cleave TNF- α target sequences *in vitro* is evaluated.

The ribozymes will be tested for function in cells by analyzing bacterial lipopolysaccharide (LPS)-induced TNF- α expression levels. Ribozymes will be delivered to cells by incorporation into liposomes, by complexing with cationic lipids, by microinjection, or by expression from DNA vectors. TNF- α expression will be monitored by ELISA, by indirect immunofluorescence, and/or by FACS analysis. TNF- α mRNA levels will be assessed by Northern analysis, RNase protection, primer extension

analysis or quantitative RT-PCR. Ribozymes that block the induction of TNF- α activity and/or TNF- α mRNA by more than 90% will be identified.

RNA ribozymes and/or genes encoding them will be locally delivered to macrophages by intraperitoneal injection. After a period of ribozyme uptake, the peritoneal macrophages are harvested and induced *ex vivo* with LPS. The ribozymes that significantly reduce TNF- α secretion are selected. The TNF- α can also be induced after ribozyme treatment with fixed *Streptococcus* in the peritoneal cavity instead of *ex vivo*. In this fashion the ability of TNF- α ribozymes to block TNF- α secretion in a localized inflammatory response are evaluated. In addition, we will determine if the ribozymes can block an ongoing inflammatory response by delivering the TNF- α ribozymes after induction by the injection of fixed *Streptococcus*.

To examine the effect of anti-TNF- α ribozymes on systemic inflammation, the ribozymes are delivered by intravenous injection. The ability of the ribozymes to inhibit TNF- α secretion and lethal shock caused by systemic LPS administration are assessed. Similarly, TNF- α ribozymes can be introduced into the joints of mice with collagen-induced arthritis. Either free delivery, liposome delivery, cationic lipid delivery, adeno-associated virus vector delivery, adenovirus vector delivery, retrovirus vector delivery or plasmid vector delivery in these animal model experiments can be used to supply ribozymes. One dose (or a few infrequent doses) of a stable anti-TNF- α ribozyme or a gene construct that constitutively expresses the ribozyme may abrogate tissue damage in these inflammatory diseases.

Macrophage isolation.

To produce responsive macrophages 1 ml of sterile fluid thioglycollate broth (Difco, Detroit, MI.) was injected i.p. into 6 week old female C57b1/6NCR mice 3 days before peritoneal lavage. Mice were maintained as specific pathogen free in autoclaved cages in a laminar flow hood and given sterilized water to minimize "spontaneous" activation of macrophages. The resulting peritoneal exudate cells (PEC) were obtained by lavage using Hanks balanced salt solution (HBSS) and were plated at 2.5×10^5 /well in 96 well plates (Costar, Cambridge, MA.) with Eagles minimal essential medium (EMEM) containing 10% heat inactivated fetal

bovine serum. After adhering for 2 hours the wells were washed to remove non-adherent cells. The resulting cultures were 97% macrophages as determined by morphology and staining for non-specific esterase.

Transfection of ribozymes into macrophages:

- 5 The ribozymes were diluted to 2X final concentration, mixed with an equal volume of 11nM lipofectamine (Life Technologies, Gaithersburg, MD.), and vortexed. 100 ml of lipid:ribozyme complex was then added directly to the cells, followed immediately by 10 ml fetal bovine serum. Three hours after ribozyme addition 100 ml of 1 mg/ml bacterial
10 lipopolysaccharide (LPS) was added to each well to stimulate TNF production.

Quantitation of TNF- α in mouse macrophages:

- Supernatants were sampled at 0, 2, 4, 8, and 24 hours post LPS stimulation and stored at -70°C. Quantitation of TNF- α was done by a
15 specific ELISA. ELISA plates were coated with rabbit anti-mouse TNF- α serum at 1:1000 dilution (Genzyme) followed by blocking with milk proteins and incubation with TNF- α containing supernatants. TNF- α was then detected using a murine TNF- α specific hamster monoclonal antibody (Genzyme). The ELISA was developed with goat anti-hamster IgG coupled
20 to alkaline phosphatase.

Assessment of reagent toxicity:

- Following ribozyme/lipid treatment of macrophages and harvesting of supernatants viability of the cells was assessed by incubation of the cells with 5 mg/ml of 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium
25 bromide (MTT). This compound is reduced by the mitochondrial dihydrogenases, the activity of which correlates well with cell viability. After 12 hours the absorbance of reduced MTT is measured at 585 nm.

Uses

- 30 The association between TNF- α and bacterial sepsis, rheumatoid arthritis, and autoimmune disease make TNF- α an attractive target for therapeutic intervention [Tracy & Cerami 1992 supra; Williams et al., 1992 Proc. Natl. Acad. Sci. USA 89, 9784-9788; Jacob, 1992 J. Autoimmun. 5 (Supp. A), 133-143].

Septic Shock

Septic shock is a complication of major surgery, bacterial infection, and polytrauma characterized by high fever, increased cardiac output, reduced blood pressure and a neutrophilic infiltrate into the lungs and other major organs. Current treatment options are limited to antibiotics to reduce the bacterial load and non-steroidal anti-inflammatories to reduce fever. Despite these treatments in the best intensive care settings, mortality from septic shock averages 50%, due primarily to multiple organ failure and disseminated vascular coagulation. Septic shock, with an incidence of 200,000 cases per year in the United States, is the major cause of death in intensive care units. In septic shock syndrome, tissue injury or bacterial products initiate massive immune activation, resulting in the secretion of pro-inflammatory cytokines which are not normally detected in the serum, such as TNF- α , interleukin-1 β (IL-1 β), γ -interferon (IFN- γ), interleukin-6 (IL-6), and interleukin-8 (IL-8). Other non-cytokine mediators such as leukotriene b₄, prostaglandin E₂, C3a and C3d also reach high levels (de Boer et al., 1992 Immunopharmacology 24, 135-148).

TNF- α is detected early in the course of septic shock in a large fraction of patients (de Boer et al., 1992 supra). In animal models, injection of TNF- α has been shown to induce shock-like symptoms similar to those induced by LPS injection (Beutler et al., 1985 Science 229, 869-871); in contrast, injection of IL-1 β , IL-6, or IL-8 does not induce shock. Injection of TNF- α also causes an elevation of IL-1 β , IL-6, IL-8, PgE₂, acute phase proteins, and TxA₂ in the serum of experimental animals (de Boer et al., 1992 supra). In animal models the lethal effects of LPS can be blocked by pre-administration of anti-TNF- α antibodies. The cumulative evidence indicates that TNF- α is a key player in the pathogenesis of septic shock, and therefore a good candidate for therapeutic intervention.

Rheumatoid Arthritis

Rheumatoid arthritis (RA) is an autoimmune disease characterized by chronic inflammation of the joints leading to bone destruction and loss of joint function. At the cellular level, autoreactive T- lymphocytes and monocytes are typically present, and the synoviocytes often have altered morphology and immunostaining patterns. RA joints have been shown to contain elevated levels of TNF- α , IL-1 α and IL-1 β , IL-6, GM-CSF, and TGF-

β (Abney et al., 1991 Imm. Rev. 119, 105-123), some or all of which may contribute to the pathological course of the disease.

Cells cultured from RA joints spontaneously secrete all of the pro-inflammatory cytokines detected *in vivo*. Addition of antisera against TNF- α to these cultures has been shown to reduce IL-1 α/β production by these cells to undetectable levels (Abney et al., 1991 Supra). Thus, TNF- α may directly induce the production of other cytokines in the RA joint. Addition of the anti-inflammatory cytokine, TGF- β , has no effect on cytokine secretion by RA cultures. Immunocytochemical studies of human RA surgical specimens clearly demonstrate the production of TNF- α , IL-1 α/β , and IL-6 from macrophages near the cartilage/pannus junction when the pannus is invading and overgrowing the cartilage (Chu et al., 1992 Br. J. Rheumatology 31, 653-661). GM-CSF was shown to be produced mainly by vascular endothelium in these samples. Both TNF- α and TGF- β have been shown to be fibroblast growth factors, and may contribute to the accumulation of scar tissue in the RA joint. TNF- α has also been shown to increase osteoclast activity and bone resorption, and may have a role in the bone erosion commonly found in the RA joint (Cooper et al., 1992 Clin. Exp. Immunol. 89, 244-250).

Elimination of TNF- α from the rheumatic joint would be predicted to reduce overall inflammation by reducing induction of MHC class II, IL-1 α/β , IL-6, and GM-CSF, and reducing T-cell activation. Osteoclast activity might also fall, reducing the rate of bone erosion at the joint. Finally, elimination of TNF- α would be expected to reduce accumulation of scar tissue within the joint by removal of a fibroblast growth factor.

Treatment with an anti-TNF- α antibody reduces joint swelling and the histological severity of collagen-induced arthritis in mice (Williams et al., 1992 Proc. Natl. Acad. Sci. USA 89, 9784-9788). In addition, a study of RA patients who have received i.v. infusions of anti-TNF- α monoclonal antibody reports a reduction in the number and severity of inflamed joints after treatment. The benefit of monoclonal antibody treatment in the long term may be limited by the expense and immunogenicity of the antibody.

Psoriasis

Psoriasis is an inflammatory disorder of the skin characterized by keratinocyte hyperproliferation and immune cell infiltrate (Kupper, 1990 J.

Clin. Invest. 86, 1783-1789). It is a fairly common condition, affecting 1.5-2.0% of the population. The disorder ranges in severity from mild, with small flaky patches of skin, to severe, involving inflammation of the entire epidermis. The cellular infiltrate of psoriasis includes T-lymphocytes, neutrophils, macrophages, and dermal dendrocytes. The majority of T-lymphocytes are activated CD4⁺ cells of the T_H-1 phenotype, although some CD8⁺ and CD4⁻/CD8⁻ are also present. B lymphocytes are typically not found in abundance in psoriatic plaques.

Numerous hypotheses have been offered as to the proximal cause of psoriasis including auto-antibodies and auto-reactive T-cells, overproduction of growth factors, and genetic predisposition. Although there is evidence to support the involvement of each of these factors in psoriasis, they are neither mutually exclusive nor are any of them necessary and sufficient for the pathogenesis of psoriasis (Reeves, 1991 Semin. Dermatol. 10, 217).

The role of cytokines in the pathogenesis of psoriasis has been investigated. Among those cytokines found to be abnormally expressed were TGF- α , IL-1 α , IL-1 β , IL-1 α , IL-6, IL-8, IFN- γ , and TNF- α . In addition to abnormal cytokine production, elevated expression of ICAM-1, ELAM-1, and VCAM has been observed (Reeves, 1991 supra). This cytokine profile is similar to that of normal wound healing, with the notable exception that cytokine levels subside upon healing. Keratinocytes themselves have recently been shown to be capable of secreting EGF, TGF- α , IL-6, and TNF- α , which could increase proliferation in an autocrine fashion (Oxholm et al., 1991 APMIS 99, 58-64).

Nickoloff et al., 1993 (J Dermatol Sci. 6, 127-33) have proposed the following model for the initiation and maintenance of the psoriatic plaque:

Tissue damage induces the wound healing response in the skin. Keratinocytes secrete IL-1 α , IL-1 β , IL-6, IL-8, TNF- α . These factors activate the endothelium of dermal capillaries, recruiting PMNs, macrophages, and T-cells into the wound site.

Dermal dendrocytes near the dermal/epidermal junction remain activated when they should return to a quiescent state, and subsequently secrete cytokines including TNF- α , IL-6, and IL-8. Cytokine expression, in

turn, maintains the activated state of the endothelium, allowing extravasation of additional immunocytes, and the activated state of the keratinocytes which secrete TGF- α and IL-8. Keratinocyte IL-8 recruits immunocytes from the dermis into the epidermis. During passage through the dermis, T-cells encounter the activated dermal dendrocytes which efficiently activate the T_H-1 phenotype. The activated T-cells continue to migrate into the epidermis, where they are stimulated by keratinocyte-expressed ICAM-1 and MHC class II. IFN- γ secreted by the T-cells synergizes with the TNF- α from dermal dendrocytes to increase keratinocyte proliferation and the levels of TGF- α , IL-8, and IL-6 production. IFN- γ also feeds back to the dermal dendrocyte, maintaining the activated phenotype and the inflammatory cycle.

Elevated serum titres of IL-6 increases synthesis of acute phase proteins including complement factors by the liver, and antibody production by plasma cells. Increased complement and antibody levels increases the probability of autoimmune reactions.

Maintenance of the psoriatic plaque requires continued expression of all of these processes, but attractive points of therapeutic intervention are TNF- α expression by the dermal dendrocyte to maintain activated endothelium and keratinocytes, and IFN- γ expression by T-cells to maintain activated dermal dendrocytes.

There are 3 million patients in the United States afflicted with psoriasis. The available treatments for psoriasis are corticosteroids. The most widely prescribed are TEMOVATE (clobetasol propionate), LIDEX (fluocinonide), DIPROLENE (betamethasone propionate), PSORCON (diflorasone diacetate) and TRIAMCINOLONE formulated for topical application. The mechanism of action of corticosteroids is multifactorial. This is a palliative therapy because the underlying cause of the disease remains, and upon discontinuation of the treatment the disease returns. Discontinuation of treatment is often prompted by the appearance of adverse effects such as atrophy, telangiectasias and purpura. Corticosteroids are not recommended for prolonged treatments or when treatment of large and/or inflamed areas is required. Alternative treatments include retinoids, such as etretinate, which has been approved for treatment of severe, refractory psoriasis. Alternative retinoid-based treatments are in advanced clinical trials. Retinoids act by converting

keratinocytes to a differentiated state and restoration of normal skin development. Immunosuppressive drugs such as cyclosporine are also in the advanced stages of clinical trials. Due to the nonspecific mechanism of action of corticosteroids, retinoids and immunosuppressives, these treatments exhibit severe side effects and should not be used for extended periods of time unless the condition is life-threatening or disabling. There is a need for a less toxic, effective therapeutic agent in psoriatic patients.

HIV and AIDS

The human immunodeficiency virus (HIV) causes several fundamental changes in the human immune system from the time of infection until the development of full-blown acquired immunodeficiency syndrome (AIDS). These changes include a shift in the ratio of CD4+ to CD8+ T-cells, sustained elevation of IL-4 levels, episodic elevation of TNF- α and TNF- β levels, hypergammaglobulinemia, and lymphoma/leukemia (Rosenberg & Fauci, 1990 Immun. Today 11, 176; Weiss 1993 Science 260, 1273). Many patients experience a unique tumor, Kaposi's sarcoma and/or unusual opportunistic infections (e.g. *Pneumocystis carinii*, cytomegalovirus, herpesviruses, hepatitis viruses, papilloma viruses, and tuberculosis). The immunological dysfunction of individuals with AIDS suggests that some of the pathology may be due to cytokine dysregulation.

Levels of serum TNF- α and IL-6 are often found to be elevated in AIDS patients (Weiss, 1993 supra). In tissue culture, HIV infection of monocytes isolated from healthy individuals stimulates secretion of both TNF- α and IL-6. This response has been reproduced using purified gp120, the viral coat protein responsible for binding to CD-4 (Buonaguro et al., 1992 J. Virol. 66, 7159). It has also been demonstrated that the viral gene regulator, Tat, can directly induce TNF transcription. The ability of HIV to directly stimulate secretion of TNF- α and IL-6 may be an adaptive mechanism of the virus. TNF- α has been shown to upregulate transcription of the LTR of HIV, increasing the number of HIV-specific transcripts in infected cells. IL-6 enhances HIV production, but at a post-transcriptional level, apparently increasing the efficiency with which HIV transcripts are translated into protein. Thus, stimulation of TNF- α secretion by the HIV virus may promote infection of neighboring CD4+ cells both by enhancing virus production from latently infected cells and by driving replication of the virus in newly infected cells.

The role of TNF- α in HIV replication has been well established in tissue culture models of infection (Sher et al., 1992 Immun. Rev. 127, 183), suggesting that the mutual induction of HIV replication and TNF- α replication may create positive feedback *in vivo*. However, evidence for the presence of such positive feedback in infected patients is not abundant. TNF- α levels are found to be elevated in some, but not all patients tested. Children with AIDS who were given zidovudine had reduced levels of TNF- α compared to those not given zidovudine (Cremoni et al., 1993 AIDS 7, 128). This correlation lends support to the hypothesis that reduced viral replication is physiologically linked to TNF- α levels. Furthermore, recently it has been shown that the polyclonal B cell activation associated with HIV infection is due to membrane-bound TNF- α . Thus, levels of secreted TNF- α may not accurately reflect the contribution of this cytokine to AIDS pathogenesis.

Chronic elevation of TNF- α has been shown to result in cachexia (Tracey et al., 1992 Am. J. Trop. Med. Hyg. 47, 2-7), increased autoimmune disease (Jacob, 1992 supra), lethargy, and immune suppression in animal models (Aderka et al., 1992 Isr. J. Med. Sci. 28, 126-130). The cachexia associated with AIDS may be associated with chronically elevated TNF- α frequently observed in AIDS patients. Similarly, TNF- α can stimulate the proliferation of spindle cells isolated from Kaposi's sarcoma lesions of AIDS patients (Barillari et al., 1992 J. Immunol 149, 3727).

A therapeutic agent that inhibits cytokine gene expression, inhibits adhesion molecule expression, and mimics the anti-inflammatory effects of glucocorticoids (without inducing steroid-responsive genes) is ideal for the treatment of inflammatory and autoimmune disorders. Disease targets for such a drug are numerous. Target indications and the delivery options each entails are summarized below. In all cases, because of the potential immunosuppressive properties of a ribozyme that cleaves the specified sites in TNF- α mRNA, uses are limited to local delivery, acute indications, or *ex vivo* treatment.

•Septic shock.

Exogenous delivery of ribozymes to macrophages can be achieved by intraperitoneal or intravenous injections. Ribozymes will be delivered by incorporation into liposomes or by complexing with cationic lipids.

•Rheumatoid arthritis (RA).

- 5 Due to the chronic nature of RA, a gene therapy approach is logical. Delivery of a ribozyme to inflamed joints is mediated by adenovirus, retrovirus, or adeno-associated virus vectors. For instance, the appropriate adenovirus vector can be administered by direct injection into the synovium: high efficiency of gene transfer and expression for several
- 10 months would be expected (B.J. Roessler, E.D. Allen, J.M. Wilson, J.W. Hartman, B. L. Davidson, J. Clin. Invest. 92, 1085-1092 (1993)). It is unlikely that the course of the disease could be reversed by the transient, local administration of an anti-inflammatory agent. Multiple administrations may be necessary. Retrovirus and adeno-associated virus
- 15 vectors would lead to permanent gene transfer and expression in the joint. However, permanent expression of a potent anti-inflammatory agent may lead to local immune deficiency.

•Psoriasis

- 20 The psoriatic plaque is a particularly good candidate for ribozyme or vector delivery. The stratum corneum of the plaque is thinned, providing access to the proliferating keratinocytes. T-cells and dermal dendrocytes can be efficiently targeted by trans-epidermal diffusion .

- 25 Organ culture systems for biopsy specimens of psoriatic and normal skin are described in current literature (Nickoloff et al., 1993 Supra). Primary human keratinocytes are easily obtained and will be grown into epidermal sheets in tissue culture. In addition to these tissue culture models, the flaky skin mouse develops psoriatic skin in response to UV light. This model would allow demonstration of animal efficacy for ribozyme treatments of psoriasis.

- 30 •Gene Therapy.

Immune responses limit the efficacy of many gene transfer techniques. Cells transfected with retrovirus vectors have short lifetimes in immune competent individuals. The length of expression of adenovirus

vectors in terminally differentiated cells is longer in neonatal or immune-compromised animals. Insertion of a small ribozyme expression cassette that modulates inflammatory and immune responses into existing adenovirus or retrovirus constructs will greatly enhance their potential.

- 5 Thus, ribozymes of the present invention that cleave TNF- α mRNA and thereby TNF- α activity have many potential therapeutic uses, and there are reasonable modes of delivering the ribozymes in a number of the possible indications. Development of an effective ribozyme that inhibits TNF- α function is described above; available cellular and activity assays
10 are number, reproducible, and accurate. Animal models for TNF- α function and for each of the suggested disease targets exist and can be used to optimize activity.

Example 5: p210bcr-abl

- 15 Chronic myelogenous leukemia exhibits a characteristic disease course, presenting initially as a chronic granulocytic hyperplasia, and invariably evolving into an acute leukemia which is caused by the clonal expansion of a cell with a less differentiated phenotype (i.e., the blast crisis stage of the disease). CML is an unstable disease which ultimately progresses to a terminal stage which resembles acute leukemia. This
20 lethal disease affects approximately 16,000 patients a year. Chemotherapeutic agents such as hydroxyurea or busulfan can reduce the leukemic burden but do not impact the life expectancy of the patient (e.g., approximately 4 years). Consequently, CML patients are candidates for bone marrow transplantation (BMT) therapy. However, for those patients
25 which survive BMT, disease recurrence remains a major obstacle (Apperley et al., 1988 Br. J. Haematol. 69, 239).

- 30 The Philadelphia (Ph) chromosome which results from the translocation of the *abl* oncogene from chromosome 9 to the *bcr* gene on chromosome 22 is found in greater than 95% of CML patients and in 10-25% of all cases of acute lymphoblastic leukemia [(ALL); Fourth International Workshop on Chromosomes in Leukemia 1982, Cancer Genet. Cytogenet. 11, 316]. In virtually all Ph⁺-positive CMLs and approximately 50% of the Ph-positive ALLs, the leukemic cells express *bcr-abl* fusion mRNAs in which exon 2 (b2-a2 junction) or exon 3 (b3-a2
35 junction) from the major breakpoint cluster region of the *bcr* gene is spliced

to exon 2 of the *abl* gene. Heisterkamp et al., 1985 Nature 315, 758; Shtivelman et al., 1987, Blood 69, 971). In the remaining cases of Ph-positive ALL, the first exon of the *bcr* gene is spliced to exon 2 of the *abl* gene (Hooberman et al., 1989 Proc. Nat. Acad. Sci. USA 86, 4259; 5 Heisterkamp et al., 1988 Nucleic Acids Res. 16, 10069).

The b3-a2 and b2-a2 fusion mRNAs encode 210 kd bcr-abl fusion proteins which exhibit oncogenic activity (Daley et al., 1990 Science 247, 824; Heisterkamp et al., 1990 Nature 344, 251). The importance of the bcr-abl fusion protein (p210^{bcr-abl}) in the evolution and maintenance of the 10 leukemic phenotype in human disease has been demonstrated using antisense oligonucleotide inhibition of p210^{bcr-abl} expression. These inhibitory molecules have been shown to inhibit the in vitro proliferation of leukemic cells in bone marrow from CML patients. Szczalik et al., 1991 Science 253, 562).

15 Reddy, U.S. Patent 5,246,921 (hereby incorporated by reference herein) describes use of ribozymes as therapeutic agents for leukemias, such as chronic myelogenous leukemia (CML) by targeting the specific junction region of *bcr-abl* fusion transcripts. It indicates causing cleavage by a ribozyme at or near the breakpoint of such a hybrid chromosome, 20 specifically it includes cleavage at the sequence GUX, where X is A, U or G. The one example presented is to cleave the sequence 5' AGC AG AGUU (cleavage site) CAA AAGCCCU-3'.

Scanlon WO 91/18625, WO 91/18624, and WO 91/18913 and Snyder et al., WO93/03141 and WO94/13793 describe a ribozyme effective 25 to cleave oncogenic variants of H-ras RNA. This ribozyme is said to inhibit H-ras expression in response to external stimuli.

The invention features use of ribozymes to inhibit the development or expression of a transformed phenotype in man and other animals by modulating expression of a gene that contributes to the expression of CML. 30 Cleavage of targeted mRNAs expressed in pre-neoplastic and transformed cells elicits inhibition of the transformed state.

The invention can be used to treat cancer or pre-neoplastic conditions. Two preferred administration protocols can be used, either in vivo administration to reduce the tumor burden, or ex vivo treatment to

eradicate transformed cells from tissues such as bone marrow prior to reimplantation.

This invention features an enzymatic RNA molecule (or ribozyme) which cleaves mRNA associated with development or maintenance of CML. The mRNA targets are present in the 425 nucleotides surrounding the fusion sites of the *bcr* and *abl* sequences in the b2-a2 and b3-a2 recombinant mRNAs. Other sequences in the 5' portion of the *bcr* mRNA or the 3' portion of the *abl* mRNA may also be targeted for ribozyme cleavage. Cleavage at any of these sites in the fusion mRNA molecules will result in inhibition of translation of the fusion protein in treated cells.

The invention provides a class of chemical cleaving agents which exhibit a high degree of specificity for the mRNA causative of CML. Such enzymatic RNA molecules can be delivered exogenously or endogenously to afflicted cells. In the preferred hammerhead motif the small size (less than 40 nucleotides, preferably between 32 and 36 nucleotides in length) of the molecule allows the cost of treatment to be reduced.

The smallest ribozyme delivered for any type of treatment reported to date (by Rossi et al., 1992 *supra*) is an *in vitro* transcript having a length of 142 nucleotides. Synthesis of ribozymes greater than 100 nucleotides in length is very difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. Delivery of ribozymes by expression vectors is primarily feasible using only *ex vivo* treatments. This limits the utility of this approach. In this invention, an alternative approach uses smaller ribozyme motifs and exogenous delivery. The simple structure of these molecules also increases the ability of the ribozyme to invade targeted regions of the mRNA structure. Thus, unlike the situation when the hammerhead structure is included within longer transcripts, there are no non-ribozyme flanking sequences to interfere with correct folding of the ribozyme structure, as well as complementary binding of the ribozyme to the mRNA target.

The enzymatic RNA molecules of this invention can be used to treat human CML or precancerous conditions. Affected animals can be treated at the time of cancer detection or in a prophylactic manner. This timing of treatment will reduce the number of affected cells and disable cellular

replication. This is possible because the ribozymes are designed to disable those structures required for successful cellular proliferation.

Ribozymes of this invention block to some extent p210*bcr-abl* expression and can be used to treat disease or diagnose such disease.
5 Ribozymes will be delivered to cells in culture and to tissues in animal models of CML. Ribozyme cleavage of *bcr/abl* mRNA in these systems may prevent or alleviate disease symptoms or conditions.

The sequence of human *bcr/abl* mRNA can be screened for accessible sites using a computer folding algorithm. Regions of the mRNA
10 that did not form secondary folding structures and that contain potential hammerhead or hairpin ribozyme cleavage sites can be identified. These sites are shown in Table 29 (All sequences are 5' to 3' in the tables). The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of ribozyme.

15 The sequences of the chemically synthesized ribozymes most useful in this study are shown in Table 30. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. For example, stem-loop II sequence of
20 hammerhead ribozymes listed in Table 30 (5'-GGCCGAAAGGCC-3') can be altered (substitution, deletion, and/or insertion) to contain any sequence provided, a minimum of two base-paired stem structure can form. The sequences listed in Tables 30 may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the
25 ribozymes described specifically in the Tables.

By engineering ribozyme motifs we have designed several ribozymes directed against *bcr-abl* mRNA sequences. These have been synthesized with modifications that improve their nuclease resistance as described above. These ribozymes cleave *bcr-abl* target sequences *in vitro*.

30 The ribozymes are tested for function *in vivo* by exogenous delivery to cells expressing *bcr-abl*. Ribozymes are delivered by incorporation into liposomes, by complexing with cationic lipids, by microinjection, or by expression from DNA vectors. Expression of *bcr-abl* is monitored by ELISA, by indirect immunofluorescence, and/or by FACS analysis. Levels of

bcr-abl mRNA are assessed by Northern analysis, RNase protection, by primer extension analysis or by quantitative RT-PCR techniques. Ribozymes that block the induction of p210^{*bcr-abl*} protein and mRNA by more than 20% are identified.

5 Example 6: RSV

This invention relates to the use of ribozymes as inhibitors of respiratory syncytial virus (RSV) production, and in particular, the inhibition of RSV replication.

RSV is a member of the virus family paramyxoviridae and is classified
10 under the genus *Pneumovirus* (for a review see McIntosh and Chanock, 1990 in Virology ed. B.N. Fields, pp. 1045, Raven Press Ltd. NY). The infectious virus particle is composed of a nucleocapsid enclosed within an envelope. The nucleocapsid is composed of a linear negative single-stranded non-segmented RNA associated with repeating subunits of
15 capsid proteins to form a compact structure and thereby protect the RNA from nuclease degradation. The entire nucleocapsid is enclosed by the envelope. The size of the virus particle ranges from 150 - 300 nm in diameter. The complete life cycle of RSV takes place in the cytoplasm of infected cells and the nucleocapsid never reaches the nuclear
20 compartment (Hall, 1990 in Principles and Practice of Infectious Diseases ed. Mandell et al., Churchill Livingstone, NY).

The RSV genome encodes ten viral proteins essential for viral production. RSV protein products include two structural glycoproteins (G and F) found in the envelope spikes, two matrix proteins [M and M2 (22K)]
25 found in the inner membrane, three proteins localized in the nucleocapsid (N, P and L), one protein that is present on the surface of the infected cell (SH), and two nonstructural proteins [NS1 (1C) and NS2 (1B)] found only in the infected cell. The mRNAs for the 10 RSV proteins have similar 5' and 3' ends. UV-inactivation studies suggest that a single promoter is used
30 with multiple transcription initiation sites (Barik *et al.*, 1992 J. Virol. 66, 6813). The order of transcription corresponding to the protein assignment on the genomic RNA is 1C, 1B, N, P, M, SH, G, F, 22K and L genes (Huang *et al.*, 1985 Virus Res. 2, 157) and transcript abundance corresponds to the order of gene assignment (for example the 1C and 1B mRNAs are
35 much more abundant than the L mRNA. Synthesis of viral message begins

immediately after RSV infection of cells and reaches a maximum at 14 hours post-infection (McIntosh and Chanock, *supra*).

There are two antigenic subgroups of RSV, A and B, which can circulate simultaneously in the community in varying proportions in different years (McIntosh and Chanock, *supra*). Subgroup A usually predominates. Within the two subgroups there are numerous strains. By the limited sequence analysis available it seems that homology at the nucleotide level is more complete within than between subgroups, although sequence divergence has been noted within subgroups as well. Antigenic determinates result primarily from both surface glycoproteins, F and G. For F, at least half of the neutralization epitopes have been stably maintained over a period of 30 years. For G however, A and B subgroups may be related antigenically by as little as a few percent. On the nucleotide level, however, the majority of the divergence in the coding region of G is found in the sequence for the extracellular domain (Johnson et al., 1987, *Proc. Natl. Acad. Sci. USA* 84, 5625).

Respiratory Syncytial Virus (RSV) is the major cause of lower respiratory tract illness during infancy and childhood (Hall, *supra*) and as such is associated with an estimated 90,000 hospitalizations and 4500 deaths in the United States alone (Update: respiratory syncytial virus activity - United States, 1993, *Mmwr Morb Mortal Wkly Rep*, 42, 971). Infection with RSV generally outranks all other microbial agents leading to both pneumonia and bronchitis. While primarily affecting children under two years of age, immunity is not complete and reinfection of older children and adults, especially hospital care givers (McIntosh and Chanock, *supra*), is not uncommon. Immunocompromised patients are severely affected and RSV infection is a major complication for patients undergoing bone marrow transplantation.

Uneventful RSV respiratory disease resembles a common cold and recovery is in 7 to 12 days. Initial symptoms (rhinorrhea, nasal congestion, slight fever, etc.) are followed in 1 to 3 days by lower respiratory tract signs of infection that include a cough and wheezing. In severe cases, these mild symptoms quickly progress to tachypnea, cyanosis, and listlessness and hospitalization is required. In infants with underlying cardiac or respiratory disease, the progression of symptoms is especially rapid and can lead to respiratory failure by the second or third day of illness. With

modern intensive care however, overall mortality is usually less than 5% of hospitalized patients (McIntosh and Chanock, *supra*).

At present, neither an efficient vaccine nor a specific antiviral agent is available. An immune response to the viral surface glycoproteins can provide resistance to RSV in a number of experimental animals, and a subunit vaccine has been shown to be effective for up to 6 months in children previously hospitalized with an RSV infection (Tristram *et al.*, 1993, J. Infect. Dis. 167, 191). An attenuated bovine RSV vaccine has also been shown to be effective in calves for a similar length of time (Kubota *et al.*, 1992 J. Vet. Med. Sci. 54, 957). Previously however, a formalin-inactivated RSV vaccine was implicated in greater frequency of severe disease in subsequent natural infections with RSV (Connors *et al.*, 1992 J. Virol. 66, 7444).

The current treatment for RSV infection requiring hospitalization is the use of aerosolized ribavirin, a guanosine analog [Antiviral Agents and Viral Diseases of Man, 3rd edition. 1990. (eds. G.J. Galasso, R.J. Whitley, and T.C. Merigan) Raven Press Ltd., NY.]. Ribavirin therapy is associated with a decrease in the severity of the symptoms, improved arterial oxygen and a decrease in the amount of viral shedding at the end of the treatment period. It is not certain, however, whether ribavirin therapy actually shortens the patients' hospital stay or diminishes the need for supportive therapies (McIntosh and Chanock, *supra*). The benefits of ribavirin therapy are especially clear for high risk infants, those with the most serious symptoms or for patients with underlying bronchopulmonary or cardiac disease. Inhibition of the viral polymerase complex is supported as the main mechanism for inhibition of RSV by ribavirin, since viral but not cellular polypeptide synthesis is inhibited by ribavirin in RSV-infected cells (Antiviral Agents and Viral Diseases of Man, 3rd edition. 1990. (eds. G.J. Galasso, R.J. Whitley, and T.C. Merigan) Raven Press Ltd., NY.]. Since ribavirin is at least partially effective against RSV infection when delivered by aerosolization, it can be assumed that the target cells are at or near the epithelial surface. In this regard, RSV antigen had not spread any deeper than the superficial layers of the respiratory epithellum in autopsy studies of fatal pneumonia (McIntosh and Chanock, *supra*).

Jennings *et al.*, WO 94/13688 indicates that targets for specific types of ribozymes include respiratory syncytical virus.

The invention features novel enzymatic RNA molecules, or ribozymes, and methods for their use for inhibiting production of respiratory syncytial virus (RSV). Such ribozymes can be used in a method for treatment of diseases caused by these related viruses in man and other animals. The invention also features cleavage of the genomic RNA and mRNA of these viruses by use of ribozymes. In particular, the ribozyme molecules described are targeted to the *NS1 (1C)*, *NS2 (1B)* and *N* viral genes. These genes are known in the art (for a review see McIntosh and Chanock, 1990 *supra*).

Ribozymes that cleave the specified sites in RSV mRNAs represent a novel therapeutic approach to respiratory disorders. Applicant indicates that ribozymes are able to inhibit the activity of RSV and that the catalytic activity of the ribozymes is required for their inhibitory effect. Those of ordinary skill in the art, will find that it is clear from the examples described that other ribozymes that cleave these sites in RSV mRNAs encoding 1C, 1B and N proteins may be readily designed and are within the invention. Also, those of ordinary skill in the art, will find that it is clear from the examples described that ribozymes cleaving other mRNAs encoded by RSV (*P*, *M*, *SH*, *G*, *F*, *22K* and *L*) and the genomic RNA may be readily designed and are within the invention.

In preferred embodiments, the ribozymes have binding arms which are complementary to the sequences in Tables 31, 33, 35, 37 and 38. Examples of such ribozymes are shown in Tables 32, 34, 36-38. Examples of such ribozymes consist essentially of sequences defined in these Tables. By "consists essentially of" is meant that the active ribozyme contains an enzymatic center equivalent to those in the examples, and binding arms able to bind mRNA such that cleavage at the target site occurs. Other sequences may be present which do not interfere with such cleavage.

Ribozymes of this invention block to some extent RSV production and can be used to treat disease or diagnose such disease. Ribozymes will be delivered to cells in culture and to cells or tissues in animal models of respiratory disorders. Ribozyme cleavage of RSV encoded mRNAs or the genomic RNA in these systems may alleviate disease symptoms.

While all ten RSV encoded proteins (1C, 1B, N, P, M, SH, 22K, F, G, and L) are essential for viral life cycle and are all potential targets for ribozyme cleavage, certain proteins (mRNAs) are more favorable for ribozyme targeting than the others. For example RSV encoded proteins 1C, 1B, SH and 22K are not found in other members of the family paramyxoviridae and appear to be unique to RSV. In contrast the ectodomain of the G protein and the signal sequence of the F protein show significant sequence divergence at the nucleotide level among various RSV sub-groups (Johnson *et al.*, 1987 *supra*). RSV proteins 1C, 1B and N are highly conserved among various subtypes at both the nucleotide and amino acid levels. Also, 1C, 1B and N are the most abundant of all RSV proteins.

The sequence of human RSV mRNAs encoding 1C, 1B and N proteins are screened for accessible sites using a computer folding algorithm. Hammerhead or hairpin ribozyme cleavage sites were identified. These sites are shown in Tables 31, 33, 34, 37 and 38 (All sequences are 5' to 3' in the tables.) The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of ribozyme.

Ribozymes of the hammerhead or hairpin motif are designed to anneal to various sites in the mRNA message. The binding arms are complementary to the target site sequences described above. The ribozymes are chemically synthesized. The method of synthesis used follows the procedure for normal RNA synthesis as described in Usman *et al.*, 1987 J. Am. Chem. Soc., 109, 7845-7854 and in Scaringe *et al.*, 1990 Nucleic Acids Res., 18, 5433-5441 and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%. Inactive ribozymes were synthesized by substituting a U for G₅ and a U for A₁₄ (numbering from Hertel *et al.*, 1992 Nucleic Acids Res., 20, 3252). Hairpin ribozymes are synthesized in two parts and annealed to reconstruct the active ribozyme (Chowrira and Burke, 1992 Nucleic Acids Res., 20, 2835-2840). Hairpin ribozymes are also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, *Methods Enzymol.* 180, 51). All ribozymes are modified extensively to enhance stability by modification with nuclease resistant

groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-o-methyl, 2'-H (for a review see Usman and Cedergren, 1992 *TIBS* 17, 34). Ribozymes are purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography and are resuspended in water.

5 The sequences of the chemically synthesized ribozymes useful in this study are shown in Tables 32, 34, 36, 37 and 38. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. For example, stem-loop II sequence of
10 hammerhead ribozymes listed in Tables 32 and 34 (5'-GGCCGAAAGGCC-3') can be altered (substitution, deletion, and/or insertion) to contain any sequences provided a minimum of two base-paired stem structure can form. Similarly, stem-loop IV sequence of hairpin ribozymes listed in Tables 37 and 38 (5'-CACGUUGUG-3') can be altered (substitution,
15 deletion, and/or insertion) to contain any sequence, provided a minimum of two base-paired stem structure can form. The sequences listed in Tables 32, 34, 36, 37 and 38 may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the ribozymes described specifically in the Tables.

20 By engineering ribozyme motifs we have designed several ribozymes directed against RSV encoded mRNA sequences. These ribozymes are synthesized with modifications that improve their nuclease resistance. The ability of ribozymes to cleave target sequences *in vitro* is evaluated.

 Numerous common cell lines can be infected with RSV for
25 experimental purposes. These include *HeLa*, *Vero* and several primary epithelial cell lines. A cotton rat animal model of experimental human RSV infection is also available, and the bovine RSV is quite homologous to the human viruses. Rapid clinical diagnosis is through the use of kits designed for the immunofluorescence staining of RSV-infected cells or an ELISA
30 assay, both of which are adaptable for experimental study. RSV encoded mRNA levels will be assessed by Northern analysis, RNase protection, primer extension analysis or quantitative RT-PCR. Ribozymes that block the induction of RSV activity and/or 1C, 1B and N protein encoding mRNAs by more than 90% will be identified.

Optimizing Ribozyme Activity

Ribozyme activity can be optimized as described by Draper et al., PCT WO93/23569. The details will not be repeated here, but include altering the length of the ribozyme binding arms or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see e.g., Eckstein et al., International Publication No. WO 92/07065; Perrault et al., 1990 Nature 344, 565; Pieken et al., 1991 Science 253, 314; Usman and Cedergren, 1992 Trends in Biochem. Sci. 17, 334; Usman et al., International Publication No. WO 93/15187; and Rossi et al., International Publication No. WO 91/03162, as well as Jennings et al., WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules. All these publications are hereby incorporated by reference herein.), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan, et al., PCT WO94/02595, incorporated by reference herein, describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. The RNA/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion pump or stent. Alternative routes of delivery include, but are not limited to, intravenous injection, intramuscular injection, subcutaneous injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Sullivan, et al., supra and Draper, et al., supra which have been incorporated by reference herein.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given

pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells

5 (Elroy-Stein and Moss, 1990 Proc. Natl. Acad. Sci. U S A, 87, 6743-7; Gao and Huang 1993 Nucleic Acids Res., 21, 2867-72; Lieber et al., 1993 Methods Enzymol., 217, 47-66; Zhou et al., 1990 Mol. Cell. Biol., 10, 4529-37). Several investigators have demonstrated that ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet

10 et al., 1992 Antisense Res. Dev., 2, 3-15; Ojwang et al., 1992 Proc. Natl. Acad. Sci. U S A, 89, 10802-6; Chen et al., 1992 Nucleic Acids Res., 20, 4581-9; Yu et al., 1993 Proc. Natl. Acad. Sci. U S A, 90, 6340-4; L'Huillier et al., 1992 EMBO J. 11, 4411-8; Lisiewicz et al., 1993 Proc. Natl. Acad. Sci. U. S. A., 90, 8000-4). The above ribozyme transcription units can be

15 incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral, or alpha virus vectors).

In a preferred embodiment of the invention, a transcription unit

20 expressing a ribozyme that cleaves target RNA is inserted into a plasmid DNA vector, a retrovirus DNA viral vector, an adenovirus DNA viral vector or an adeno-associated virus vector or alpha virus vector. These and other vectors have been used to transfer genes to live animals (for a review see Friedman, 1989 Science 244, 1275-1281; Roemer and Friedman, 1992

25 Eur. J. Biochem. 208, 211-225) and leads to transient or stable gene expression. The vectors are delivered as recombinant viral particles. DNA may be delivered alone or complexed with vehicles (as described for RNA above). The DNA, DNA/vehicle complexes, or the recombinant virus particles are locally administered to the site of treatment, e.g., through the

30 use of a catheter, stent or infusion pump.

Diagnostic uses

Ribozymes of this invention may be used as diagnostic tools to examine genetic drift and mutations within diseased cells. The close relationship between ribozyme activity and the structure of the target RNA

35 allows the detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By

using multiple ribozymes described in this invention, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with ribozymes may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets may be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combinational therapies (e.g., multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes and/or other chemical or biological molecules). Other *in vitro* uses of ribozymes of this invention are well known in the art, and include detection of the presence of mRNA associated with ICAM-1, relA, TNF- α , p210, bcr-abl or RSV related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a ribozyme using standard methodology.

In a specific example, ribozymes which can cleave only wild-type or mutant forms of the target RNA are used for the assay. The first ribozyme is used to identify wild-type RNA present in the sample and the second ribozyme will be used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA will be cleaved by both ribozymes to demonstrate the relative ribozyme efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates will also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus each analysis will require two ribozymes, two substrates and one unknown sample which will be combined into six reactions. The presence of cleavage products will be determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (i.e., ICAM-1, rel A, TNF α , p210bcr-abl or RSV) is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels will be adequate and will

decrease the cost of the initial diagnosis. Higher mutant form to wild-type ratios will be correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

II. Chemical Synthesis Of Ribozymes

5 There follows the chemical synthesis, deprotection, and purification of RNA, enzymatic RNA or modified RNA molecules in greater than milligram quantities with high biological activity. Applicant has determined that the synthesis of enzymatically active RNA in high yield and quantity is dependent upon certain critical steps used during its preparation.
10 Specifically, it is important that the RNA phosphoramidites are coupled efficiently in terms of both yield and time, that correct exocyclic amino protecting groups be used, that the appropriate conditions for the removal of the exocyclic amino protecting groups and the alkylsilyl protecting groups on the 2'-hydroxyl are used, and that the correct work-up and
15 purification procedure of the resulting ribozyme be used.

 To obtain a correct synthesis in terms of yield and biological activity of a large RNA molecule (*i.e.*, about 30 to 40 nucleotide bases), the protection of the amino functions of the bases requires either amide or substituted amide protecting groups, which must be, on the one hand, stable enough
20 to survive the conditions of synthesis, and on the other hand, removable at the end of the synthesis. These requirements are met by the amide protecting groups shown in Figure 8, in particular, benzoyl for adenosine, isobutyryl or benzoyl for cytidine, and isobutyryl for guanosine, which may be removed at the end of the synthesis by incubating the RNA in NH₃/EtOH
25 (ethanolic ammonia) for 20 h at 65 °C. In the case of the phenoxyacetyl type protecting groups shown in Figure 8 on guanosine and adenosine and acetyl protecting groups on cytidine, an incubation in ethanolic ammonia for 4 h at 65 °C is used to obtain complete removal of these protecting groups. Removal of the alkylsilyl 2'-hydroxyl protecting groups
30 can be accomplished using a tetrahydrofuran solution of TBAF at room temperature for 8-24 h.

 The most quantitative procedure for recovering the fully deprotected RNA molecule is by either ethanol precipitation, or an anion exchange cartridge desalting, as described in Scaringe *et al. Nucleic Acids Res.*
35 1990, 18, 5433-5341. The purification of the long RNA sequences may be

accomplished by a two-step chromatographic procedure in which the molecule is first purified on a reverse phase column with either the trityl group at the 5' position on or off. This purification is accomplished using an acetonitrile gradient with triethylammonium or bicarbonate salts as the aqueous phase. In the case of the trityl on purification, the trityl group may be removed by the addition of an acid and drying of the partially purified RNA molecule. The final purification is carried out on an anion exchange column, using alkali metal perchlorate salt gradients to elute the fully purified RNA molecule as the appropriate metal salts, e.g. Na⁺, Li⁺ etc. A final de-salting step on a small reverse-phase cartridge completes the purification procedure. Applicant has found that such a procedure not only fails to adversely affect activity of a ribozyme, but may improve its activity to cleave target RNA molecules.

Applicant has also determined that significant (see Tables 39-41) improvements in the yield of desired full length product (FLP) can be obtained by:

1. Using 5-S-alkyltetrazole at a delivered or effective concentration of 0.25-0.5 M or 0.15-0.35 M for the activation of the RNA (or analogue) amidite during the coupling step. (By delivered is meant that the actual amount of chemical in the reaction mix is known. This is possible for large scale synthesis since the reaction vessel is of size sufficient to allow such manipulations. The term effective means that available amount of chemical actually provided to the reaction mixture that is able to react with the other reagents present in the mixture. Those skilled in the art will recognize the meaning of these terms from the examples provided herein.) The time for this step is shortened from 10-15 m, *vide supra*, to 5-10 m. Alkyl, as used herein, refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino, or SH. The term also includes alkenyl groups which are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably it is a lower alkenyl of from 1 to

7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂, halogen, N(CH₃)₂, amino, or SH. The term "alkyl" also includes alkynyl groups which have an
5 unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the
10 substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino or SH.

Such alkyl groups may also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group which has at least one ring having a conjugated π electron
15 system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as
20 described above. Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur,
25 and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

30 2. Using 5-S-alkyltetrazole at an effective, or final, concentration of 0.1-0.35 M for the activation of the RNA (or analogue) amidite during the coupling step. The time for this step is shortened from 10-15 m, *vide supra*, to 5-10 m.

35 3. Using alkylamine (MA, where alkyl is preferably methyl, ethyl, propyl or butyl) or NH₄OH/alkylamine (AMA, with the same preferred alkyl groups as noted for MA) @ 65 °C for 10-15 m to remove the exocyclic

amino protecting groups (vs 4-20 h @ 55-65 °C using $\text{NH}_4\text{OH}/\text{EtOH}$ or NH_3/EtOH , *vide supra*). Other alkylamines, e.g. ethylamine, propylamine, butylamine etc. may also be used.

4. Using anhydrous triethylamine-hydrogen fluoride ($\text{aHF}\cdot\text{TEA}$)
5 @ 65 °C for 0.5-1.5 h to remove the 2'-hydroxyl alkylsilyl protecting group (vs 8 - 24 h using TBAF, *vide supra* or $\text{TEA}\cdot 3\text{HF}$ for 24 h (Gasparutto *et al. Nucleic Acids Res.* 1992, 20, 5159-5166). Other alkylamine-HF complexes may also be used, e.g. trimethylamine or diisopropylethylamine.

5. The use of anion-exchange resins to purify and/or analyze the
10 fully deprotected RNA. These resins include, but are not limited to, quaternary or tertiary amino derivatized stationary phases such as silica or polystyrene. Specific examples include Dionex-NA100®, Mono-Q®, Poros-Q®.

- Thus, the invention features an improved method for the coupling of
15 RNA phosphoramidites; for the removal of amide or substituted amide protecting groups; and for the removal of 2'-hydroxyl alkylsilyl protecting groups. Such methods enhance the production of RNA or analogs of the type described above (e.g., with substituted 2'-groups), and allow efficient synthesis of large amounts of such RNA. Such RNA may also have
20 enzymatic activity and be purified without loss of that activity. While specific examples are given herein, those in the art will recognize that equivalent chemical reactions can be performed with the alternative chemicals noted above, which can be optimized and selected by routine experimentation.

- In another aspect, the invention features an improved method for the
25 purification or analysis of RNA or enzymatic RNA molecules (e.g. 28-70 nucleotides in length) by passing said RNA or enzymatic RNA molecule over an HPLC, e.g., reverse phase and/or an anion exchange chromatography column. The method of purification improves the catalytic activity of enzymatic RNAs over the gel purification method (see Figure 10).

- 30 Draper *et al.*, PCT WO93/23569, incorporated by reference herein, disclosed reverse phase HPLC purification. The purification of long RNA molecules may be accomplished using anion exchange chromatography, particularly in conjunction with alkali perchlorate salts. This system may be used to purify very long RNA molecules. In particular, it is advantageous to

use a Dionex NucleoPak 100[®] or a Pharmacia Mono Q[®] anion exchange column for the purification of RNA by the anion exchange method. This anion exchange purification may be used following a reverse-phase purification or prior to reverse phase purification. This method results in the formation of a sodium salt of the ribozyme during the chromatography. Replacement of the sodium alkali earth salt by other metal salts, e.g., lithium, magnesium or calcium perchlorate, yields the corresponding salt of the RNA molecule during the purification.

In the case of the 2-step purification procedure, in which the first step is a reverse phase purification followed by an anion exchange step, the reverse phase purification is best accomplished using polymeric, e.g. polystyrene based, reverse-phase media, using either a 5'-trityl-on or 5'-trityl-off method. Either molecule may be recovered using this reverse-phase method, and then, once detritylated, the two fractions may be pooled and then submitted to an anion exchange purification step as described above.

The method includes passing the enzymatically active RNA molecule over a reverse phase HPLC column; the enzymatically active RNA molecule is produced in a synthetic chemical method and not by an enzymatic process; and the enzymatic RNA molecule is partially blocked, and the partially blocked enzymatically active RNA molecule is passed over a reverse phase HPLC column to separate it from other RNA molecules.

In more preferred embodiments, the enzymatically active RNA molecule, after passage over the reverse phase HPLC column, is deprotected and passed over a second reverse phase HPLC column (which may be the same as the reverse phase HPLC column), to remove the enzymatic RNA molecule from other components. In addition, the column is a silica or organic polymer-based C4, C8 or C18 column having a porosity of at least 125 Å, preferably 300 Å, and a particle size of at least 2 µm, preferably 5 µm.

Activation

The synthesis of RNA molecules may be accomplished chemically or enzymatically. In the case of chemical synthesis the use of tetrazole as an activator of RNA phosphoramidites is known (Usman *et al.* *J. Am. Chem.*

Soc. 1987, 109, 7845-7854). In this, and subsequent reports, a 0.5 M solution of tetrazole is allowed to react with the RNA phosphoramidite and couple with the polymer bound 5'-hydroxyl group for 10 m. Applicant has determined that using 0.25-0.5 M solutions of 5-S-alkyltetrazoles for only 5 min gives equivalent or better results. The following exemplifies the procedure.

Example 7: Synthesis of RNA and Ribozymes Using 5-S-Alkyltetrazoles as Activating Agent

The method of synthesis used follows the general procedure for RNA synthesis as described in Usman et al., 1987*supra* and in Scaringe et al., *Nucleic Acids Res.* 1990, 18, 5433-5441 and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The major difference used was the activating agent, 5-S-ethyl or -methyltetrazole @ 0.25 M concentration for 5 min.

All small scale syntheses were conducted on a 394 (ABI) synthesizer using a modified 2.5 μ mol scale protocol with a reduced 5 min coupling step for alkylsilyl protected RNA and 2.5 m coupling step for 2'-O-methylated RNA. A 6.5-fold excess (162.5 μ L of 0.1 M = 32.5 μ mol) of phosphoramidite and a 40-fold excess of S-ethyl tetrazole (400 μ L of 0.25 M = 100 μ mol) relative to polymer-bound 5'-hydroxyl was used in each coupling cycle. Average coupling yields on the 394, determined by colorimetric quantitation of the trityl fractions, was 97.5-99%. Other oligonucleotide synthesis reagents for the 394: Detritylation solution was 2% TCA in methylene chloride; capping was performed with 16% N-Methyl imidazole in THF and 10% acetic anhydride/10% 2,6-lutidine in THF; oxidation solution was 16.9 mM I₂, 49 mM pyridine, 9% water in THF. Fisher Synthesis Grade acetonitrile was used directly from the reagent bottle. S-Ethyl tetrazole solution (0.25 M in acetonitrile) was made up from the solid obtained from Applied Biosystems.

All large scale syntheses were conducted on a modified (eight amidite port capacity) 390Z (ABI) synthesizer using a 25 μ mol scale protocol with a 5-15 min coupling step for alkylsilyl protected RNA and 7.5 m coupling step for 2'-O-methylated RNA. A six-fold excess (1.5 mL of 0.1 M = 150 μ mol) of phosphoramidite and a forty-five-fold excess of S-ethyl tetrazole (4.5 mL of

0.25 M = 1125 μ mol) relative to polymer-bound 5'-hydroxyl was used in each coupling cycle. Average coupling yields on the 390Z, determined by colorimetric quantitation of the trityl fractions, was 95.0-96.7%. Oligonucleotide synthesis reagents for the 390Z: Detritylation solution was
5 2% DCA in methylene chloride; capping was performed with 16% *N*-Methylimidazole in THF and 10% acetic anhydride/10% 2,6-lutidine in THF; oxidation solution was 16.9 mM I₂, 49 mM pyridine, 9% water in THF. Fisher Synthesis Grade acetonitrile was used directly from the reagent bottle. *S*-Ethyl tetrazole solution (0.25-0.5 M in acetonitrile) was made up
10 from the solid obtained from Applied Biosystems.

Deprotection

The first step of the deprotection of RNA molecules may be accomplished by removal of the exocyclic amino protecting groups with either NH₄OH/EtOH:3/1 (Usman *et al.* *J. Am. Chem. Soc.* 1987, 109, 7845-
15 7854) or NH₃/EtOH (Scaringe *et al.* *Nucleic Acids Res.* 1990, 18, 5433-5341) for -20 h @ 55-65 °C. Applicant has determined that the use of methylamine or NH₄OH/methylamine for 10-15 min @ 55-65 °C gives equivalent or better results. The following exemplifies the procedure.

Example 8: RNA and Ribozyme Deprotection of Exocyclic Amino 20 Protecting Groups Using Methylamine (MA) or NH₄OH/Methylamine (AMA)

The polymer-bound oligonucleotide, either trityl-on or off, was suspended in a solution of methylamine (MA) or NH₄OH/methylamine (AMA) @ 55-65 °C for 5-15 min to remove the exocyclic amino protecting groups. The polymer-bound oligoribonucleotide was transferred from the
25 synthesis column to a 4 mL glass screw top vial. NH₄OH and aqueous methylamine were pre-mixed in equal volumes. 4 mL of the resulting reagent was added to the vial, equilibrated for 5 m at RT and then heated at 55 or 65 °C for 5-15 min. After cooling to -20 °C, the supernatant was removed from the polymer support. The support was washed with 1.0 mL
30 of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant was then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, were dried to a white powder. The same procedure was followed for the aqueous methylamine reagent.

Table 40 is a summary of the results obtained using the improvements
35 outlined in this application for base deprotection.

The second step of the deprotection of RNA molecules may be accomplished by removal of the 2'-hydroxyl alkylsilyl protecting group using TBAF for 8-24 h (Usman *et al.* *J. Am. Chem. Soc.* 1987, 109, 7845-7854). Applicant has determined that the use of anhydrous TEA•HF in *N*-methylpyrrolidine (NMP) for 0.5-1.5 h @ 55-65 °C gives equivalent or better results. The following exemplifies this procedure.

Example 9: RNA and Ribozyme Deprotection of 2'-Hydroxyl Alkylsilyl Protecting Groups Using Anhydrous TEA•HF

To remove the alkylsilyl protecting groups, the ammonia-deprotected oligoribonucleotide was resuspended in 250 µL of 1.4 M anhydrous HF solution (1.5 mL *N*-methylpyrrolidine, 750 µL TEA and 1.0 mL TEA•3HF) and heated to 65 °C for 1.5 h. 9 mL of 50 mM TEAB was added to quench the reaction. The resulting solution was loaded onto a Qiagen 500® anion exchange cartridge (Qiagen Inc.) prewashed with 10 mL of 50 mM TEAB. After washing the cartridge with 10 mL of 50 mM TEAB, the RNA was eluted with 10 mL of 2 M TEAB and dried down to a white powder.

Table 41 is a summary of the results obtained using the improvements outlined in this application for alkylsilyl deprotection.

Example 10: HPLC Purification, Anion Exchange column

For a small scale synthesis, the crude material was diluted to 5 mL with diethylpyrocarbonate treated water. The sample was injected onto either a Pharmacia Mono Q® 16/10 or Dionex NucleoPac® column with 100% buffer A (10 mM NaClO₄). A gradient from 180-210 mM NaClO₄ at a rate of 0.85 mM/void volume for a Pharmacia Mono Q® anion-exchange column or 100-150 mM NaClO₄ at a rate of 1.7 mM/void volume for a Dionex NucleoPac® anion-exchange column was used to elute the RNA. Fractions were analyzed by a HP-1090 HPLC with a Dionex NucleoPac® column. Fractions containing full length product at ≥80% by peak area were pooled.

For a trityl-off large scale synthesis, the crude material was desalted by applying the solution that resulted from quenching of the desilylation reaction to a 53 mL Pharmacia HiLoad 26/10 Q-Sepharose® Fast Flow column. The column was thoroughly washed with 10 mM sodium perchlorate buffer. The oligonucleotide was eluted from the column with

300 mM sodium perchlorate. The eluent was quantitated and an analytical HPLC was run to determine the percent full length material in the synthesis. The eluent was diluted four fold in sterile H₂O to lower the salt concentration and applied to a Pharmacia Mono Q[®] 16/10 column. A
5 gradient from 10-185 mM sodium perchlorate was run over 4 column volumes to elute shorter sequences, the full length product was then eluted in a gradient from 185-214 mM sodium perchlorate in 30 column volumes. The fractions of interest were analyzed on a HP-1090 HPLC with a Dionex NucleoPac[®] column. Fractions containing over 85% full length material
10 were pooled. The pool was applied to a Pharmacia RPC[®] column for desalting.

For a trityl-on large scale synthesis, the crude material was desalted by applying the solution that resulted from quenching of the desilylation reaction to a 53 mL Pharmacia HiLoad 26/10 Q-Sepharose[®] Fast Flow
15 column. The column was thoroughly washed with 20 mM NH₄CO₃H/10% CH₃CN buffer. The oligonucleotide was eluted from the column with 1.5 M NH₄CO₃H/10% acetonitrile. The eluent was quantitated and an analytical HPLC was run to determine the percent full length material present in the synthesis. The oligonucleotide was then applied to a Pharmacia Resource
20 RPC column. A gradient from 20-55% B (20 mM NH₄CO₃H/25% CH₃CN, buffer A = 20 mM NH₄CO₃H/10% CH₃CN) was run over 35 column volumes. The fractions of interest were analyzed on a HP-1090 HPLC with a Dionex NucleoPac[®] column. Fractions containing over 60% full length material were pooled. The pooled fractions were then submitted to manual
25 detritylation with 80% acetic acid, dried down immediately, resuspended in sterile H₂O, dried down and resuspended in H₂O again. This material was analyzed on a HP 1090-HPLC with a Dionex NucleoPac[®] column. The material was purified by anion exchange chromatography as in the trityl-off scheme (*vide supra*).

30 Example 11. Ribozyme Activity Assay

Purified 5'-end labeled RNA substrates (15-25-mers) and purified 5'-end labeled ribozymes (~36-mers) were both heated to 95 °C, quenched on ice and equilibrated at 37 °C, separately. Ribozyme stock solutions were 1 μM, 200 nM, 40 nM or 8 nM and the final substrate RNA
35 concentrations were ~ 1 nM. Total reaction volumes were 50 μL. The assay buffer was 50 mM Tris-Cl, pH 7.5 and 10 mM MgCl₂. Reactions were

initiated by mixing substrate and ribozyme solutions at $t = 0$. Aliquots of 5 μL were removed at time points of 1, 5, 15, 30, 60 and 120 m. Each aliquot was quenched in formamide loading buffer and loaded onto a 15% denaturing polyacrylamide gel for analysis. Quantitative analyses were performed using a phosphorimager (Molecular Dynamics).

Example 12: One pot deprotection of RNA

Applicant has shown that aqueous methyl amine is an efficient reagent to deprotect bases in an RNA molecule. However, in a time consuming step (2-24 hrs), the RNA sample needs to be dried completely prior to the deprotection of the sugar 2'-hydroxyl groups. Additionally, deprotection of RNA synthesized on a large scale (e.g., 100 μmol) becomes challenging since the volume of solid support used is quite large. In an attempt to minimize the time required for deprotection and to simplify the process of deprotection of RNA synthesized on a large scale, applicant describes a one pot deprotection protocol (Fig. 12). According to this protocol, anhydrous methylamine is used in place of aqueous methyl amine. Base deprotection is carried out at 65 °C for 15 min and the reaction is allowed to cool for 10 min. Deprotection of 2'-hydroxyl groups is then carried out in the same container for 90 min in a TEA•3HF reagent. The reaction is quenched with 16 mM TEAB solution.

Referring to Fig. 13, hammerhead ribozyme targeted to site B is synthesized using RNA phosphoramidite chemistry and deprotected using either a two pot or a one pot protocol. Profiles of these ribozymes on an HPLC column are compared. The figure shows that RNAs deprotected by either the one pot or the two pot protocols yield similar full-length product profiles. Applicant has shown that using a one pot deprotection protocol, time required for RNA deprotection can be reduced considerably without compromising the quality or the yield of full length RNA.

Referring to Fig. 14, hammerhead ribozymes targeted to site B (from Fig. 13) are tested for their ability to cleave RNA. As shown in the figure 14, ribozymes that are deprotected using one pot protocol have catalytic activity comparable to ribozymes that are deprotected using a two pot protocol.

Example 12a: Improved protocol for the synthesis of phosphorothioate containing RNA and ribozymes using 5-S-Alkyltetrazoles as Activating Agent

5 The two sulfurizing reagents that have been used to synthesize ribophosphorothioates are tetraethylthiuram disulfide (TETD; Vu and Hirschbein, 1991 *Tetrahedron Letter* 31, 3005), and 3H-1,2-benzodithiol-3-one 1,1-dioxide (Beaucage reagent; Vu and Hirschbein, 1991 *supra*). TETD requires long sulfurization times (600 seconds for DNA and 3600 seconds for RNA). It has recently been shown that for sulfurization of DNA
10 oligonucleotides, Beaucage reagent is more efficient than TETD (Wyrzykiewicz and Ravikumar, 1994 *Bioorganic Med. Chem.* 4, 1519). Beaucage reagent has also been used to synthesize phosphorothioate oligonucleotides containing 2'-deoxy-2'-fluoro modifications wherein the wait time is 10 min (Kawasaki et al., 1992 *J. Med. Chem.*).

15 The method of synthesis used follows the procedure for RNA synthesis as described herein and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The sulfurization step for RNA described in the literature is a 8 second delivery and 10 min wait steps (Beaucage
20 and Iyer, 1991 *Tetrahedron* 49, 6123). These conditions produced about 95% sulfurization as measured by HPLC analysis (Morvan et al., 1990 *Tetrahedron Letter* 31, 7149). This 5% contaminating oxidation could arise from the presence of oxygen dissolved in solvents and/or slow release of traces of iodine adsorbed on the inner surface of delivery lines during
25 previous synthesis.

A major improvement is the use of an activating agent, 5-S-ethyltetrazole or 5-S-methyltetrazole at a concentration of 0.25 M for 5 min. Additionally, for those linkages which are phosphorothioate, the iodine solution is replaced with a 0.05 M solution of 3H-1,2-benzodithiole-3-one
30 1,1-dioxide (Beaucage reagent) in acetonitrile. The delivery time for the sulfurization step is reduced to 5 seconds and the wait time is reduced to 300 seconds.

RNA synthesis is conducted on a 394 (ABI) synthesizer using a modified 2.5 μ mol scale protocol with a reduced 5 min coupling step for
35 alkylsilyl protected RNA and 2.5 min coupling step for 2'-O-methylated RNA. A 6.5-fold excess (162.5 μ L of 0.1 M = 32.5 μ mol) of phosphoramidite

and a 40-fold excess of *S*-ethyl tetrazole (400 μ L of 0.25 M = 100 μ mol) relative to polymer-bound 5'-hydroxyl was used in each coupling cycle. Average coupling yields on the 394 synthesizer, determined by colorimetric quantitation of the trityl fractions, was 97.5-99%. Other oligonucleotide synthesis reagents for the 394 synthesizer: detritylation solution was 2% TCA in methylene chloride; capping was performed with 16% *N*-Methyl imidazole in THF and 10% acetic anhydride/10% 2,6-lutidine in THF; oxidation solution was 16.9 mM I_2 , 49 mM pyridine, 9% water in THF. Fisher Synthesis Grade acetonitrile was used directly from the reagent bottle. *S*-Ethyl tetrazole solution (0.25 M in acetonitrile) was made up from the solid obtained from Applied Biosystems. Sulfurizing reagent was obtained from Glen Research.

Average sulfurization efficiency (ASE) is determined using the formula: $ASE = (PS/Total)^{1/n-1}$

where, PS = integrated ^{31}P NMR values of the P=S diester

Total = integration value of all peaks

n = length of oligo

Referring to tables 42 and 43, effects of varying the delivery and the wait time for sulfurization with Beaucage's reagent is described. These data suggest that 5 second wait time and 300 second delivery time is the condition under which ASE is maximum.

Using the above conditions a 36 mer hammerhead ribozyme is synthesized which is targeted to site C. The ribozyme is synthesized to contain phosphorothioate linkages at four positions towards the 5' end. RNA cleavage activity of this ribozyme is shown in Fig. 16. Activity of the phosphorothioate ribozyme is comparable to the activity of a ribozyme lacking any phosphorothioate linkages.

Example 13: Protocol for the synthesis of 2'-N-phthalimido-nucleoside phosphoramidite

The 2'-amino group of a 2'-deoxy-2'-amino nucleoside is normally protected with *N*-(9-fluorenylmethoxycarbonyl) (Fmoc; Imazawa and Eckstein, 1979 *supra*; Pieken et al., 1991 *Science* 253, 314). This protecting group is not stable in CH_3CN solution or even in dry form during

prolonged storage at -20 °C. These problems need to be overcome in order to achieve large scale synthesis of RNA.

Applicant describes the use of alternative protecting groups for the 2'-amino group of 2'-deoxy-2'-amino nucleoside. Referring to Figure 17,
5 phosphoramidite 17 was synthesized starting from 2'-deoxy-2'-aminonucleoside (12) using transient protection with Markievich reagent (Markiewicz *J. Chem. Res.* 1979, S, 24). An intermediate 13 was obtained in 50% yield, however subsequent introduction of N-phtaloyl (Pht) group by Nefken's method (Nefkens, 1960 *Nature* 185, 306), desilylation (15),
10 dimethoxytrytilation (16) and phosphitylation led to phosphoramidite 17. Since overall yield of this multi-step procedure was low (20%) applicant investigated some alternative approaches, concentrating on selective introduction of N-phtaloyl group without acylation of 5' and 3' hydroxyls.

When 2'-deoxy-2'-amino-nucleoside was reacted with 1.05
15 equivalents of Nefkens reagent in DMF overnight with subsequent treatment with Et₃N (1 hour) only 10-15% of N and 5'(3')-bis-phtaloyl derivatives were formed with the major component being N-Pht-derivative 15. The N,O-bis by-products could be selectively and quantitatively converted to N-Pht derivative 15 by treatment of crude reaction mixture
20 with cat. KCN/MeOH.

A convenient "one-pot" procedure for the synthesis of key intermediate 16 involves selective N-phthaloylation with subsequent dimethoxytrytilation by DMTCl/Et₃N and resulting in the preparation of DMT derivative 16 in 85% overall yield as follows. Standard phosphitylation of
25 16 produced phosphoramidite 17 in 87% yield. One gram of 2'-amino nucleoside, for example 2'-amino uridine (US Biochemicals® part # 77140) was co-evaporated twice from dry dimethyl formamide (Dmf) and dried in vacuo overnight. 50 mls of Aldrich sure-seal Dmf was added to the dry 2'-amino uridine via syringe and the mixture was stirred for 10 minutes
30 to produce a clear solution. 1.0 grams (1.05 eq.) of N-carbethoxyphthalimide (Nefken's reagent, 98% Janssen Chimica) was added and the solution was stirred overnight. Thin layer chromatography (TLC) showed 90% conversion to a faster moving products (10% ETOH in CHCl₃) and 57 µl of TEA (0.1 eq.) was added to effect closure of the phthalimide ring. After 1 hour an additional 855 µl (1.5 eq.) of TEA was
35 added followed by the addition of 1.53 grams (1.1 eq.) of DMT-Cl

(Lancaster Synthesis®, 98%). The reaction mixture was left to stir overnight and quenched with ETOH after TLC showed greater than 90% desired product. Dmf was removed under vacuum and the mixture was washed with sodium bicarbonate solution (5% aq., 500 mls) and extracted with ethyl acetate (2x 200 mls). A 25mm x 300mm flash column (75 grams Merck flash silica) was used for purification. Compound eluted at 80 to 85% ethyl acetate in hexanes (yield: 80% purity: >95% by ¹HNMR). Phosphoramidites were then prepared using standard protocols described above.

With phosphoramidite 17 in hand applicant synthesized several ribozymes with 2'-deoxy-2'-amino modifications. Analysis of the synthesis demonstrated coupling efficiency in 97-98% range. RNA cleavage activity of ribozymes containing 2'-deoxy-2'-amino-U modifications at U4 and/or U7 positions (see Figure 1), wherein the 2'-amino positions were either protected with Fmoc or Pht, was identical. Additionally, complete deprotection of 2'-deoxy-2'-amino-Uridine was confirmed by base-composition analysis. The coupling efficiency of phosphoramidite 17 was not effected over prolonged storage (1-2 months) at low temperatures.

Protecting 2' Position with a SEM Group

There follows a method using the 2'-(trimethylsilyl)ethoxymethyl protecting group (SEM) in the synthesis of oligoribonucleotides, and in particular those enzymatic molecules described above. For the synthesis of RNA it is important that the 2'-hydroxyl protecting group be stable throughout the various steps of the synthesis and base deprotection. At the same time, this group should also be readily removed when desired. To that end the *t*-butyldimethylsilyl group has been efficacious (Usman,N.; Ogilvie,K.K.; Jiang,M.-Y.; Cedergren,R.J. *J. Am. Chem. Soc.* 1987, 109, 7845-7854 and Scaringe,S.A.; Franklyn,C.; Usman,N. *Nucl. Acids Res.* 1990, 18, 5433-5441). However, long exposure times to tetra-*n*-butylammonium fluoride (TBAF) are generally required to fully remove this protecting group from the 2'-hydroxyl. In addition, the bulky alkyl substituents can prove to be a hindrance to coupling thereby necessitating longer coupling times. Finally, it has been shown that the TBDMS group is base labile and is partially deprotected during treatment with ethanolic ammonia (Scaringe,S.A.; Franklyn,C.; Usman,N. *Nucl. Acids Res.* 1990,

18, 5433-5441 and Stawinski,J.; Stromberg,R.; Thelin,M.; Westman,E. *Nucleic Acids Res.* 1988, 16, 9285-9298).

5 The (trimethylsilyl)ethoxymethyl ether (SEM) seems a suitable substitute. This protecting group is stable to base and all but the harshest acidic conditions. Therefore it is stable under the conditions required for oligonucleotide synthesis. It can be readily introduced and the oxygen carbon bond makes it unable to migrate. Finally, the SEM group can be removed with $\text{BF}_3 \cdot \text{OEt}_2$ very quickly.

10 There follows a method for synthesis of RNA by protecting the 2'-position of a nucleotide during RNA synthesis with a (trimethylsilyl)ethoxymethyl (SEM) group. The method can involve use of standard RNA synthesis conditions as discussed below, or any other equivalent steps. Those in the art are familiar with such steps. The nucleotide used can be any normal nucleotide or may be substituted in
15 various positions by methods well known in the art, e.g., as described by Eckstein *et al.*, *International Publication No. WO 92/07065*, Perrault *et al.*, *Nature* 1990, 344, 565-568, Pieken *et al.*, *Science* 1991, 253, 314-317, Usman,N.; Cedergren,R.J. *Trends in Biochem. Sci.* 1992, 17, 334-339, Usman *et al.*, PCT WO93/15187, and Sproat,B. *European Patent*
20 *Application 92110298.4*.

This invention also features a method for covalently linking a SEM group to the 2'-position of a nucleotide. The method involves contacting a nucleoside with an SEM-containing molecule under SEM bonding conditions. In a preferred embodiment, the conditions are dibutyltin oxide,
25 tetrabutylammonium fluoride and SEM-Cl. Those in the art, however, will recognize that other equivalent conditions can also be used.

In another aspect, the invention features a method for removal of an SEM group from a nucleoside molecule or an oligonucleotide. The method involves contacting the molecule or oligonucleotide with boron trifluoride
30 etherate ($\text{BF}_3 \cdot \text{OEt}_2$) under SEM removing conditions, e.g., in acetonitrile.

Referring to Figure 18, there is shown the method for solid phase synthesis of RNA. A 2',5'-protected nucleotide is contacted with a solid phase bound nucleotide under RNA synthesis conditions to form a dinucleotide. The protecting group (R) at the 2'-position in prior art

methods can be a silyl ether, as shown in the Figure. In the method of the present invention, an SEM group is used in place of the silyl ether. Otherwise RNA synthesis can be performed by standard methodology.

Referring to Figure 19, there is shown the synthesis of 2'-O-SEM protected nucleosides and phosphoramidites. Briefly, a 5'-protected nucleoside (1) is protected at the 2'- or 3'-position by contacting with a derivative of SEM under appropriate conditions. Specifically, those conditions include contacting the nucleoside with dibutyltin oxide and SEM chloride. The 2 regioisomers are separated by chromatography and the 2'-protected moiety is converted into a phosphoramidite by standard procedure. The 3'-protected nucleoside is converted into a succinate derivative suitable for derivatization of a solid support.

Referring to Figure 20, a prior art method for deprotection of RNA using silyl ethers is shown. This contrasts with the method shown in Figure 21 in which deprotection of RNA containing an SEM group is performed. In step 1, the base protecting groups and cyanoethyl groups are removed by standard procedure. The SEM group is then removed as shown in the Figure. The details of the synthesis of phosphoramidites and SEM protected nucleosides and their use in synthesis of oligonucleotides and subsequent deprotection of

Example 14: Synthesis of 2'-O-((trimethylsilyl)ethoxymethyl)-5'-O-Dimethoxytrityl Uridine (2)

Referring to Figure 19, 5'-O-dimethoxytrityl uridine 1 (1.0 g, 1.83 mmol) in CH₃CN (18 mL) was added dibutyltin oxide (1.0 g, 4.03 mmol) and TBAF (1 M, 2.38 mL, 2.38 mmol). The mixture was stirred for 2 h at RT (about 20-25°C) at which time (trimethylsilyl)ethoxymethyl chloride (SEM-Cl) (487 µL, 2.75 mmol) was added. The reaction mixture was stirred overnight and then filtered and evaporated. Flash chromatography (30% hexanes in ethyl acetate) yielded 347 mg (28.0%) of 2'-hydroxyl protected nucleoside 2 and 314 mg (25.3%) of 3'-hydroxyl protected nucleoside 3.

Example 15: Synthesis of 2'-O-((trimethylsilyl)ethoxymethyl) Uridine (4)

Nucleoside 2 was detritylated following standard methods, as shown in Figure 19.

Example 16: Synthesis of 2'-O-((trimethylsilyl)ethoxymethyl)-5',3'-O-Acetyl Uridine (5)

Nucleoside 4 was acetylated following standard methods, as shown in Figure 19.

5 Example 17: Synthesis of 5',3'-O-Acetyl Uridine (6)

Referring to Figure 19, the fully protected uridine 5 (32 mg, 0.07 mmol) was dissolved in CH₃CN (700 µL) and BF₃•OEt₂ (17.5 µL, 0.14 mmol) was added. The reaction was stirred 15 m and MeOH was added to quench the reaction. Flash chromatography (5% MeOH in CH₂Cl₂) gave
10 20 mg (88%) of SEM deprotected nucleoside 6.

Example 18: Synthesis of 2'-O-((trimethylsilyl)ethoxymethyl)-3'-O-Succinyl-5'-O-Dimethoxytrityl Uridine (2)

Nucleoside 3 was succinylated and coupled to the support following standard procedures, as shown in Figure 19.

15 Example 19: Synthesis of 2'-O-((trimethylsilyl)ethoxymethyl)-5'-O-Dimethoxytrityl Uridine 3'-(2-Cyanoethyl N,N-diisopropylphosphoramidite) (8)

Nucleoside 3 was phosphitylated following standard methods, as shown in Figure 19.

20 Example 20: Synthesis of RNA Using 2'-O-SEM Protection

Referring to Figure 18, the method of synthesis used follows the general procedure for RNA synthesis as described in Usman,N.; Ogilvie,K.K.; Jiang,M.-Y.; Cedergren,R.J. *J. Am. Chem. Soc.* 1987, 109, 7845-7854 and in Scaringe,S.A.; Franklyn,C.; Usman,N. *Nucl. Acids Res.*
25 1990, 18, 5433-5441. The phosphoramidite 8 was coupled following standard RNA methods to provide a 10-mer of uridylic acid. Syntheses were conducted on a 394 (ABI) synthesizer using a modified 2.5 µmol scale protocol with a 10 m coupling step. A thirteen-fold excess (325 µL of 0.1 M = 32.5 µmol) of phosphoramidite and a 80-fold excess of tetrazole
30 (400 µL of 0.5 M = 200 µmol) relative to polymer-bound 5'-hydroxyl was used in each coupling cycle. Average coupling yields on the 394, determined by colorimetric quantitation of the trityl fractions, were 98-99%. Other oligonucleotide synthesis reagents for the 394: Detritylation solution was 2% TCA in methylene chloride; capping was performed with 16% N-

Methyl imidazole in THF and 10% acetic anhydride/10% 2,6-lutidine in THF; oxidation solution was 16.9 mM I₂, 49 mM pyridine, 9% water in THF. Fisher Synthesis Grade acetonitrile was used directly from the reagent bottle.

- 5 Referring to Figure 21, the homopolymer was base deprotected with NH₃/EtOH at 65 °C. The solution was decanted and the support was washed twice with a solution of 1:1:1 H₂O:CH₃CN:MeOH. The combined solutions were dried down and then diluted with CH₃CN (1 mL). BF₃•OEt₂ (2.5 μL, 30 μmol) was added to the solution and aliquots were removed at
10 ten time points. The results indicate that after 30 min deprotection is complete, as shown in Figure 22.

III. Vectors Expressing Ribozymes

- There follows a method for expression of a ribozyme in a bacterial or eucaryotic cell, and for production of large amounts of such a ribozyme. In
15 general, the invention features a method for preparing multi-copy cassettes encoding a defined ribozyme structure for production of a ribozyme at a decreased cost. A vector is produced which encodes a plurality of ribozymes which are cleaved at their 3' and 5' ends from an RNA transcript produced from the vector by only one other ribozyme. The system is useful
20 for scaling up production of a ribozyme, which may be either modified or unmodified, *in situ* or *in vitro*. Such vector systems can be used to express a desired ribozyme in a specific cell, or can be used in an *in vitro* system to allow production of large amounts of a desired ribozyme. The vectors of this invention allow a higher yield synthesis of a ribozyme in the form of an
25 RNA transcript which is cleaved *in situ* or *in vitro* before or after transcript isolation.

- Thus, this invention is distinct from the prior art in that a single ribozyme is used to process the 3' and 5' ends of each therapeutic, trans-acting or desired ribozyme instead of processing only one end, or only one
30 ribozyme. This allows smaller vectors to be derived with multiple trans-acting ribozymes released by only one other ribozyme from the mRNA transcript. Applicant has also provided methods by which the activity of such ribozymes is increased compared to those in the art, by designing ribozyme-encoding vectors and the corresponding transcript such that

folding of the mRNA does not interfere with processing by the releasing ribozyme.

The stability of the ribozyme produced in this method can be enhanced by provision of sequences at the termini of the ribozymes as described by Draper et al., PCT WO 93/23509, hereby incorporated by reference herein.

The method of this invention is advantageous since it provides high yield synthesis of ribozymes by use of low cost transcription-based protocols, compared to existing chemical ribozyme synthesis, and can use isolation techniques currently used to purify chemically synthesized oligonucleotides. Thus, the method allows synthesis of ribozymes in high yield at low cost for analytical, diagnostic, or therapeutic applications.

The method is also useful for synthesis of ribozymes *in vitro* for ribozyme structural studies, enzymatic studies, target RNA accessibility studies, transcription inhibition studies and nuclease protection studies, much is described by Draper et al., PCT WO 93/23509 hereby incorporated by reference herein.

The method can also be used to produce ribozymes *in situ* either to increase the intracellular concentration of a desired therapeutic ribozyme, or to produce a concatameric transcript for subsequent *in vitro* isolation of unit length ribozyme. The desired ribozyme can be used to inhibit gene expression in molecular genetic analyses or in infectious cell systems, and to test the efficacy of a therapeutic molecule or treat afflicted cells.

Thus, in general, the invention features a vector which includes a bacterial, viral or eucaryotic promoter within a plasmid, cosmid, phagmid, virus, viroid, virusoid or phage vector. Other vectors are equally suitable and include double-stranded, or partially double-stranded DNA, formed by an amplification method such as the polymerase chain reaction, or double-stranded, partially double-stranded or single-stranded RNA, formed by site-directed homologous recombination into viral or viroid RNA genomes. Such vectors need not be circular. Transcriptionally linked to the promoter region is a first ribozyme-encoding region, and nucleotide sequences encoding a ribozyme cleavage sequence which is placed on either side of a region encoding a therapeutic or otherwise desired second ribozyme.

Suitable restriction endonuclease sites can be provided to ease construction of this vector in DNA vectors or in requisite DNA vectors of an RNA expression system. The desired second ribozyme may be any desired type of ribozyme, such as a hammerhead, hairpin, hepatitis delta virus (HDV) or other catalytic center, and can include group I and group II introns, as discussed above. The first ribozyme is chosen to cleave the encoded cleavage sequence, and may also be any desired ribozyme, for example, a *Tetrahymena* derived ribozyme, which may, for example, include an imbedded restriction endonuclease site in the center of a self-recognition sequence to aid in vector construction. This endonuclease site is useful for construction of the vector, and subsequent analysis of the vector.

When the promoter of such a vector is activated an RNA transcript is produced which includes the first and second ribozyme sequences. The first ribozyme sequence is able to act, under appropriate conditions, to cause cleavage at the cleavage sites to release the second ribozyme sequences. These second ribozyme sequences can then act at their target RNA sites, or can be isolated for later use or analysis.

Thus, in one aspect the invention features a vector which includes a first nucleic acid sequence (encoding a first ribozyme having intramolecular cleaving activity), and a second nucleic acid sequence (encoding a second ribozyme having intermolecular cleaving enzymatic activity) flanked by nucleic acid sequences encoding RNA which is cleaved by the first ribozyme to release the second ribozyme from the RNA transcript encoded by the vector. The second ribozyme may be flanked by the first ribozyme either on the 5' side or 3' side. If desired, the first ribozyme may be encoded on a separate vector and may have intermolecular cleaving activity.

As discussed above, the first ribozyme can be chosen to be any self-cleaving ribozyme, and the second ribozyme may be chosen to be any desired ribozyme. The flanking sequences are chosen to include sequences recognized by the first ribozyme. When the vector is caused to express RNA from these nucleic acid sequences, that RNA has the ability under appropriate conditions to cleave each of the flanking regions and thereby release one or more copies of the second ribozyme. If desired, several different second ribozymes can be produced by the same vector, or

but includes the modifications of Been et al., 1992 (Biochemistry 31, 11843) in which cis-cleavage activity of the ribozyme was improved by the substitution of a shortened helix 4 for a wild-type stem-loop (Figure 25).

5 To prepare DNA inserts that encode self-processing ribozyme cassettes, partially overlapping top- and bottom-strand oligonucleotides (60-90 nucleotides) were designed to include sequences for the T7 promoter, the trans-acting ribozyme, the cis-cleaving ribozyme and appropriate restriction sites for use in cloning (see Fig. 26). The single-strand portions of annealed oligonucleotides were converted to double-
10 strands using Sequenase® (U.S. Biochemicals). Insert DNA was ligated into *EcoRI/HindIII*-digested puc18 and transformed into *E. coli* strain DH5 α using standard protocols (Maniatis et al., 1982 in Molecular Cloning Cold Spring Harbor Press). The identity of positive clones was confirmed by sequencing small-scale plasmid preparations.

15 Larger scale preparations of plasmid DNA for use as *in vitro* transcription templates and in transactions were prepared using the protocol and columns from QIAGEN Inc. (Studio City, CA) except that an additional ethanol precipitation was included as the final step.

Example 22: RNA Processing *in vitro*

20 Transcription reactions containing linear plasmid templates were carried out essentially as described (Milligan & Uhlenbeck, 1989 Supra; Chowrira & Burke, 1991 Supra). In order to prepare 5' end-labeled transcripts, standard transcription reactions were carried out in the presence of 10-20 μ Ci [γ -³²P]GTP, 200 μ M each NTP and 0.5 to 1 μ g of
25 linearized plasmid template. The concentration of MgCl₂ was maintained at 10 mM above the total nucleotide concentration.

To compare the ability of the different ribozyme cassettes to self-process *in vitro*, each construct was transcribed and allowed to undergo self-processing under identical conditions at 37°C. For these comparisons,
30 equal amounts of linearized DNA templates bearing the various ribozyme cassettes were transcribed in the presence of [γ -³²P]GTP to generate 5' end-labeled transcripts. In this manner only the full-length, unprocessed transcripts and the released trans-ribozymes are visualized by autoradiography. In all reactions, Mg²⁺ was included at 10 mM above the
35 nucleotide concentration so that cleavage by all the ribozyme cassettes

would be supported. Transcription templates were linearized at several positions by digestion with different restriction enzymes so that self-processing in the presence of increasing lengths of downstream sequence could be compared (see Fig. 26). The resulting transcripts have either 4-5 non-ribozyme nucleotides at the 3' end (*HindIII*-digested template), 220 nucleotides (*NdeI* digested templates) or 454 nucleotides of downstream sequence (*RcaI* digested template).

As shown in Figure 27, all four ribozyme cassettes are capable of self-processing and yield RNA products of expected sizes. Two nucleotides essential for hammerhead ribozyme activity (Ruffner et al., 1990 *supra*) have been changed in the HH(mutant) core sequence (see Figure 23) and so this transcript is unable to undergo self-processing (Fig. 27). This is evidenced by the lack of a released 5' RNA in the HH(mutant), although the full-length RNAs are present. Comparison of the amounts of released trans-ribozyme (Fig. 27) indicate that there are differences in the ability of these ribozymes to self-process *in vitro*, especially with respect to the presence of downstream sequence. For the two HP constructs, it is clear that HP(GC) is more efficient than the HP(GU) ribozyme, both in the presence and in the absence of extra downstream sequence. In addition, the activity of HP(GU) falls off more dramatically when downstream sequence is present. The stronger G:C base pair likely contributes to the HP(GC) construct's ability to fold correctly (and/or more quickly) into the productive structure, even when as much as 216 extra nucleotides are present downstream. The HH ribozyme construct is also quite efficient at self-processing, and slightly better than the HP(GU) construct even when downstream sequence is present.

Of the three ribozyme motifs, the presence of extra downstream sequence seems to most affect the efficiency of HDV. When no extra sequence is present downstream, HDV is quite efficient and self-processes to approximately the same level as the HH and HP(GC) cassettes. However, when extra downstream sequence is present, the self-processing activity seems to decrease almost as dramatically as is seen with the (sub-optimal) HP(GU) cassette.

Example 23: Kinetics of self-processing reaction

*Hind*III-digested template (250 ng) was used in a standard transcription reaction mixture containing: 50 mM Tris-HCl pH 8.3; 1 mM ATP, GTP and UTP; 50 μ M CTP; 40 μ Ci [α -³²P]CTP; 12 mM MgCl₂; 10 mM DTT. The transcription/self-processing reaction was initiated by the addition of T7 RNA polymerase (15 U/ μ l). Aliquots of 5 μ l were taken at regular time intervals and the reaction was stopped by adding an equal volume of 2x formamide loading buffer (95% formamide, 15 mM EDTA, & dyes) and freezing on dry ice. The samples were resolved on a 10% polyacrylamide sequencing gel and results were quantitated by PhosphorImager (Molecular Dynamics, Sunnyvale, CA). Ribozyme self-cleavage rates were determined from non-linear, least-squares fits (KaleidaGraph, Synergy Software, Reading, PA) of the data to the equation:

$$(\text{Fraction Uncleaved Transcript}) = \frac{1}{kt} (1 - e^{-kt})$$

where *t* represents time and *k* represents the unimolecular rate constant for cleavage (Long & Uhlenbeck, 1994 Proc. Natl. Acad. Sci. USA 91, 6977).

Linear templates were prepared by digesting the plasmids with *Hind*III so that transcripts will contain only four to five vector-derived nucleotides at the 3' end (see Figure 23-25). By comparison of the unimolecular rate constant (*k*) determined for each construct, it is clear that HH is the most efficient at self-processing (Table 44). The HH transcript self-processes 2-fold faster than HDV and 3-fold faster than HP(GC) transcripts. Although the HP(GU) RNA undergoes self-processing, it is at least 6-fold slower than the HP(GC) construct. This is consistent with previous observations that the stability of helix 2 is essential for self-processing and trans-cleavage activity of the hairpin ribozyme (Hampel et al., 1990 supra; Chowrira & Burke, 1991 supra). The rate of HH self-cleavage during transcription measured here (1.2 min⁻¹) is similar to the rate measured by Long and Uhlenbeck 1994 supra using a HH that has a different stem I and stem III. Self-processing rates during transcription for HP and HDV have not been previously reported. However, self-processing of the HDV ribozyme—as measured here during transcription—is significantly slower than when tested after isolation from a denaturing gel (Been et al., 1992 supra). This decrease likely reflects the difference in protocol as well as the presence of 5' flanking sequence in the HDV construct used here.

Example 24: Effect of downstream sequences on trans-cleavage *in vitro*

Transcripts containing the trans ribozyme with or without 3' flanking sequences were assayed for their ability to cleave their target *in trans*. To this end, transcripts from three templates were resolved on a preparative gel and bands corresponding both to processed trans-acting ribozymes from the HH transcription reaction, and to full-length HH(mutant) and Δ HDV transcripts were isolated. In all three transcripts the trans-acting ribozyme portion is identical with the exception of sequences at their 3' ends. The HH trans-acting ribozyme contains only an additional UC at its 3' end, while HH(mutant) and Δ HDV have 52 and 37 nucleotides, respectively, at their 3' ends. A 622 nucleotide, internally-labeled target RNA was incubated, under ribozyme excess conditions, along with the three ribozyme transcripts in a standard reaction buffer.

To make internally-labeled substrate RNA for trans-ribozyme cleavage reactions, a 622 nt region (containing hammerhead site P) was synthesized by PCR using primers that place the T7 RNA promoter upstream of the amplified sequence. Target RNA was transcribed in a standard transcription buffer in the presence of [α -³²P]CTP (Chowrira & Burke, 1991 *supra*). The reaction mixture was treated with 15 units of ribonuclease-free DNaseI, extracted with phenol followed by chloroform:isoamyl alcohol (25:1), precipitated with isopropanol and washed with 70% ethanol. The dried pellet was resuspended in 20 μ l DEPC-treated water and stored at -20°C.

Unlabeled ribozyme (1 μ M) and internally labeled 622 nt substrate RNA (<10 nM) were denatured and renatured separately in a standard cleavage buffer (containing 50 mM Tris-HCl pH 7.5 and 10 mM MgCl₂) by heating to 90°C for 2 min. and slow cooling to 37°C for 10 min. The reaction was initiated by mixing the ribozyme and substrate mixtures and incubating at 37°C. Aliquots of 5 μ l were taken at regular time intervals, quenched by adding an equal volume of 2X formamide gel loading buffer and frozen on dry ice. The samples were resolved on 5% polyacrylamide sequencing gel and results were quantitatively analyzed by radioanalytic imaging of gels with a PhosphorImager[®] (Molecular Dynamics, Sunnyvale, CA).

The HH trans-acting ribozyme cleaves the target RNA approximately 10-fold faster than the Δ HDV transcript and greater than 20-fold faster than

the HH(mutant) transcript (Figure 28). The additional nucleotides at the end of HH(mutant) form 7 base-pairs with the 3' target-binding arm of the trans-acting ribozyme (Figure 23). This interaction must be disrupted (at a cost of 6 kcal/mole) to make the trans-acting ribozyme available for binding the target sequence. In contrast, the additional nucleotides at the end of Δ HDV were not designed to form any strong, alternative base-pairing with the trans-ribozyme. Nevertheless, the Δ HDV sequences are predicted to form multiple structures involving the 3' target-binding arm of the trans ribozyme that have stabilities ranging from 1-2 kcal/mole. Thus, the observed reductions in activity for the Δ HDV and HH(mutant) constructs are consistent with the predicted folded structures, and it reinforces the view that the flanking sequences can decrease the catalytic efficiency of a ribozyme through nonproductive interactions with either the ribozyme or the substrate or both.

Example 25: RNA self-processing *in vivo*

Since three of the constructs (HH, HDV and HP(GC)) self-process efficiently in solution, the affect of the mammalian cellular milieu on ribozyme self-processing was next explored by applicant. A transient expression system was employed to investigate ribozyme activity *in vivo*. A mouse cell line (OST7-1) that constitutively expresses T7 RNA polymerase in the cytoplasm was chosen for this study (Elroy-Stein and Moss, 1990 Proc. Natl. Acad. Sci. USA 87, 6743). In these cells plasmids containing a ribozyme cassette downstream of the T7 promoter will be transcribed efficiently in the cytoplasm (Elroy-Stein & Moss, 1990 supra).

Monolayers of a mouse L9 fibroblast cell line (OST7-1; Elroy-Stein and Moss, 1990 supra) were grown in 6-well plates with $\sim 5 \times 10^5$ cells/well. Cells were transfected with circular plasmids (5 μ g/well) using the calcium phosphate-DNA precipitation method (Maniatis et al., 1982 supra). Cells were lysed (4 hours post-transfection) by the addition of standard lysis buffer (200 μ l/well) containing 4M guanadinium isothiocyanate, 25 mM sodium citrate (pH 7.0), 0.5% sarkosyl (Chomczynski and Sacchi, 1987 Anal. Biochem. 162, 156), and 50 mM EDTA pH 8.0. The lysate was extracted once with water-saturated phenol followed by one extraction with chloroform:isoamyl alcohol (25:1). Total cellular RNA was precipitated with an equal volume of isopropanol. The RNA pellet was resuspended in 0.2

M ammonium acetate and reprecipitated with ethanol. The pellet was then washed with 70% ethanol and resuspended in DEPC-treated water.

Purified cellular RNA (3 µg/reaction) was first denatured in the presence of a 5' end-labeled DNA primer (100 pmol) by heating to 90°C for 2 min. in the absence of Mg²⁺, and then snap-cooling on ice for at least 15 min. This protocol allows for efficient annealing of the primer to its complementary RNA sequence. The primer was extended using Superscript II reverse transcriptase (8 U/µl; BRL) in a buffer containing 50 mM Tris-HCl pH 8.3; 10 mM DTT; 75 mM KCl; 1 mM MgCl₂; 1 mM each dNTP. The extension reaction was carried out at 42°C for 10 min. The reaction was terminated by adding an equal volume of 2x formamide gel loading buffer and freezing on crushed dry ice. The samples were resolved on a 10% polyacrylamide sequencing gel. The primer sequences are as follows: HH primer, 5'-CTCCAGTTTCGAGCTTT-3'; HDV primer, 5'-AAGTAGCCCAGGTCGGACC-3'; HP primer, 5'-ACCAGGTAATATACCACAAC-3'.

As shown in Figure 29, specific bands corresponding to full-length precursor RNA and 3' cleavage products were detected from cells transfected with the self-processing cassettes. All three constructs, in addition to being transcriptionally active, appear to self-process efficiently in the cytoplasm of OST7-1 cells. In particular, the HH and HP(GC) constructs self-process to greater than 95%. The overall extent of self-processing in OST7-1 cells appears to be strikingly similar to the extent of self-processing *in vitro* (Figure 29 "In Vitro +MgCl₂" vs. "Cellular").

Consistent with the *in vitro* self-processing results, the HP(GU) cassette self-processed to approximately 50% in OST7-1 cells. As expected, transfection with plasmids containing the HH(mutant) cassette yielded a primer-extension product corresponding to the full-length RNA with no detectable cleavage products (Figure 29). The latter result strongly suggests that the primer extension band corresponding to the 3' cleavage product is not an artifact of reverse transcription.

Applicant was concerned with the possibility that RNA self-processing might occur during cell lysis, RNA isolation and /or the primer extension assay. Two precautions were taken to exclude this possibility. First, 50 mM EDTA was included in the lysis buffer. EDTA is a strong chelator of divalent

metal ions such as Mg^{2+} and Ca^{2+} that are necessary for ribozyme activity. Divalent metal ions are therefore unavailable to self-processing RNAs following cell lysis. A second precaution involved using primers in the primer-extension assay that were designed to hybridize to essential regions of the processing ribozyme. Binding of these primers should prevent the 3' cis-acting ribozymes from folding into the conformation essential for catalytic activity.

Two experiments were carried out to further eliminate the possibility that self-processing is occurring either during RNA preparations or during the primer extension analysis. The first experiment involves primer extension analysis on full-length precursor RNAs that were added to non-transfected OST7-1 lysates after cell lysis. Thus, only if self-processing is occurring at some point after lysis would cleavage products be detected. Full-length precursor RNAs were prepared by transcribing under conditions of low Mg^{2+} (5 mM) and high NTP concentration (total 12 mM) in an attempt to eliminate the free Mg^{2+} required for the self-processing reaction (Michel et al. 1992 *Genes & Dev.* 6, 1373). The full-length precursor RNAs were gel-purified, and a known amount was added to lysates of non-transfected OST7-1 cells. RNA was purified from these lysates and incubated for 1 hr in DEPC-treated water at 37° C prior to the standard primer extension analysis (Figure 29, *in vitro* "-MgCl₂" control). The predominant RNA detected in all cases corresponds to the primer extension product of full-length precursor RNAs. If, instead, the purified RNA containing the full-length precursor is incubated in 10 mM MgCl₂ prior to the primer extension analysis, most or all of the RNA detected by primer extension analysis undergoes cleavage (Figure 29, *in vitro* "+MgCl₂" control). These results indicate that the standard RNA isolation and primer extension protocols used here do not provide a favorable environment for RNA self-processing, even though the RNA in question is inherently able to undergo self-cleavage.

In a second experiment to demonstrate lack of self-processing during work up, internally-labeled precursor RNAs were prepared and added to non-transfected OST7-1 lysates as in the previous control. The internally-labeled precursor RNAs were carried through the RNA purification and primer extension reactions (in the presence of unlabeled primers) and analyzed to determine the extent of self-processing. By this analysis, the

vast majority of the added full-length RNA remained intact during the entire process of RNA isolation and primer extension.

These two control experiments validate the protocols used and support applicant's conclusion that the self-processing reactions catalyzed by HH, HDV and HP(GC) cassettes are occurring in the cytoplasm of OST7-1 cells.

Sequences in figures 23 through 25 are meant to be non-limiting examples. Those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art.

In addition, those in the art will recognize that Applicant provides guidance through the above examples as to how to best design vectors of this invention so that secondary structure of the mRNA allows efficient cleavage by releasing ribozymes. Thus, the specific constructs are not limiting in this invention. Such constructs can be readily tested as described above for such secondary structure, either by computer folding algorithms or empirically. Such constructs will then allow at least 80% completion of release of ribozymes, which can be readily determined as described above or by methods known in the art. That is, any such secondary structure in the RNA does not reduce release of the ribozymes by more than 20%.

IV. Ribozymes Expressed by RNA Polymerase III

Applicant has determined that the level of production of a foreign RNA, using a RNA polymerase III (pol III) based system, can be significantly enhanced by ensuring that the RNA is produced with the 5' terminus and a 3' region of the RNA molecule base-paired together to form a stable intramolecular stem structure. This stem structure is formed by hydrogen bond interactions (either Watson-Crick or non-Watson-Crick) between nucleotides in the 3' region (at least 8 bases) and complementary nucleotides in the 5' terminus of the same RNA molecule.

Although the example provided below involves a type 2 pol III gene unit, a number of other pol III promoter systems can also be used, for example, tRNA (Hall et al., 1982 *Cell* 29, 3-5), 5S RNA (Nielsen et al., 1993, *Nucleic Acids Res.* 21, 3631-3636), adenovirus VA RNA (Fowlkes and Shenk, 1980 *Cell* 22, 405-413), U6 snRNA (Gupta and Reddy, 1990

Nucleic Acids Res. 19, 2073-2075), vault RNA (Kickoefer et al., 1993 *J. Biol. Chem.* 268, 7868-7873), telomerase RNA (Romero and Blackburn, 1991 *Cell* 67, 343-353), and others.

5 The construct described in this invention is able to accumulate RNA to a significantly higher level than other constructs, even those in which 5' and 3' ends are involved in hairpin loops. Using such a construct the level of expression of a foreign RNA can be increased to between 20,000 and 50,000 copies per cell. This makes such constructs, and the vectors encoding such constructs, excellent for use in decoy, therapeutic editing
10 and antisense protocols as well as for ribozyme formation. In addition, the molecules can be used as agonist or antagonist RNAs (affinity RNAs). Generally, applicant believes that the intramolecular base-paired interaction between the 5' terminus and the 3' region of the RNA should be in a double-stranded structure in order to achieve enhanced RNA
15 accumulation.

Thus, in one preferred embodiment the invention features a pol III promoter system (e.g., a type 2 system) used to synthesize a chimeric RNA molecule which includes tRNA sequences and a desired RNA (e.g., a tRNA-based molecule).

20 The following exemplifies this invention with a type 2 pol III promoter and a tRNA gene. Specifically to illustrate the broad invention, the RNA molecule in the following example has an A box and a B box of the type 2 pol III promoter system and has a 5' terminus or region able to base-pair with at least 8 bases of a complementary 3' end or region of the same RNA
25 molecule. This is meant to be a specific example. Those in the art will recognize that this is but one example, and other embodiments can be readily generated using other pol III promoter systems and techniques generally known in the art.

30 By "terminus" is meant the terminal bases of an RNA molecule, ending in a 3' hydroxyl or 5' phosphate or 5' cap moiety. By "region" is meant a stretch of bases 5' or 3' from the terminus that are involved in base-paired interactions. It need not be adjacent to the end of the RNA. Applicant has determined that base pairing of at least one end of the RNA molecule with a region not more than about 50 bases, and preferably only 20 bases, from

the other end of the molecule provides a useful molecule able to be expressed at high levels.

By "3' region" is meant a stretch of bases 3' from the terminus that are involved in intramolecular base-paired interaction with complementary nucleotides in the 5' terminus of the same molecule. The 3' region can be designed to include the 3' terminus. The 3' region therefore is ≥ 0 nucleotides from the 3' terminus. For example, in the S35 construct described in the present invention (Fig. 40) the 3' region is one nucleotide from the 3' terminus. In another example, the 3' region is ~ 43 nt from 3' terminus. These examples are not meant to be limiting. Those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. Generally, it is preferred to have the 3' region within 100 bases of the 3' terminus.

By "tRNA molecule" is meant a type 2 pol III driven RNA molecule that is generally derived from any recognized tRNA gene. Those in the art will recognize that DNA encoding such molecules is readily available and can be modified as desired to alter one or more bases within the DNA encoding the RNA molecule and/or the promoter system. Generally, but not always, such molecules include an A box and a B box that consist of sequences which are well known in the art (and examples of which can be found throughout the literature). These A and B boxes have a certain consensus sequence which is essential for a optimal pol III transcription.

By "chimeric tRNA molecule" is meant a RNA molecule that includes a pol III promoter (type 2) region. A chimeric tRNA molecule, for example, might contain an intramolecular base-paired structure between the 3' region and complementary 5' terminus of the molecule, and includes a foreign RNA sequence at any location within the molecule which does not affect the activity of the type 2 pol III promoter boxes. Thus, such a foreign RNA may be provided at the 3' end of the B box, or may be provided in between the A and the B box, with the B box moved to an appropriate location either within the foreign RNA or another location such that it is effective to provide pol III transcription. In one example, the RNA molecule may include a hammerhead ribozyme with the B box of a type 2 pol III promoter provided in stem II of the ribozyme. In a second example, the B box may be provided in stem IV region of a hairpin ribozyme. A specific example of such RNA molecules is provided below. Those in the art will

recognize that this is but one example, and other embodiments can be readily generated using techniques generally known in the art.

By "desired RNA" molecule is meant any foreign RNA molecule which is useful from a therapeutic, diagnostic, or other viewpoint. Such molecules include antisense RNA molecules, decoy RNA molecules, enzymatic RNA, therapeutic editing RNA and agonist and antagonist RNA.

By "antisense RNA" is meant a non-enzymatic RNA molecule that binds to another RNA (target RNA) by means of RNA-RNA interactions and alters the activity of the target RNA (Eguchi et al., 1991 *Annu. Rev. Biochem.* 60, 631-652). By "enzymatic RNA" is meant an RNA molecule with enzymatic activity (Cech, 1988 *J. American. Med. Assoc.* 260, 3030-3035). Enzymatic nucleic acids (ribozymes) act by first binding to a target RNA. Such binding occurs through the target binding portion of an enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA.

By "decoy RNA" is meant an RNA molecule that mimics the natural binding domain for a ligand. The decoy RNA therefore competes with natural binding target for the binding of a specific ligand. For example, it has been shown that over-expression of HIV trans-activation response (TAR) RNA can act as a "decoy" and efficiently binds HIV *tat* protein, thereby preventing it from binding to TAR sequences encoded in the HIV RNA (Sullenger et al., 1990 *Cell* 63, 601-608). This is meant to be a specific example. Those in the art will recognize that this is but one example, and other embodiments can be readily generated using techniques generally known in the art.

By "therapeutic editing RNA" is meant an antisense RNA that can bind to its cellular target (RNA or DNA) and mediate the modification of a specific base.

By "agonist RNA" is meant an RNA molecule that can bind to protein receptors with high affinity and cause the stimulation of specific cellular pathways.

By "antagonist RNA" is meant an RNA molecule that can bind to cellular proteins and prevent it from performing its normal biological function (for example, see Tsai et al., 1992 *Proc. Natl. Acad. Sci. USA* 89, 8864-8868).

- 5 In other aspects, the invention includes vectors encoding RNA molecules as described above, cells including such vectors, methods for producing the desired RNA, and use of the vectors and cells to produce this RNA.

- 10 Thus, the invention features a transcribed non-naturally occurring RNA molecule which includes a desired therapeutic RNA portion and an intramolecular stem formed by base-pairing interactions between a 3' region and complementary nucleotides at the 5' terminus in the RNA. The stem preferably includes at least 8 base pairs, but may have more, for example, 15 or 16 base pairs.

- 15 In preferred embodiments, the 5' terminus of the chimeric tRNA includes a portion of the precursor molecule of the primary tRNA molecule, of which ≥ 8 nucleotides are involved in base-pairing interaction with the 3' region; the chimeric tRNA contains A and B boxes; natural sequences 3' of the B box are deleted, which prevents endogenous RNA processing; the
20 desired RNA molecule is at the 3' end of the B box; the desired RNA molecule is between the A and the B box; the desired RNA molecule includes the B box; the desired RNA molecule is selected from the group consisting of antisense RNA, decoy RNA, therapeutic editing RNA, enzymatic RNA, agonist RNA and antagonist RNA; the molecule has an
25 intramolecular stem resulting from a base-paired interaction between the 5' terminus of the RNA and a complementary 3' region within the same RNA, and includes at least 8 bases; and the 5' terminus is able to base pair with at least 15 bases of the 3' region.

- 30 In most preferred embodiments, the molecule is transcribed by a RNA polymerase III based promoter system, e.g., a type 2 pol III promoter system; the molecule is a chimeric tRNA, and may have the A and B boxes of a type 2 pol III promoter separated by between 0 and 300 bases; DNA vector encoding the RNA molecule of claim 51.

In other related aspects, the invention features an RNA or DNA vector encoding the above RNA molecule, with the portions of the vector encoding the RNA functioning as a RNA pol III promoter; or a cell containing the vector ; or a method to provide a desired RNA molecule in a cell, by
5 introducing the molecule into a cell with an RNA molecule as described above. The cells can be derived from animals, plants or human beings.

In order for RNA-based gene therapy approaches to be effective, sufficient amounts of the therapeutic RNA must accumulate in the appropriate intracellular compartment of the treated cells. Accumulation is
10 a function of both promoter strength of the antiviral gene, and the intracellular stability of the antiviral RNA. Both RNA polymerase II (pol II) and RNA polymerase III (pol III) based expression systems have been used to produce therapeutic RNAs in cells (Sarver & Rossi, 1993 *AIDS Res. & Human Retroviruses* 9, 483-487; Yu et al., 1993 *P.N.A.S.(USA)* 90, 6340-
15 6344). However, pol III based expression cassettes are theoretically more attractive for use in expressing antiviral RNAs for the following reasons. Pol II produces messenger RNAs located exclusively in the cytoplasm, whereas pol III produces functional RNAs found in both the nucleus and the cytoplasm. Pol II promoters tend to be more tissue restricted, whereas pol
20 III genes encode tRNAs and other functional RNAs necessary for basic "housekeeping" functions in all cell types. Therefore, pol III promoters are likely to be expressed in all tissue types. Finally, pol III transcripts from a given gene accumulate to much greater levels in cells relative to pol II genes.

25 Intracellular accumulation of therapeutic RNAs is also dependent on the method of gene transfer used. For example, the retroviral vectors presently used to accomplish stable gene transfer, integrate randomly into the genome of target cells. This random integration leads to varied expression of the transferred gene in individual cells comprising the bulk
30 treated cell population. Therefore, for maximum effectiveness, the transferred gene must have the capacity to express therapeutic amounts of the antiviral RNA in the entire treated cell population, regardless of the integration site.

Pol III System

The following is just one non-limiting example of the invention. A pol III based genetic element derived from a human tRNAⁱmet gene and termed $\Delta 3-5$ (Fig. 33; Adeniyi-Jones et al., 1984 *supra*), has been adapted to express antiviral RNAs (Sullenger et al., 1990 *Mol. Cell. Biol.* 10, 6512-6523). This element was inserted into the DC retroviral vector (Sullenger et al., 1990 *Mol. Cell. Biol.* 10, 6512-6523) to accomplish stable gene transfer, and used to express antisense RNAs against moloney murine leukemia virus and anti-HIV decoy RNAs (Sullenger et al., 1990 *Mol. Cell. Biol.* 10, 6512-6523; Sullenger et al., 1990 *Cell* 63, 601-608; Sullenger et al., 1991 *J. Virol.* 65, 6811-6816; Lee et al., 1992 *The New Biologist* 4, 66-74). Clonal lines are expanded from individual cells present in the bulk population, and therefore express similar amounts of the therapeutic RNA in all cells. Development of a vector system that generates therapeutic levels of therapeutic RNA in all treated cells would represent a significant advancement in RNA based gene therapy modalities.

Applicant examined hammerhead (HHI) ribozyme (RNA with enzymatic activity) expression in human T cell lines using the $\Delta 3-5$ vector system (These constructs are termed " $\Delta 3-5$ /HHI"; Fig. 34). On average, ribozymes were found to accumulate to less than 100 copies per cell in the bulk T cell populations. In an attempt to improve expression levels of the $\Delta 3-5$ chimera, the applicant made a series of modified $\Delta 3-5$ gene units containing enhanced promoter elements to increase transcription rates, and inserted structural elements to improve the intracellular stability of the ribozyme transcripts (Fig. 34). One of these modified gene units, termed S35, gave rise to more than a 100-fold increase in ribozyme accumulation in bulk T cell populations relative to the original $\Delta 3-5$ /HHI vector system. Ribozyme accumulation in individual clonal lines from the pooled T cell populations ranged from 10 to greater than 100 fold more than those achieved with the original $\Delta 3-5$ /HHI version of this vector.

The S35 gene unit may be used to express other therapeutic RNAs including, but not limited to, ribozymes, antisense, decoy, therapeutic editing, agonist and antagonist RNAs. Application of the S35 gene unit would not be limited to antiviral therapies, but also to other diseases, such as cancer, in which therapeutic RNAs may be effective. The S35 gene unit may be used in the context of other vector systems besides retroviral

vectors, including but not limited to, other stable gene transfer systems such as adeno-associated virus (AAV; Carter, 1992 *Curr. Opin. Genet. Dev.* 3, 74), as well as transient vector systems such as plasmid delivery and adenoviral vectors (Berkner, 1988 *BioTechniques* 6, 616-629).

- 5 As described below, the S35 vector encodes a truncated version of a tRNA wherein the 3' region of the RNA is base-paired to complementary nucleotides at the 5' terminus, which includes the 5' precursor portion that is normally processed off during tRNA maturation. Without being bound by any theory, Applicant believes this feature is important in the level of
10 expression observed. Thus, those in the art can now design equivalent RNA molecules with such high expression levels. Below are provided examples of the methodology by which such vectors and tRNA molecules can be made.

Δ 3-5 Vectors

- 15 The use of a truncated human tRNA^{i^{met}} gene, termed Δ 3-5 (Fig. 33; Adeniyi-Jones et al., 1984 *supra*), to drive expression of antisense RNAs, and subsequently decoy RNAs (Sullenger et al., 1990 *supra*) has recently been reported. Because tRNA genes utilize internal pol III promoters, the antisense and decoy RNA sequences were expressed as chimeras
20 containing tRNA^{i^{met}} sequences. The truncated tRNA genes were placed into the U3 region of the 3' moloney murine leukemia virus vector LTR (Sullenger et al., 1990 *supra*).

Base-Paired Structures

- 25 Since the Δ 3-5 vector combination has been successfully used to express inhibitory levels of both antisense and decoy RNAs, applicant cloned ribozyme-encoding sequences (termed as " Δ 3-5/HHI") into this vector to explore its utility for expressing therapeutic ribozymes. However, low ribozyme accumulation in human T cell lines stably transduced with this vector was observed (Fig. 35). To try and improve accumulation of the
30 ribozyme, applicant incorporated various RNA structural elements (Fig. 34) into one of the ribozyme chimeras (Δ 3-5/HHI).

Two strategies were used to try and protect the termini of the chimeric transcripts from exonucleolytic degradation. One strategy involved the incorporation of stem-loop structures into the termini of the transcript. Two

such constructs were cloned, S3 which contains a stem-loop structure at the 3' end, and S5 which contains stem-loop structures at both ends of the transcript (Figure 34). The second strategy involved modification of the 3' terminal sequences such that the 5' terminus and the 3' end sequences can form a stable base-paired stem. Two such constructs were made: S35 in which the 3' end was altered to hybridize to the 5' leader and acceptor stem of the tRNAⁱmet domain, and S35Plus which was identical to S35 but included more extensive structure formation within the non-ribozyme portion of the $\Delta 3-5$ chimeras (Figure 34). These stem-loop structures are also intended to sequester non-ribozyme sequences in structures that will prevent them from interfering with the catalytic activity of the ribozyme. These constructs were cloned, producer cell lines were generated, and stably-transduced human MT2 (Harada et al., 1985 *supra*) and CEM (Nara & Fischinger, 1988 *supra*) cell lines were established (*Curr. Protocols Mol. Biol.* 1992, ed. Ausubel et al., Wiley & Sons, NY). The RNA sequences and structure of S35 and S35 Plus are provided in Figures 40-47.

Referring to Figure 48, there is provided a general structure for a chimeric RNA molecule of this invention. Each N independently represents none or a number of bases which may or may not be base paired. The A and B boxes are optional and can be any known A or B box, or a consensus sequence as exemplified in the figure. The desired nucleic acid to be expressed can be any location in the molecule, but preferably is on those places shown adjacent to or between the A and B boxes (designated by arrows). Figure 49 shows one example of such a structure in which a desired RNA is provided 3' of the intramolecular stem. A specific example of such a construct is provided in Figures 50 and 51.

Example 26: Cloning of $\Delta 3-5$ -Ribozyme Chimera

Oligonucleotides encoding the S35 insert that overlap by at least 15 nucleotides were designed (5' GATCCACTCTGCTGTTCTGTTTTTGA 3' and 5' CGCGTCAAAAACAGAACAGCAGAGTG 3'). The oligonucleotides (10 μ M each) were denatured by boiling for 5 min in a buffer containing 40 mM Tris.HCl, pH8.0. The oligonucleotides were allowed to anneal by snap cooling on ice for 10-15 min.

The annealed oligonucleotide mixture was converted into a double-stranded molecule using Sequenase[®] enzyme (US Biochemicals) in a

buffer containing 40 mM Tris.HCl, pH7.5, 20 mM MgCl₂, 50 mM NaCl, 0.5 mM each of the four deoxyribonucleotide triphosphates, 10 mM DTT. The reaction was allowed to proceed at 37°C for 30 min. The reaction was stopped by heating to 70°C for 15 min.

- 5 The double stranded DNA was digested with appropriate restriction endonucleases (*Bam*HI and *Mlu*I) to generate ends that were suitable for cloning into the Δ3-5 vector.

- 10 The double-stranded insert DNA was ligated to the Δ3-5 vector DNA by incubating at room temperature (about 20°C) for 60 min in a buffer containing 66 mM Tris.HCl, pH 7.6, 6.6 mM MgCl₂, 10 mM DTT, 0.066 μM ATP and 0.1U/μl T4 DNA Ligase (US Biochemicals).

- 15 Competent *E. coli* bacterial strain was transformed with the recombinant vector DNA by mixing the cells and DNA on ice for 60 min. The mixture was heat-shocked by heating to 37°C for 1 min. The reaction mixture was diluted with LB media and the cells were allowed to recover for 60 min at 37°C. The cells were plated on LB agar plates and incubated at 37°C for ~ 18 h.

- 20 Plasmid DNA was isolated from an overnight culture of recombinant clones using standard protocols (Ausubel et al., *Curr. Protocols Mol. Biology* 1990, Wiley & Sons, NY).

The identity of the clones were determined by sequencing the plasmid DNA using the Sequenase[®] DNA sequencing kit (US Biochemicals).

- 25 The resulting recombinant Δ3-5 vector contains the S35 sequence. The HHI encoding DNA was cloned into this Δ3-5-S35 containing vector using *Sac*II and *Bam*HI restriction sites.

Example 27: Northern analysis

- 30 RNA from the transduced MT2 cells were extracted and the presence of Δ3-5/ribozyme chimeric transcripts were assayed by Northern analysis (*Curr. Protocols Mol. Biol.* 1992, ed. Ausubel et al., Wiley & Sons, NY). Northern analysis of RNA extracted from MT2 transductants showed that Δ3-5/ribozyme chimeras of appropriate sizes were expressed (Fig. 35.36). In addition, these results demonstrated the relative differences in accumulation among the different constructs (Figure 35.36). The pattern of

expression seen from the $\Delta 3$ -5/HHI ribozyme chimera was similar to 12 other ribozymes cloned into the $\Delta 3$ -5 vector (not shown). In MT-2 cell line, $\Delta 3$ -5/HHI ribozyme chimeras accumulated, on average, to less than 100 copies per cell.

- 5 Addition of a stem-loop onto the 3' end of $\Delta 3$ -5/HHI did not lead to increased $\Delta 3$ -5 levels (S3 in Fig. 35.36). The S5 construct containing both 5' and 3' stem-loop structures also did not lead to increased ribozyme levels (Fig. 35.36).

- 10 Interestingly, the S35 construct expression in MT2 cells was about 100-fold more abundant relative to the original $\Delta 3$ -5/HHI vector transcripts (Fig. 35.36). This may be due to increased stability of the S35 transcript.

Example 28: Cleavage activity

- 15 To assay whether ribozymes transcribed in the transduced cells contained cleavage activity, total RNA extracted from the transduced MT2 T cells were incubated with a labeled substrate containing the HHI cleavage site (Figure 37). Ribozyme activity in all but the S35 constructs, was too low to detect. However, ribozyme activity was detectable in S35-transduced T cell RNA. Comparison of the activity observed in the S35-transduced MT2 RNA with that seen with MT2 RNA in which varying
- 20 amounts of in vitro transcribed S5 ribozyme chimeras, indicated that between 1-3 nM of S35 ribozyme was present in S35-transduced MT2 RNA. This level of activity corresponds to an intracellular concentration of 5,000-15,000 ribozyme molecules per cell.

Example 29: Clonal variation

- 25 Variation in the ribozyme expression levels among cells making up the bulk population was determined by generating several clonal cell lines from the bulk S35 transduced CEM line (*Curr. Protocols Mol. Biol.* 1992, ed. Ausubel et al., Wiley & Sons, NY) and the ribozyme expression and activity levels in the individual clones were measured (Figure 38 and 39).
- 30 All the individual clones were found to express active ribozyme. The ribozyme activity detected from each clone correlated well with the relative amounts of ribozyme observed by Northern analysis. Steady state ribozyme levels among the clones ranged from approximately 1,000 molecules per cell in clone G to 11,000 molecules per cell in clone H (Fig.

38). The mean accumulation among the clones, calculated by averaging the ribozyme levels of the clones, exactly equaled the level measured in the parent bulk population. This suggests that the individual clones are representative of the variation present in the bulk population.

- 5 The fact that all 14 clones were found to express ribozyme indicate that the percentage of cells in the bulk population expressing ribozyme is also very high. In addition, the lowest level of expression in the clones was still more than 10-fold that seen in bulk cells transduced with the original $\Delta 3-5$ vector. Therefore, the S35 gene unit should be much more effective
10 in a gene therapy setting in which bulk cells are removed, transduced and then reintroduced back into a patient.

Example 30: Stability

- Finally, the bulk S35-transduced line, resistant to G418, was propagated for a period of 3 months (in the absence of G418) to determine
15 if ribozyme expression was stable over extended periods of time. This situation mimicks that found in the clinic in which bulk cells are transduced and then reintroduced into the patient and allowed to propagate. There was a modest 30% reduction of ribozyme expression after 3 months. This difference probably arose from cells with varying amount of ribozyme
20 expression and exhibiting different growth rates in the culture becoming slightly more prevalent in the culture. However, ribozyme expression is apparently stable for at least this period of time.

Example 31: Design and construction of TRZ-tRNA Chimera

- A transcription unit, termed TRZ, is designed that contains the S35
25 motif (Figure 52). A desired RNA (e.g. ribozyme) can be inserted into the indicated region of TRZ tRNA chimera. This construct might provide additional stability to the desired RNA. TRZ-A and TRZ-B are non-limiting examples of the TRZ-tRNA chimera.

- Referring to Fig. 53-54, a hammerhead ribozyme targeted to site I
30 (HHITRZ-A; Fig. 53) and a hairpin ribozyme (HPITRZ-A; Fig. 54), also targeted to site I, is cloned individually into the indicated region of TRZ tRNA chimera. The resulting ribozyme transcripts retain full RNA cleavage activity (see for example Fig. 55). Applicant has shown that efficient

expression of these TRZ tRNA chimera can be achieved in mammalian cells.

Besides ribozymes, desired RNAs like antisense, therapeutic editing RNAs, decoys, can be readily inserted into the indicated region of TRZ-
5 tRNA chimera to achieve therapeutic levels of RNA expression in mammalian cells.

Sequences listed in Figures 40-47 and 50 - 54 are meant to be non-limiting examples. Those skilled in the art will recognize that variants (mutations, insertions and deletions) of the above examples can be readily
10 generated using techniques known in the art, are within the scope of the present invention.

Example 32: Ribozyme expression in T cell lines

Ribozyme expression in T cell lines stably-transduced with either a retroviral-based or an Adeno-associated virus (AAV)-based ribozyme
15 expression vector (Figure 56). The human T cell lines MT2 and CEM were transduced with either retroviral or AAV vectors encoding a neomycin selectable marker and a ribozyme (S35/HHI) expressed from pol III met; tRNA-driven promoter. Cells stably-transduced with the vectors were
20 selectively expanded in medium containing the neomycin antibiotic derivative, G418 (0.7 mg/ml). Ribozyme expression in the stable cell lines was then analyzed by Northern analysis. The probe used to detect ribozyme transcripts also cross-hybridized with human met; tRNA sequences. Referring to Figure 56, S35/HHI RNA accumulates to significant
25 levels in MT2 and CEM cells when transduced with either the retrovirus or the AAV vector.

These are meant to be non-limiting examples, those skilled in the art will recognize that other vectors such as adenovirus vector (Figure 57), plasmid DNA vector, alpha virus vectors and the other derivatives thereof, can be readily generated to deliver the desired RNA, using techniques
30 known in the art and are within the scope of this invention. Additionally, the transcription units can be expressed individually or in multiples using pol II and/or pol III promoters.

References cited herein, as well as Draper WO 93/23569, 94/02495, 94/06331, Sullenger WO 93/12657, Thompson WO 93/04573, and Sullivan

WO 94/04609, and 93/11253 describe methods for use of vectors described herein, and are incorporated by reference herein. In particular these vectors are useful for administration of antisense and decoy RNA molecules.

5 Example 33: Ligated Ribozymes are catalytically active

The ability of ribozymes generated by ligation methods, described in Draper et al., PCT WO 93/23569, to cleave target RNA was tested on either matched substrate RNA (Fig. 58) or long (622 nt) RNA (Fig. 59, 60 and 61).

10 Matched substrate RNAs were chemically synthesized using solid-phase RNA synthesis chemistry (Scaringe et al., 1990 Nucleic Acids Res. 18, 5433-5441). Substrate RNA was 5' end-labeled using [γ - 32 P] ATP and polynucleotide kinase (Curr. Protocols Mol. Biol. 1992, ed. Ausubel et al., Wiley & Sons, NY). Ribozyme reactions were carried out under ribozyme excess conditions (k_{cat}/K_M ; Herschlag and Cech, 1990 Biochemistry 29, 15 10159-10171). Briefly, ribozyme and substrate RNA were denatured and renatured separately by heating to 90°C and snap cooling on ice for 10 min in a buffer containing 50 mM Tris. HCl pH 7.5 and 10 mM MgCl₂. Cleavage reaction was initiated by mixing the ribozyme with the substrate at 37°C. Aliquots of 5 μ l were taken at regular intervals of time and the 20 reaction was stopped by mixing with equal volume of formamide gel loading buffer (Curr. Protocols Mol. Biol. 1992, ed. Ausubel et al., Wiley & Sons, NY). The samples were resolved on 20 % polyacrylamide-urea gel. Referring to Fig. 58, $-\Delta G$ refers to the free energy of binding calculated for base-paired interactions between the ribozyme and the substrate RNA 25 (Turner and Sugimoto, 1988 Supra). RPI A is a HH ribozyme with 6/6 binding arms. This ribozyme was synthesized chemically either as a one piece ribozyme or was synthesized in two fragments followed by ligation to generate a one piece ribozyme. The k_{cat}/K_M values for the two ribozymes were comparable.

30 A template containing T7 RNA polymerase promoter upstream of 622 nt long target sequence, was PCR amplified from a DNA clone. The target RNA (containing HH ribozyme cleavage sites B, C and D) was transcribed from this PCR amplified template using T7 RNA polymerase. The transcript was internally labeled during transcription by including [α - 32 P] CTP as one 35 of the four ribonucleotide triphosphates. The transcription mixture was

treated with DNase-1, following transcription at 37°C for 2 hours, to digest away the DNA template used in the transcription. RNA was precipitated with Isopropanol and the pellet was washed two times with 70% ethanol to get rid of salt and nucleotides used in the transcription reaction. RNA is resuspended in DEPC-treated water and stored at 4°C. Ribozyme cleavage reactions were carried out under ribozyme excess (k_{cat}/K_M) conditions [Herschlag and Cech 1990 supra]. Briefly, 1000 nM ribozyme and 10 nM internally labeled target RNA were denatured separately by heating to 90°C for 2 min in the presence of 50 mM Tris.HCl, pH 7.5 and 10 mM $MgCl_2$. The RNAs were renatured by cooling to 37°C for 10-20 min. Cleavage reaction was initiated by mixing the ribozyme and target RNA at 37°C. Aliquots of 5 μ l were taken at regular intervals of time and the reaction was quenched by adding equal volume of stop buffer. The samples were resolved on a sequencing gel.

Example 34: Hammerhead ribozymes with ≥ 2 base-paired stem II are catalytically active

To decrease the cost of chemical synthesis of RNA, applicant was interested in determining whether the length of stem II region of a typical hammerhead ribozyme (≥ 4 bp stem II) can be shortened without decreasing the catalytic efficiency of the HH ribozyme. The length of stem II was systematically shortened by one base-pair at a time. HH ribozymes with three and two base-paired stem II were chemically synthesized using solid-phase RNA phosphoramidite chemistry (Scaringe et al., 1990 supra).

Matched and long substrate RNAs were synthesized and ribozyme assays were carried out as described in example 33. Referring to figures 62, 63 and 64, data shows that shortening stem II of a hammerhead ribozyme does not significantly alter the catalytic efficiency. It is applicant's opinion that hammerhead ribozymes with ≥ 2 base-paired stem II region are catalytically active.

Example 35: Synthesis of catalytically active hairpin ribozymes

RNA molecules were chemically synthesized having the nucleotide base sequence shown in Fig. 65 for both the 5' and 3' fragments. The 3' fragments are phosphorylated and ligated to the 5' fragment essentially as described in example 37. As is evident from the Figure 65, the 3' and 5' fragments can hybridize together at helix 4 and are covalently linked via

GAAA sequence. When this structure hybridizes to a substrate, a ribozyme-substrate complex structure is formed. While helix 4 is shown as 3 base pairs it may be formed with only 1 or 2 base pairs.

40 nM mixtures of ligated ribozymes were incubated with 1-5 nM 5' end-labeled matched substrates (chemically synthesized by solid-phase synthesis using RNA phosphoramidite chemistry) for different times in 50 mM Tris/HCl pH 7.5, 10 mM MgCl₂ and shown to cleave the substrate efficiently (Fig.66).

The target and the ribozyme sequences shown in Fig. 62 and 65 are meant to be non-limiting examples. Those in the art will recognize that other embodiments can be readily generated using other sequences and techniques generally known in the art.

V. Constructs of Hairpin Ribozymes

There follows an improved trans-cleaving hairpin ribozyme in which a new helix (*i.e.*, a sequence able to form a double-stranded region with another single-stranded nucleic acid) is provided in the ribozyme to base-pair with a 5' region of a separate substrate nucleic acid. This helix is provided at the 3' end of the ribozyme after helix 3 as shown in Figure 3. In addition, at least two extra bases may be provided in helix 2 and a portion of the substrate corresponding to helix 2 may be either directly linked to the 5' portion able to hydrogen bond to the 3' end of the hairpin or may have a linker of atleast one base. By trans-cleaving is meant that the ribozyme is able to act in *trans* to cleave another RNA molecule which is not covalently linked to the ribozyme itself. Thus, the ribozyme is not able to act on itself in an intramolecular cleavage reaction.

By "base-pair" is meant a nucleic acid that can form hydrogen bond(s) with other RNA sequence by either traditional Watson-Crick or other non-traditional types (for example Hoogsteen type) of interactions.

The increase in length of helix 2 of a hairpin ribozyme (with or without helix 5) has several advantages. These include improved stability of the ribozyme-target complex *in vivo*. In addition, an increase in the recognition sequence of the hairpin ribozyme improves the specificity of the ribozyme. This also makes possible the targeting of potential hairpin

ribozyme sites that would otherwise be inaccessible due to neighboring secondary structure.

The increase in length of helix 2 of a hairpin ribozyme (with or without helix 5) enhances *trans*-ligation reaction catalyzed by the ribozyme. *Trans*-ligation reactions catalyzed by the regular hairpin ribozyme (4 bp helix 2) is very inefficient (Komatsu *et al.*, 1993 *Nucleic Acids Res.* 21, 185). This is attributed to weak base-pairing interactions between substrate RNAs and the ribozyme. By increasing the length of helix 2 (with or without helix 5) the rate of ligation (*in vitro* and *in vivo*) can be enhanced several fold.

Results of experiments suggest that the length of H2 can be 6 bp without significantly reducing the activity of the hairpin ribozyme. The H2 arm length variation does not appear to be sequence dependent. HP ribozymes with 6 bp H2 have been designed against five different target RNAs and all five ribozymes efficiently cleaved their cognate target RNA. Additionally, two of these ribozymes were able to successfully inhibit gene expression (e.g., TNF- α) in mammalian cells. Results of these experiments are shown below.

HP ribozymes with 7 and 8 bp H2 are also capable of cleaving target RNA in a sequence-specific manner, however, the rate of the cleavage reaction is lower than those catalyzed by HP ribozymes with 6 bp H2.

Example 36: 4 and 6 base pair H2

Referring to Figures 67-72, HP ribozymes were synthesized as described above and tested for activity. Surprisingly, those with 6 base pairs in H2 were still as active as those with 4 base pairs.

25 VI. Chemical Modification

Oligonucleotides with 5'-C-alkyl Group

The introduction of an alkyl group at the 5'-position of a nucleoside or nucleotide sugar introduces an additional center of chirality into the sugar moiety. Referring to Fig. 75, the general structures of 5'-C-alkylnucleotides belonging to the D-allose, 2, and L-talose, 3, sugar families are shown. The family names are derived from the known sugars D-allose and L-talose ($R_1 = CH_3$ in 2 and 3 in Figure 75). Useful specific D-allose and L-talose

nucleotide derivatives are shown in Figure 76, 29-32 and Figure 77, 58-61 respectively.

5 This invention relates to the use of 5'-C-alkylnucleotides in oligonucleotides, which are particularly useful for enzymatic cleavage of RNA or single-stranded DNA, and also as antisense oligonucleotides. As the term is used in this application, 5'-C-alkylnucleotide-containing enzymatic nucleic acids are catalytic nucleic molecules that contain 5'-C-alkylnucleotide components replacing, but not limited to, double stranded stems, single stranded "catalytic core" sequences, single-stranded loops or
10 single-stranded recognition sequences. These molecules are able to cleave (preferably, repeatedly cleave) separate RNA or DNA molecules in a nucleotide base sequence specific manner. Such catalytic nucleic acids can also act to cleave intramolecularly if that is desired. Such enzymatic molecules can be targeted to virtually any RNA transcript.

15 Also within the invention are 5'-C-alkylnucleotides which may be present in enzymatic nucleic acid or even in antisense oligonucleotides. Such nucleotides are useful since they enhance the stability of the antisense or enzymatic molecule, and can be used in locations which do not affect the desired activity of the molecule. That is, while the presence of
20 the 5'-C-alkyl group may reduce binding affinity of the oligonucleotide containing this modification, if that moiety is not in an essential base pair forming region then the enhanced stability that it provides to the molecule is advantageous. In addition, while the reduced binding may reduce enzymatic activity, the enhanced stability may make the loss of activity of
25 less consequence. Thus, for example, if a 5'-C-alkyl-containing molecule has 10% the activity of the unmodified molecule, but has 10-fold higher stability *in vivo* then it has utility in the present invention. The same analysis is true for antisense oligonucleotides containing such modifications. The invention also relates to novel intermediates useful in
30 the synthesis of such nucleotides and oligonucleotides (examples of which are shown in the Figures), and to methods for their synthesis.

Thus, in one aspect, the invention features 5'-C-alkylnucleosides, that is a nucleotide base having at the 5'-position on the sugar molecule an alkyl moiety. In a related aspect, the invention also features 5'-C-
35 alkylnucleotides, and in preferred embodiments features those where the nucleotide is not uridine or thymidine. That is, the invention preferably

includes all those nucleotides useful for making enzymatic nucleic acids or antisense molecules that are not described by the art discussed above. In preferred embodiments, the sugar of the nucleoside or nucleotide is in an optically pure form, as the talose or allose sugar.

- 5 Examples of various alkyl groups useful in this invention are shown in Figure 75, where each R_1 group is any alkyl. These examples are not limiting in the invention. Specifically, an "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More
- 10 preferably it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $\text{N}(\text{CH}_3)_2$, amino, or SH. The term also includes alkenyl groups which are unsaturated hydrocarbon groups containing at least one
- 15 carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy,
- 20 =O, =S, NO_2 , halogen, $\text{N}(\text{CH}_3)_2$, amino, or SH. The term "alkyl" also includes alkynyl groups which have an unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably it is a lower alkynyl of from 1 to 7 carbons,
- 25 more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $\text{N}(\text{CH}_3)_2$, amino or SH.

- Such alkyl groups may also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an
- 30 aromatic group which has at least one ring having a conjugated π electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an
- 35 alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring

atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

10 In other aspects, also related to those discussed above, the invention features oligonucleotides having one or more 5'-C-alkylnucleotides; *e.g.* enzymatic nucleic acids having a 5'-C-alkylnucleotide; and a method for producing an enzymatic nucleic acid molecule having enhanced activity to cleave an RNA or single-stranded DNA molecule, by forming the enzymatic
15 molecule with at least one nucleotide having at its 5'-position an alkyl group. In other related aspects, the invention features 5'-C-alkylnucleotide triphosphates. These triphosphates can be used in standard protocols to form useful oligonucleotides of this invention.

20 The 5'-C-alkyl derivatives of this invention provide enhanced stability to the oligonucleotides containing them. While they may also reduce absolute activity in an *in vitro* assay they will provide enhanced overall activity *in vivo*. Below are provided assays to determine which such molecules are useful. Those in the art will recognize that equivalent assays can be readily devised.

25 In another aspect, the invention features a method for conversion of a protected allo sugar to a protected talo sugar. In the method, the protected allo sugar is contacted with triphenyl phosphine, diethylazodicarboxylate, and *p*-nitrobenzoic acid under inversion causing conditions to provide the protected talo sugar. While one example of such conditions is provided
30 below, those in the art will recognize other such conditions. Applicant has found that such conversion allows for ready synthesis of all types of nucleotide bases as exemplified in the figures.

While this invention is applicable to all oligonucleotides, applicant has found that the modified molecules of this invention are particularly useful for
35 enzymatic RNA molecules. Thus, below is provided examples of such

molecules. Those in the art will recognize that equivalent procedures can be used to make other molecules without such enzymatic activity. Specifically, Figure 1 shows base numbering of a hammerhead motif in which the numbering of various nucleotides in a hammerhead ribozyme is provided. This is not to be taken as an indication that the Figure is prior art to the pending claims, or that the art discussed is prior art to those claims. Referring to Figure 1, the preferred sequence of a hammerhead ribozyme in a 5'- to 3'-direction of the catalytic core is CUGANGAG[base paired with]CGAAA. In this invention, the use of 5'-C-alkyl substituted nucleotides that maintain or enhance the catalytic activity and or nuclease resistance of the hammerhead ribozyme is described. Substitutions of any nucleotide with any of the modified nucleotides shown in Figure 75 are possible.

The following are non-limiting examples showing the synthesis of nucleic acids using 5'-C-alkyl-substituted phosphoramidites and the syntheses of the amidites.

Example 37: Synthesis of Hammerhead Ribozymes Containing 5'-C-Alkyl-nucleotides & Other Modified Nucleotides

The method of synthesis would follow the procedure for normal RNA synthesis as described in Usman, N.; Ogilvie, K.K.; Jiang, M.-Y.; Cedergren, R.J. *J. Am. Chem. Soc.* 1987, 109, 7845-7854 and in Scaringe, S.A.; Franklyn, C.; Usman, N. *Nucleic Acids Res.* 1990, 18, 5433-5441 and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end (compounds 26-29 and 56-59). These 5'-C-alkyl substituted phosphoramidites may be incorporated not only into hammerhead ribozymes, but also into hairpin, hepatitis delta virus, Group 1 or Group 2 intron catalytic nucleic acids, or into antisense oligonucleotides. They are, therefore, of general use in any nucleic acid structure.

Example 38: Methyl-2,3-O-Isopropylidene-6-Deoxy-β-D-allofuranoside (4)

A suspension of L-rhamnose (100 g, 0.55 mol), CuSO₄ (120 g) and conc. H₂SO₄ (4.0 mL) in 1.0 L of dry acetone was mixed for 24 h at RT, then filtered. Conc. NH₄OH (5 mL) was added to the filtrate and the newly formed precipitate was filtered. The residue was concentrated *in vacuo*, coevaporated with pyridine (2 x 300 mL), dissolved in pyridine (500 mL) and cooled to 0 °C. A solution of *p*-toluenesulfonylchloride (107 g, 0.56

mmol) in dry DCE (500 mL) was added dropwise over 0.5 h. The reaction mixture was left for 16 h at RT. The reaction was quenched by adding ice-water (0.5 L) and, after mixing for 0.5 h, was extracted with chloroform (0.75 L). The organic layer was washed with H₂O (2 x 500 mL), 10% H₂SO₄ (2 x 300 mL), water (2 x 300 mL), sat. NaHCO₃ (2 x 300 mL), brine (2 x 300 mL), dried over MgSO₄ and evaporated to dryness. The residue (115 g) was dissolved in dry MeOH (1 L) and treated with NaOMe (23.2 g, 0.42 mmol) in MeOH. The reaction mixture was left for 16 h at 20 °C, neutralized with dry CO₂ and evaporated to dryness. The residue was suspended in chloroform (750 mL), filtered, concentrated to 100 mL and purified by flash chromatography in CHCl₃ to yield 45 g (37%) of compound 4.

Example 39: Methyl-2,3-O-Isopropylidene-5-O-*t*-Butyldiphenylsilyl-6-Deoxy-β-D-Allofuranoside (5).

To solution of methylfuranoside 4 (12.5 g 62.2 mmol) and AgNO₃ (21.25 g, 125.0 mmol) in dry DMF (300 mL) *t*-butyldiphenylsilyl chloride (22.2 g, 81 mmol) was added dropwise under Ar over 0.5 h. The reaction mixture was stirred for 4 h at RT, diluted with CHCl₃ (200 mL), filtered and evaporated to dryness (below 40 °C using a high vacuum oil pump). The residue was dissolved in CH₂Cl₂ (300 mL) washed with sat. NaHCO₃ (2 x 50 mL), brine (2 x 50 mL), dried over MgSO₄ and evaporated to dryness. The residue was purified by flash chromatography in CH₂Cl₂ to yield 20.0 g (75%) of compound 5.

Example 40: Methyl-5-O-*t*-Butyldiphenylsilyl-6-Deoxy-β-D-Allofuranoside (6).

Methylfuranoside 5 (13.5 g, 30.6 mmol) was dissolved in CF₃COOH:dioxane:H₂O / 2:1:1 (v/v/v, 200 mL) and stirred at 24 °C for 45 m. The reaction mixture was cooled to -10 °C, neutralized with conc. NH₄OH (140 mL) and extracted with CH₂Cl₂ (500 mL). The organic layer was separated, washed with sat. NaHCO₃ (2 x 75 mL), brine (2 x 75 mL), dried over MgSO₄ and evaporated to dryness. The product 6 was purified by flash chromatography using a 0-10% MeOH gradient in CH₂Cl₂. Yield 9.0 g (76%).

Example 41: Methyl-2,3-di-O-Benzoyl-5-O-t-Butyldiphenylsilyl-6-Deoxy- β -D-Allofuranoside (7).

Methylfuranoside 6 (7.0 g, 17.5 mmol) was coevaporated with pyridine (2 x 100 mL) and dissolved in pyridine (100 mL). Benzoyl chloride (5.4 g, 38.5 mmol) was added and the reaction mixture was left at RT for 16 h. Dry EtOH (50 mL) was added and the reaction mixture was evaporated to dryness after 0.5 h. The residue was dissolved in CH₂Cl₂ (300 mL), washed with sat. NaHCO₃ (2 x 75 mL), brine (2 x 75 mL) dried over MgSO₄ and evaporated to dryness. The product was purified by flash chromatography in CH₂Cl₂ to yield 9.5 g (89%) of compound 7.

Example 42: 1-O-Acetyl-2,3-di-O-benzoyl-5-O-t-Butyldiphenylsilyl-6-Deoxy- β -D-Allofuranose (8).

Dibenzoate 7 (4.7 g, 7.7 mmol) was dissolved in a mixture of AcOH (10.0 mL), Ac₂O (20.0 mL) and EtOAc (30 mL) and the reaction mixture was cooled 0 °C. 98% H₂SO₄ (0.15 mL) was then added. The reaction mixture was kept at 0 °C for 16 h, and then poured into a cold 1:1 mixture of sat. NaHCO₃ and EtOAc (150 mL). After 0.5 h of vigorous stirring the organic phase was separated, washed with brine (2 x 75 mL), dried over MgSO₄, evaporated to dryness and coevaporated with toluene (2 x 50 mL). The product was purified by flash chromatography using a gradient of 0-5% MeOH in CH₂Cl₂. Yield: 4.0 g (82% as a mixture of α and β isomers).

Example 43: 1-(2',3'-di-O-Benzoyl-5'-O-t-Butyldiphenylsilyl-6'-Deoxy- β -D-Allofuranosyl)uracil (9).

Uracil (1.44 g, 11.5 mmol) was suspended in mixture of hexamethyldisilazane (100 mL) and pyridine (50 mL) and boiled under reflux until complete dissolution (3 h) occurred, and then for an additional hour. The reaction mixture was cooled to RT, evaporated to dryness and coevaporated with dry toluene (2 x 50 mL). To the residue was added a solution of acetates 8 (6.36 g, 10.0 mmol) in dry CH₃CN (100 mL), followed by CF₃SO₃SiMe₃ (2.8 g, 12.6 mmol). The reaction mixture was kept at 24 °C for 16 h, concentrated to 1/3 of its original volume, diluted with 100 mL of CH₂Cl₂ and extracted with sat. NaHCO₃ (2 x 50 mL), brine (2 x 50 mL) dried over MgSO₄, and evaporated to dryness. The product 9 was purified by flash chromatography using a gradient of 0-5% MeOH in CH₂Cl₂. Yield: 5.7 g (80%).

Example 44: N⁴-Benzoyl-1-(2',3'-Di-O-Benzoyl-5'-O-*t*-Butyldiphenylsilyl-6'-Deoxy-β-D-Allofuranosyl)Cytosine (10).

N⁴-benzoylcytosine (1.84 g, 8.56 mmol) was suspended in mixture of hexamethyldisilazane (100 mL) and pyridine (50 mL) and boiled under reflux until complete dissolution (3 h) occurred, and then for an additional hour. The reaction mixture was cooled to RT evaporated to dryness and coevaporated with dry toluene (2 x 50 mL). To the residue was added a solution of acetates 8 (3.6 g, 5.6 mmol) in dry CH₃CN (100 mL), followed by CF₃SO₃SiMe₃ (4.76 g, 21.4 mmol). The reaction mixture was boiled under reflux for 5 h, cooled to RT, concentrated to 1/3 of its original volume, diluted with CH₂Cl₂ (100 mL) and extracted with sat. NaHCO₃ (2 x 50 mL), brine (2 x 50 mL) dried over MgSO₄ and evaporated to dryness. Purification by flash chromatography using a gradient of 0-5% MeOH in CH₂Cl₂ yielded 1.8 g (55%) of compound 10.

Example 45: N⁶-Benzoyl-9-(2',3'-di-O-Benzoyl-5'-O-*t*-Butyldiphenylsilyl-6'-Deoxy-β-D-Allofuranosyl)adenine (11).

N⁶-benzoyladenine (2.86 g, 11.86 mmol) was suspended in mixture of hexamethyldisilazane (100 mL) and pyridine (50 mL) and boiled under reflux until complete dissolution (7 h) occurred, and then for an additional hour. The reaction mixture was cooled to RT evaporated to dryness and coevaporated with dry toluene (2 x 50 mL). To the residue was added a solution of acetates 8 (3.6 g, 5.6 mmol) in dry CH₃CN (100 mL) followed by CF₃SO₃SiMe₃ (6.59 g, 29.7 mmol). The reaction mixture was boiled under reflux for 8 h, cooled to RT, concentrated to 1/3 of its original volume, diluted with CH₂Cl₂ (100 mL) and extracted with sat. NaHCO₃ (2 x 50 mL), brine (2 x 50 mL) dried over MgSO₄ and evaporated to dryness. The product 11 was purified by flash chromatography using a gradient of 0-5% MeOH in CH₂Cl₂. Yield: 2.7 g (60%).

Example 46: N²-Isobutyryl-9-(2',3'-di-O-Benzoyl-5'-O-*t*-Butyldiphenylsilyl-6'-Deoxy-β-D-Allofuranosyl)guanine (12).

N²-Isobutyrylguanine (1.47 g, 11.2 mmol) was suspended in mixture of hexamethyldisilazane (100 mL) and pyridine (50 mL) and boiled under reflux until complete dissolution (6 h) occurred, and then for an additional hour. The reaction mixture was cooled to RT evaporated to dryness and coevaporated with dry toluene (2 x 50 mL). To the residue was added a

- 5 solution of acetates 8 (3.4 g, 5.3 mmol) in dry CH₃CN (100 mL) followed by CF₃SO₃SiMe₃ (6.22 g, 28.0 mmol). The reaction mixture was boiled under reflux for 8 h, cooled to RT, concentrated to 1/3 of its original volume, diluted with CH₂Cl₂ (100 mL) and extracted with sat. NaHCO₃ (2 x 50 mL), brine (2 x 50 mL) dried over MgSO₄ and evaporated to dryness. The product 12 was purified by flash chromatography using a gradient of 0-2% MeOH in CH₂Cl₂. Yield: 2.1g (54%).

Example 47: N⁶-Benzoyl-9-(2',3'-di-O-benzoyl-6'-Deoxy-β-D-Allofuranosyl)adenine (15).

- 10 Nucleoside 11 (1.65 g, 2.0 mmol) was dissolved in THF (50 mL) and a 1 M solution of TBAF in THF (4 mL) was added. The reaction mixture was kept at RT for 4 h, evaporated to dryness and the product purified by flash chromatography using a gradient of 0-5% MeOH in CH₂Cl₂ to yield 1.0 g (85%) of compound 15.

15 Example 48: N⁶-Benzoyl-9-(2',3'-di-O-Benzoyl-5'-O-Dimethoxytrityl-6'-Deoxy-β-D-Allofuranosyl)-adenine (19).

- 20 Nucleoside 15 (0.55 g, 0.92 mmol) was dissolved in dry CH₂Cl₂ (50 mL). AgNO₃ (0.34 g, 2.0 mmol), dimethoxytrityl chloride (0.68 g, 2.0 mmol) and sym-collidine (0.48 g) were added under Ar. The reaction mixture was stirred for 2h, diluted with CH₂Cl₂ (100 mL), filtered, evaporated to dryness and coevaporated with toluene (2 x 50 mL). Purification by flash chromatography using a gradient of 0-5% MeOH in CH₂Cl₂ yielded 0.8 g (97%) of compound 19.

25 Example 49: N⁶-Benzoyl-9-(5'-O-Dimethoxytrityl-6'-Deoxy-β-D-Allofuranosyl)adenine (23).

- 30 Nucleoside 19 (1.8 g, 2 mmol) was dissolved in dioxane (50 mL), cooled to 0 °C and 2 M NaOH (50 mL) was added. The reaction mixture was kept at 0 °C for 45 m, neutralized with Dowex 50 (Pyr⁺ form), filtered and the resin was washed with MeOH (2 x 50 mL). The filtrate was then evaporated to dryness. Purification by flash chromatography using a gradient of 0-10% MeOH in CH₂Cl₂ yielded 1.1 g (80%) of 23.

Example 50: N⁶-Benzoyl-9-(-5'-O-Dimethoxytrityl-2'-O-*t*-butyldimethylsilyl-6'-Deoxy-β-D-Allofuranosyl)adenine (27).

Nucleoside 23 (1.2 g, 1.8 mmol) was dissolved in dry THF (50 mL). Pyridine (0.50 g, 8 mmol) and AgNO₃ (0.4 g, 2.3 mmol) were added. After the AgNO₃ dissolved (1.5 h), *t*-butyldimethylsilyl chloride (0.35 g, 2.3 mmol) was added and the reaction mixture was stirred at RT for 16 h. The reaction mixture was diluted with CH₂Cl₂ (100 mL), filtered into sat. NaHCO₃ (50 mL), extracted, the organic layer washed with brine (2 x 50 mL), dried over MgSO₄ and evaporated to dryness. The product 27 was purified by flash chromatography using a hexanes:EtOAc / 7:3 gradient. Yield: 0.7 g (50%).

Example 51: N⁶-Benzoyl-9-(-5'-O-Dimethoxytrityl-2'-O-*t*-butyldimethylsilyl-6'-Deoxy-β-D-Allofuranosyl)adenine-3'-(2-Cyanoethyl *N,N*-diisopropylphosphoramidite) (31).

Standard phosphitylation of 27 according to Scaringe, S.A.; Franklyn, C.; Usman, N. *Nucleic Acids Res.* 1990, 18, 5433-5441 yielded phosphoramidite 31 in 73% yield.

Example 52: Methyl-5-O-*p*-Nitrobenzoyl-2,3-O-Isopropylidene-6-deoxy-β-L-Tallofuranoside (5)

Methylfuranoside 4 (3.1 g 14.2 mmol) was dissolved in dry dioxane (200 mL), *p*-nitrobenzoic acid (10.0 g, 60 mmol) and triphenylphosphine (15.74 g, 60.0 mmol) were added followed by DEAD (10.45 g, 60.0 mmol). The reaction mixture was left at RT for 16 h, EtOH (5 mL) was added, and after 0.5 h the reaction mixture was evaporated to dryness. The residue was dissolved in CH₂Cl₂ (300 mL) washed with sat. NaHCO₃ (2 x 75 mL), brine (2 x 75 mL) dried over MgSO₄ and evaporated to dryness. Purification by flash chromatography using a hexanes:EtOAc / 9:1 gradient yielded 4.1 g (78%) of compound 33. Subsequent debenzoylation (NaOMe/MeOH) and silylation (see preparation of 5) led to L-talofuranoside 34 which was converted to phosphoramidites 58-61 using the same methodology as described above for the preparation of the phosphoramidites of the D-allo-isomers 29-32.

The alkyl substituted nucleotides of this invention can be used to form stable oligonucleotides as discussed above for use in enzymatic cleavage

or antisense situations. Such oligonucleotides can be formed enzymatically using triphosphate forms by standard procedure. Administration of such oligonucleotides is by standard procedure. See Sullivan et al., PCT WO 94/ 02595.

- 5 The ribozymes and the target RNA containing site O were synthesized, deprotected and purified as described above. RNA cleavage assay was carried out at 37°C in the presence of 10 mM MgCl₂ as described above.

- 10 Applicant has substituted 5'-C-Me-L-talo nucleotides at positions A6, A9, A9 + G10, C11.1 and C11.1 + G10, as shown in Figure 78 (HH-O1 to HH-05). HH-O 1,2,4 and 5 showed almost wild type activity (Figure 79). However, HH-03 demonstrated low catalytic activity. Ribozymes HH-01, 2, 3, 4 and 5 are also extremely resistant to degradation by human serum nucleases.

15 Oligonucleotides with 2'-Deoxy-2'-Alkyl nucleotide

- 20 This invention uses 2'-deoxy-2'-alkyl nucleotides in oligonucleotides, which are particularly useful for enzymatic cleavage of RNA or single-stranded DNA, and also as antisense oligonucleotides. As the term is used in this application, 2'-deoxy-2'-alkyl nucleotide-containing enzymatic nucleic acids are catalytic nucleic molecules that contain 2'-deoxy-2'-alkyl nucleotide components replacing, but not limited to, double stranded stems, single stranded "catalytic core" sequences, single-stranded loops or single-stranded recognition sequences. These molecules are able to cleave (preferably, repeatedly cleave) separate RNA or DNA molecules in a nucleotide base sequence specific manner. Such catalytic nucleic acids can also act to cleave intramolecularly if that is desired. Such enzymatic molecules can be targeted to virtually any RNA transcript.

- 30 Also within the invention are 2'-deoxy-2'-alkyl nucleotides which may be present in enzymatic nucleic acid or even in antisense oligonucleotides. Contrary to the findings of De Mesmaeker *et al.* applicant has found that such nucleotides are useful since they enhance the stability of the antisense or enzymatic molecule, and can be used in locations which do not affect the desired activity of the molecule. That is, while the presence of the 2'-alkyl group may reduce binding affinity of the oligonucleotide containing this modification, if that moiety is not in an essential base pair
- 35

forming region then the enhanced stability that it provides to the molecule is advantageous. In addition, while the reduced binding may reduce enzymatic activity, the enhanced stability may make the loss of activity of less consequence. Thus, for example, if a 2'-deoxy-2'-alkyl-containing molecule has 10% the activity of the unmodified molecule, but has 10-fold higher stability *in vivo* then it has utility in the present invention. The same analysis is true for antisense oligonucleotides containing such modifications. The invention also relates to novel intermediates useful in the synthesis of such nucleotides and oligonucleotides (examples of which are shown in the Figures), and to methods for their synthesis.

Thus, in one aspect, the invention features 2'-deoxy-2'-alkylnucleotides, that is a nucleotide base having at the 2'-position on the sugar molecule an alkyl moiety and in preferred embodiments features those where the nucleotide is not uridine or thymidine. That is, the invention preferably includes all those nucleotides useful for making enzymatic nucleic acids or antisense molecules that are not described by the art discussed above.

Examples of various alkyl groups useful in this invention are shown in Figure 81, where each R group is any alkyl. The term "alkyl" does not include alkoxy groups which have an "-O-alkyl" group, where "alkyl" is defined as described above, where the O is adjacent the 2'-position of the sugar molecule.

In other aspects, also related to those discussed above, the invention features oligonucleotides having one or more 2'-deoxy-2'-alkylnucleotides (preferably not a 2'-alkyl- uridine or thymidine); *e.g.* enzymatic nucleic acids having a 2'-deoxy-2'-alkylnucleotide; and a method for producing an enzymatic nucleic acid molecule having enhanced activity to cleave an RNA or single-stranded DNA molecule, by forming the enzymatic molecule with at least one nucleotide having at its 2'-position an alkyl group. In other related aspects, the invention features 2'-deoxy-2'-alkylnucleotide triphosphates. These triphosphates can be used in standard protocols to form useful oligonucleotides of this invention.

The 2'-alkyl derivatives of this invention provide enhanced stability to the oligonucleotides containing them. While they may also reduce absolute activity in an *in vitro* assay they will provide enhanced overall

activity *in vivo*. Below are provided assays to determine which such molecules are useful. Those in the art will recognize that equivalent assays can be readily devised.

5 In another aspect, the invention features hammerhead motifs having enzymatic activity having ribonucleotides at locations shown in Figure 80 at 5, 6, 8, 12, and 15.1, and having substituted ribonucleotides at other positions in the core and in the substrate binding arms if desired. (The term "core" refers to positions between bases 3 and 14 in Figure 80, and the binding arms correspond to the bases from the 3'-end to base 15.1, and 10 from the 5'-end to base 2). Applicant has found that use of ribonucleotides at these five locations in the core provide a molecule having sufficient enzymatic activity even when modified nucleotides are present at other sites in the motif. Other such combinations of useful ribonucleotides can be determined as described by Usman *et al. supra*.

15 Figure 80 shows base numbering of a hammerhead motif in which the numbering of various nucleotides in a hammerhead ribozyme is provided. This is not to be taken as an indication that the Figure is prior art to the pending claims, or that the art discussed is prior art to those claims. Referring to Figure 80 the preferred sequence of a hammerhead ribozyme 20 in a 5'- to 3'-direction of the catalytic core is CUGANGAG[base paired with]CGAAA. In this invention, the use of 2'-C-alkyl substituted nucleotides that maintain or enhance the catalytic activity and or nuclease resistance of the hammerhead ribozyme is described. Although substitutions of any nucleotide with any of the modified nucleotides shown in Figure 81 are 25 possible, and were indeed synthesized, the basic structure composed of promarily 2'-O-Me nucleotides weth selected substitutions was chosen to maintain maximal catalytic activity (Yang *et al. Biochemistry* 1992, 31, 5005-5009 and Paoletta *et al. , EMBO J.* 1992, 11, 1913-1919) and ease of synthesis, but is not limiting to this invention.

30 Ribozymes from Figure 80 and Table 45 were synthesized and assayed for catalytic activity and nuclease resistance. With the exception of entries 8 and 17, all of the modified ribozymes retained at lease 1/10 of the wild-type catalytic activity. From Table 45, all 2'-modified ribozymes showed very large and significant increases in stability in human serum 35 (shown) and in the other fluids described below (Example 55, data not shown). The order of most aggressive nuclease activity was fetal bovine

serum, > human serum > human plasma > human synovial fluid. As an overall measure of the effect of these 2'-substitutions on stability and activity, a ratio β was calculated (Table 45). This β value indicated that all modified ribozymes tested had significant, >100 - >1700 fold, increases in overall stability and activity. These increases in β indicate that the lifetime of these modified ribozymes *in vivo* are significantly increased which should lead to a more pronounced biological effect.

More general substitutions of the 2'-modified nucleotides from Figure 81 also increased the $t_{1/2}$ of the resulting modified ribozymes. However the catalytic activity of these ribozymes was decreased > 10-fold.

In Figure 86 compound 37 may be used as a general intermediate to prepare derivatized 2'-C-alkyl phosphoramidites, where X is CH₃, or an alkyl, or other group described above.

The following are non-limiting examples showing the synthesis of nucleic acids using 2'-C-alkyl substituted phosphoramidites, the syntheses of the amidites, their testing for enzymatic activity and nuclease resistance.

Example 53: Synthesis of Hammerhead Ribozymes Containing 2'-Deoxy-2'-Alkyl nucleotides & Other 2'-Modified Nucleotides

The method of synthesis used generally follows the procedure for normal RNA synthesis as described in Usman, N.; Ogilvie, K.K.; Jiang, M.-Y.; Cedergren, R.J. *J. Am. Chem. Soc.* 1987, 109, 7845-7854 and in Scaringe, S.A.; Franklyn, C.; Usman, N. *Nucleic Acids Res.* 1990, 18, 5433-5441 and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end (compounds 10, 12, 17, 22, 31, 18, 26, 32, 36 and 38). Other 2'-modified phosphoramidites were prepared according to: 3 & 4, Eckstein *et al.* *International Publication No.* WO 92/07065; and 5 Kois *et al.* *Nucleosides & Nucleotides* 1993, 12, 1093-1109. The average stepwise coupling yields were ~98%. The 2'-substituted phosphoramidites were incorporated into hammerhead ribozymes as shown in Figure 80. However, these 2'-alkyl substituted phosphoramidites may be incorporated not only into hammerhead ribozymes, but also into hairpin, hepatitis delta virus, Group I or Group II intron catalytic nucleic acids, or into antisense

oligonucleotides. They are, therefore, of general use in any nucleic acid structure.

Example 54: Ribozyme Activity Assay

Purified 5'-end labeled RNA substrates (15-25-mers) and purified 5'-end labeled ribozymes (~36-mers) were both heated to 95 °C, quenched on ice and equilibrated at 37 °C, separately. Ribozyme stock solutions were 1 mM, 200 nM, 40 nM or 8 nM and the final substrate RNA concentrations were ~1 nM. Total reaction volumes were 50 µL. The assay buffer was 50 mM Tris-Cl, pH 7.5 and 10 mM MgCl₂. Reactions were initiated by mixing substrate and ribozyme solutions at t = 0. Aliquots of 5 µL were removed at time points of 1, 5, 15, 30, 60 and 120 m. Each time point was quenched in formamide loading buffer and loaded onto a 15% denaturing polyacrylamide gel for analysis. Quantitative analyses were performed using a phosphorimager (Molecular Dynamics).

Example 55: Stability Assay

500 pmol of gel-purified 5'-end-labeled ribozymes were precipitated in ethanol and pelleted by centrifugation. Each pellet was resuspended in 20 µL of appropriate fluid (human serum, human plasma, human synovial fluid or fetal bovine serum) by vortexing for 20 s at room temperature. The samples were placed into a 37 °C incubator and 2 µL aliquots were withdrawn after incubation for 0, 15, 30, 45, 60, 120, 240 and 480 m. Aliquots were added to 20 µL of a solution containing 95% formamide and 0.5X TBE (50 mM Tris, 50 mM borate, 1 mM EDTA) to quench further nuclease activity and the samples were frozen until loading onto gels. Ribozymes were size-fractionated by electrophoresis in 20% acrylamide/8M urea gels. The amount of intact ribozyme at each time point was quantified by scanning the bands with a phosphorimager (Molecular Dynamics) and the half-life of each ribozyme in the fluids was determined by plotting the percent intact ribozyme vs the time of incubation and extrapolation from the graph.

Example 56: 3',5'-O-(Tetraisopropyl-disiloxane-1,3-diyl)-2'-O-Phenoxythio-carbonyl-Uridine (7)

To a stirred solution of 3',5'-O-(tetraisopropyl-disiloxane-1,3-diyl)-uridine, 6, (15.1 g, 31 mmol, synthesized according to *Nucleic Acid*

Chemistry, ed. Leroy Townsend, 1986 pp. 229-231) and dimethylamino-pyridine (7.57 g, 62 mmol) a solution of phenylchlorothionoformate (5.15 mL, 37.2 mmol) in 50 mL of acetonitrile was added dropwise and the reaction stirred for 8 h. TLC (EtOAc:hexanes / 1:1) showed disappearance of the starting material. The reaction mixture was evaporated, the residue dissolved in chloroform, washed with water and brine, the organic layer was dried over sodium sulfate, filtered and evaporated to dryness. The residue was purified by flash chromatography on silica gel with EtOAc:hexanes / 2:1 as eluent to give 16.44 g (85%) of 7.

10 Example 57: 3',5'-O-(Tetraisopropyl-disiloxane-1,3-diyl)-2'-C-Allyl -Uridine (8)

To a refluxing, under argon, solution of 3',5'-O-(tetraisopropyl-disiloxane-1,3-diyl)-2'-O-phenoxythiocarbonyl-uridine, 7, (5 g, 8.03 mmol) and allyltributyltin (12.3 mL, 40.15 mmol) in dry toluene, benzoyl peroxide (0.5 g) was added portionwise during 1 h. The resulting mixture was allowed to reflux under argon for an additional 7-8 h. The reaction was then evaporated and the product 8 purified by flash chromatography on silica gel with EtOAc:hexanes / 1:3 as eluent. Yield 2.82 g (68.7%).

Example 58: 5'-O-Dimethoxytrityl-2'-C-Allyl-Uridine (9)

20 A solution of 8 (1.25 g, 2.45 mmol) in 10 mL of dry tetrahydrofuran (THF) was treated with a 1 M solution of tetrabutylammoniumfluoride in THF (3.7 mL) for 10 m at room temperature. The resulting mixture was evaporated, the residue was loaded onto a silica gel column, washed with 1 L of chloroform, and the desired deprotected compound was eluted with 25 chloroform:methanol / 9:1. Appropriate fractions were combined, solvents removed by evaporation, and the residue was dried by coevaporation with dry pyridine. The oily residue was redissolved in dry pyridine, dimethoxytritylchloride (1.2 eq) was added and the reaction mixture was left under anhydrous conditions overnight. The reaction was quenched 30 with methanol (20 mL), evaporated, dissolved in chloroform, washed with 5% aq. sodium bicarbonate and brine. The organic layer was dried over sodium sulfate and evaporated. The residue was purified by flash chromatography on silica gel, EtOAc:hexanes / 1:1 as eluent, to give 0.85 g (57%) of 9 as a white foam.

Example 59: 5'-O-Dimethoxytrityl-2'-C-Allyl-Uridine 3'-(2-Cyanoethyl N,N-diisopropylphosphoramidite) (10)

5'-O-Dimethoxytrityl-2'-C-allyl-uridine (0.64 g, 1.12 mmol) was dissolved in dry dichloromethane under dry argon. N,N-Diisopropylethyl-amine (0.39 mL, 2.24 mmol) was added and the solution was ice-cooled. 2-Cyanoethyl N,N-diisopropylchlorophosphoramidite (0.35 mL, 1.57 mmol) was added dropwise to the stirred reaction solution and stirring was continued for 2 h at RT. The reaction mixture was then ice-cooled and quenched with 12 mL of dry methanol. After stirring for 5 m, the mixture was concentrated *in vacuo* (40 °C) and purified by flash chromatography on silica gel using a gradient of 10-60% EtOAc in hexanes containing 1% triethylamine mixture as eluent. Yield: 0.78 g (90%), white foam.

Example 60: 3',5'-O-(Tetraisopropyl-disiloxane-1,3-diyl)-2'-C-Allyl-N⁴-Acetyl-Cytidine (11)

Triethylamine (6.35 mL, 45.55 mmol) was added dropwise to a stirred ice-cooled mixture of 1,2,4-triazole (5.66 g, 81.99 mmol) and phosphorous oxychloride (0.86 mL, 9.11 mmol) in 50 mL of anhydrous acetonitrile. To the resulting suspension a solution of 3',5'-O-(tetraisopropyl-disiloxane-1,3-diyl)-2'-C-allyl uridine (2.32 g, 4.55 mmol) in 30 mL of acetonitrile was added dropwise and the reaction mixture was stirred for 4 h at room temperature. The reaction was concentrated *in vacuo* to a minimal volume (not to dryness). The residue was dissolved in chloroform and washed with water, saturated aq. sodium bicarbonate and brine. The organic layer was dried over sodium sulfate and the solvent was removed *in vacuo*. The resulting foam was dissolved in 50 mL of 1,4-dioxane and treated with 29% aq. NH₄OH overnight at room temperature. TLC (chloroform:methanol / 9:1) showed complete conversion of the starting material. The solution was evaporated, dried by coevaporation with anhydrous pyridine and acetylated with acetic anhydride (0.52 mL, 5.46 mmol) in pyridine overnight. The reaction mixture was quenched with methanol, evaporated, the residue was dissolved in chloroform, washed with sodium bicarbonate and brine. The organic layer was dried over sodium sulfate, evaporated to dryness and purified by flash chromatography on silica gel (3% MeOH in chloroform). Yield 2.3 g (90%) as a white foam.

Example 61: 5'-O-Dimethoxytrityl-2'-C-Allyl-N⁴-Acetyl-Cytidine

This compound was obtained analogously to the uridine derivative 9 in 55% yield.

Example 62: 5'-O-Dimethoxytrityl-2'-C-allyl-N⁴-Acetyl-Cytidine 3'-(2-Cyanoethyl N,N-diisopropylphosphoramidite) (12)

2'-O-Dimethoxytrityl-2'-C-allyl-N⁴-acetyl cytidine (0.8 g, 1.31 mmol) was dissolved in dry dichloromethane under argon. N,N-Diisopropylethylamine (0.46 mL, 2.62 mmol) was added and the solution was ice-cooled. 2-Cyanoethyl N,N-diisopropylchlorophosphoramidite (0.38 mL, 1.7 mmol) was added dropwise to a stirred reaction solution and stirring was continued for 2 h at room temperature. The reaction mixture was then ice-cooled and quenched with 12 mL of dry methanol. After stirring for 5 m, the mixture was concentrated *in vacuo* (40 °C) and purified by flash chromatography on silica gel using chloroform:ethanol / 98:2 with 2% triethylamine mixture as eluent. Yield: 0.91 g (85%), white foam.

Example 63: 2'-Deoxy-2'-Methylene-Uridine

2'-Deoxy-2'-methylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-uridine 14 (Hansske, F.; Madej, D.; Robins, M. J. *Tetrahedron* 1984, 40, 125 and Matsuda, A.; Takenuki, K.; Tanaka, S.; Sasaki, T.; Ueda, T. *J. Med. Chem.* 1991, 34, 812) (2.2 g, 4.55 mmol) dissolved in THF (20 mL) was treated with 1 M TBAF in THF (10 mL) for 20 m and concentrated *in vacuo*. The residue was triturated with petroleum ether and chromatographed on a silica gel column. 2'-Deoxy-2'-methylene-uridine (1.0 g, 3.3 mmol, 72.5%) was eluted with 20% MeOH in CH₂Cl₂.

Example 64: 5'-O-DMT-2'-Deoxy-2'-Methylene-Uridine (15)

2'-Deoxy-2'-methylene-uridine (0.91 g, 3.79 mmol) was dissolved in pyridine (10 mL) and a solution of DMT-Cl in pyridine (10 mL) was added dropwise over 15 m. The resulting mixture was stirred at RT for 12 h and MeOH (2 mL) was added to quench the reaction. The mixture was concentrated *in vacuo* and the residue taken up in CH₂Cl₂ (100 mL) and washed with sat. NaHCO₃, water and brine. The organic extracts were dried over MgSO₄, concentrated *in vacuo* and purified over a silica gel column using EtOAc:hexanes as eluant to yield 15 (0.43 g, 0.79 mmol, 22%).

Example 65: 5'-O-DMT-2'-Deoxy-2'-Methylene-Uridine 3'-(2-Cyanoethyl N,N-diisopropylphosphoramidite) (17)

1-(2'-Deoxy-2'-methylene-5'-O-dimethoxytrityl-β-D-ribofuranosyl)-uracil (0.43 g, 0.8 mmol) dissolved in dry CH₂Cl₂ (15 mL) was placed in a round-bottom flask under Ar. Diisopropylethylamine (0.28 mL, 1.6 mmol) was added, followed by the dropwise addition of 2-cyanoethyl N,N-diisopropylchlorophosphoramidite (0.25 mL, 1.12 mmol). The reaction mixture was stirred 2 h at RT and quenched with ethanol (1 mL). After 10 m the mixture evaporated to a syrup *in vacuo* (40 °C). The product (0.3 g, 0.4 mmol, 50%) was purified by flash column chromatography over silica gel using a 25-70% EtOAc gradient in hexanes, containing 1% triethylamine, as eluant. R_f 0.42 (CH₂Cl₂: MeOH / 15:1)

Example 66: 2'-Deoxy-2'-Difluoromethylene-3',5'-O-(Tetraisopropylidisiloxane-1,3-diyl)-Uridine

2'-Keto-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)uridine **14** (1.92 g, 12.6 mmol) and triphenylphosphine (2.5 g, 9.25 mmol) were dissolved in diglyme (20 mL), and heated to a bath temperature of 160 °C. A warm (60 °C) solution of sodium chlorodifluoroacetate in diglyme (50 mL) was added (dropwise from an equilibrating dropping funnel) over a period of ~1 h. The resulting mixture was further stirred for 2 h and concentrated *in vacuo*. The residue was dissolved in CH₂Cl₂ and chromatographed over silica gel. 2'-Deoxy-2'-difluoromethylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-uridine (3.1 g, 5.9 mmol, 70%) eluted with 25% hexanes in EtOAc.

Example 67: 2'-Deoxy-2'-Difluoromethylene-Uridine

2'-Deoxy-2'-methylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-uridine (3.1 g, 5.9 mmol) dissolved in THF (20 mL) was treated with 1 M TBAF in THF (10 mL) for 20 m and concentrated *in vacuo*. The residue was triturated with petroleum ether and chromatographed on silica gel column. 2'-Deoxy-2'-difluoromethylene-uridine (1.1 g, 4.0 mmol, 68%) was eluted with 20% MeOH in CH₂Cl₂.

Example 68: 5'-O-DMT-2'-Deoxy-2'-Difluoromethylene-Uridine (16)

2'-Deoxy-2'-difluoromethylene-uridine (1.1 g, 4.0 mmol) was dissolved in pyridine (10 mL) and a solution of DMT-Cl (1.42 g, 4.18 mmol) in pyridine (10 mL) was added dropwise over 15 m. The resulting mixture

was stirred at RT for 12 h and MeOH (2 mL) was added to quench the reaction. The mixture was concentrated *in vacuo* and the residue taken up in CH₂Cl₂ (100 mL) and washed with sat. NaHCO₃, water and brine. The organic extracts were dried over MgSO₄, concentrated *in vacuo* and
5 purified over a silica gel column using 40% EtOAc:hexanes as eluant to yield 5'-O-DMT-2'-deoxy-2'-difluoromethylene-uridine 16 (1.05 g, 1.8 mmol, 45%).

Example 69: 5'-O-DMT-2'-Deoxy-2'-Difluoromethylene-Uridine 3'-(2-Cyanoethyl N,N-diisopropylphosphoramidite) (18)

10 1-(2'-Deoxy-2'-difluoromethylene-5'-O-dimethoxytrityl-β-D-ribofuranosyl)-uracil (0.577 g, 1 mmol) dissolved in dry CH₂Cl₂ (15 mL) was placed in a round-bottom flask under Ar. Diisopropylethylamine (0.36 mL, 2 mmol) was added, followed by the dropwise addition of 2-cyanoethyl N,N-diisopropylchlorophosphoramidite (0.44 mL, 1.4 mmol). The reaction mixture
15 was stirred for 2 h at RT and quenched with ethanol (1 mL). After 10 m the mixture evaporated to a syrup *in vacuo* (40 °C). The product (0.404 g, 0.52 mmol, 52%) was purified by flash chromatography over silica gel using 20-50% EtOAc gradient in hexanes, containing 1% triethylamine, as eluant. R_f 0.48 (CH₂Cl₂: MeOH / 15:1).

20 Example 70: 2'-Deoxy-2'-Methylene-3',5'-O-(Tetraisopropylidisiloxane-1,3-diyl)-4-N-Acetyl-Cytidine 20

Triethylamine (4.8 mL, 34 mmol) was added to a solution of POCl₃ (0.65 mL, 6.8 mmol) and 1,2,4-triazole (2.1 g, 30.6 mmol) in acetonitrile (20 mL) at 0 °C. A solution of 2'-deoxy-2'-methylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl) uridine 19 (1.65 g, 3.4 mmol) in acetonitrile (20 mL) was
25 added dropwise to the above reaction mixture and left to stir at room temperature for 4 h. The mixture was concentrated *in vacuo*, dissolved in CH₂Cl₂ (2 x 100 mL) and washed with 5% NaHCO₃ (1 x 100 mL). The organic extracts were dried over Na₂SO₄ concentrated *in vacuo*, dissolved
30 in dioxane (10 mL) and aq. ammonia (20 mL). The mixture was stirred for 12 h and concentrated *in vacuo*. The residue was azeotroped with anhydrous pyridine (2 x 20 mL). Acetic anhydride (3 mL) was added to the residue dissolved in pyridine, stirred at RT for 4 h and quenched with sat. NaHCO₃ (5 mL). The mixture was concentrated *in vacuo*, dissolved in
35 CH₂Cl₂ (2 x 100 mL) and washed with 5% NaHCO₃ (1 x 100 mL). The

organic extracts were dried over Na_2SO_4 , concentrated *in vacuo* and the residue chromatographed over silica gel. 2'-Deoxy-2'-methylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-4-N-acetyl-cytidine **20** (1.3 g, 2.5 mmol, 73%) was eluted with 20% EtOAc in hexanes.

5 Example 71: 1-(2'-Deoxy-2'-Methylene-5'-O-Dimethoxytrityl-β-D-ribofuranosyl)-4-N-Acetyl-Cytosine **21**

2'-Deoxy-2'-methylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-4-N-acetyl-cytidine **20** (1.3 g, 2.5 mmol) dissolved in THF (20 mL) was treated with 1 M TBAF in THF (3 mL) for 20 m and concentrated *in vacuo*. The residue was triturated with petroleum ether and chromatographed on silica gel column. 2'-Deoxy-2'-methylene-4-N-acetyl-cytidine (0.56 g, 1.99 mmol, 80%) was eluted with 10% MeOH in CH_2Cl_2 . 2'-Deoxy-2'-methylene-4-N-acetyl-cytidine (0.56 g, 1.99 mmol) was dissolved in pyridine (10 mL) and a solution of DMT-Cl (0.81 g, 2.4 mmol) in pyridine (10 mL) was added dropwise over 15 m. The resulting mixture was stirred at RT for 12 h and MeOH (2 mL) was added to quench the reaction. The mixture was concentrated *in vacuo* and the residue taken up in CH_2Cl_2 (100 mL) and washed with sat. NaHCO_3 (50 mL), water (50 mL) and brine (50 mL). The organic extracts were dried over MgSO_4 , concentrated *in vacuo* and purified over a silica gel column using EtOAc:hexanes / 60:40 as eluant to yield **21** (0.88 g, 1.5 mmol, 75%).

Example 72: 1-(2'-Deoxy-2'-Methylene-5'-O-Dimethoxytrityl-β-D-ribofuranosyl)-4-N-Acetyl-Cytosine 3'-(2-Cyanoethyl-N,N-diisopropylphosphoramidite) (**22**)

25 1-(2'-Deoxy-2'-methylene-5'-O-dimethoxytrityl-β-D-ribofuranosyl)-4-N-acetyl-cytosine **21** (0.88 g, 1.5 mmol) dissolved in dry CH_2Cl_2 (10 mL) was placed in a round-bottom flask under Ar. Diisopropylethylamine (0.8 mL, 4.5 mmol) was added, followed by the dropwise addition of 2-cyanoethyl N,N-diisopropylchlorophosphoramidite (0.4 mL, 1.8 mmol). The reaction mixture was stirred 2 h at room temperature and quenched with ethanol (1 mL). After 10 m the mixture evaporated to a syrup *in vacuo* (40 °C). The product **22** (0.82 g, 1.04 mmol, 69%) was purified by flash chromatography over silica gel using 50-70% EtOAc gradient in hexanes, containing 1% triethylamine, as eluant. R_f 0.36 (CH_2Cl_2 :MeOH / 20:1).

**Example 73: 2'-Deoxy-2'-Difluoromethylene-3',5'-O-(Tetraisopropyl
disiloxane-1,3-diyl)-4-N-Acetyl-Cytidine (24)**

Et₃N (6.9 mL, 50 mmol) was added to a solution of POCl₃ (0.94 mL, 10 mmol) and 1,2,4-triazole (3.1 g, 45 mmol) in acetonitrile (20 mL) at 0 °C. A solution of 2'-deoxy-2'-difluoromethylene-3',5'-O-(tetraisopropyl-
disiloxane-1,3-diyl)uridine 23 ([described in example 14] 2.6 g, 5 mmol) in acetonitrile (20 mL) was added dropwise to the above reaction mixture and left to stir at RT for 4 h. The mixture was concentrated *in vacuo*, dissolved in CH₂Cl₂ (2 x 100 mL) and washed with 5% NaHCO₃ (1 x 100 mL). The organic extracts were dried over Na₂SO₄ concentrated *in vacuo*, dissolved in dioxane (20 mL) and aq. ammonia (30 mL). The mixture was stirred for 12 h and concentrated *in vacuo*. The residue was azeotroped with anhydrous pyridine (2 x 20 mL). Acetic anhydride (5 mL) was added to the residue dissolved in pyridine, stirred at RT for 4 h and quenched with sat. NaHCO₃ (5mL). The mixture was concentrated *in vacuo*, dissolved in CH₂Cl₂ (2 x 100 mL) and washed with 5% NaHCO₃ (1 x 100 mL). The organic extracts were dried over Na₂SO₄, concentrated *in vacuo* and the residue chromatographed over silica gel. 2'-Deoxy-2'-difluoromethylene-3',5'-O-(tetraisopropyl-
disiloxane-1,3-diyl)-4-N-acetyl-cytidine 24 (2.2 g, 3.9 mmol, 78%) was eluted with 20% EtOAc in hexanes.

**Example 74: 1-(2'-Deoxy-2'-Difluoromethylene-5'-O-Dimethoxytrityl-β-D-
ribofuranosyl)-4-N-Acetyl-Cytosine (25)**

2'-Deoxy-2'-difluoromethylene-3',5'-O-(tetraisopropyl-
disiloxane-1,3-diyl)-4-N-acetyl-cytidine 24 (2.2 g, 3.9 mmol) dissolved in THF (20 mL) was treated with 1 M TBAF in THF (3 mL) for 20 m and concentrated *in vacuo*. The residue was triturated with petroleum ether and chromatographed on a silica gel column. 2'-Deoxy-2'-difluoromethylene-4-N-acetyl-cytidine (0.89 g, 2.8 mmol, 72%) was eluted with 10% MeOH in CH₂Cl₂. 2'-Deoxy-2'-difluoromethylene-4-N-acetyl-cytidine (0.89 g, 2.8 mmol) was dissolved in pyridine (10 mL) and a solution of DMT-Cl (1.03 g, 3.1 mmol) in pyridine (10 mL) was added dropwise over 15 m. The resulting mixture was stirred at RT for 12 h and MeOH (2 mL) was added to quench the reaction. The mixture was concentrated *in vacuo* and the residue taken up in CH₂Cl₂ (100 mL) and washed with sat. NaHCO₃ (50 mL), water (50 mL) and brine (50 mL). The organic extracts were dried over MgSO₄, concentrated *in*

vacuo and purified over a silica gel column using EtOAc:hexanes / 60:40 as eluant to yield 25 (1.2 g, 1.9 mmol, 68%).

5 Example 75: 1-(2'-Deoxy-2'-Difluoromethylene-5'-O-Dimethoxytrityl-β-D-ribofuranosyl)-4-N-Acetylcytosine 3'-(2-cyanoethyl-N,N-diisopropylphosphoramidite) (26)

1-(2'-Deoxy-2'-difluoromethylene-5'-O-dimethoxytrityl-β-D-ribofuranosyl)-4-N-acetylcytosine 25 (0.6 g, 0.97 mmol) dissolved in dry CH₂Cl₂ (10 mL) was placed in a round-bottom flask under Ar. Diisopropylethylamine (0.5 mL, 2.9 mmol) was added, followed by the dropwise addition of 2-cyanoethyl N,N-diisopropylchlorophosphoramidite (0.4 mL, 1.8 mmol). The reaction mixture was stirred 2 h at RT and quenched with ethanol (1 mL). After 10 m the mixture was evaporated to a syrup *in vacuo* (40 °C). The product 26, a white foam (0.52 g, 0.63 mmol, 65%) was purified by flash chromatography over silica gel using 30-70% EtOAc gradient in hexanes, containing 1% triethylamine, as eluant. R_f 0.48 (CH₂Cl₂:MeOH / 20:1).

Example 76: 2'-Keto-3',5'-O-(Tetraisopropylidisiloxane-1,3-diyl)-6-N-(4-*t*-Butylbenzoyl)-Adenosine (28)

Acetic anhydride (4.6 mL) was added to a solution of 3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-N-(4-*t*-butylbenzoyl)-adenosine (Brown, J.; Christodolou, C.; Jones, S.; Modak, A.; Reese, C.; Sibanda, S.; Ubasawa A. *J. Chem. Soc. Perkin Trans. I* 1989, 1735) (6.2 g, 9.2 mmol) in DMSO (37 mL) and the resulting mixture was stirred at room temperature for 24 h. The mixture was concentrated *in vacuo*. The residue was taken up in EtOAc and washed with water. The organic layer was dried over MgSO₄ and concentrated *in vacuo*. The residue was purified on a silica gel column to yield 2'-keto-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-N-(4-*t*-butylbenzoyl)-adenosine 28 (4.8 g, 7.2 mmol, 78%).

Example 77: 2'-Deoxy-2'-methylene-3',5'-O-(Tetraisopropylidisiloxane-1,3-diyl)-6-N-(4-*t*-Butylbenzoyl)-Adenosine (29)

30 Under a pressure of argon, sec-butyllithium in hexanes (11.2 mL, 14.6 mmol) was added to a suspension of triphenylmethylphosphonium iodide (7.07 g, 17.5 mmol) in THF (25 mL) cooled at -78 °C. The homogeneous orange solution was allowed to warm to -30 °C and a solution of 2'-keto-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-N-(4-*t*-butylbenzoyl)-adenosine

- 28 (4.87 g, 7.3 mmol) in THF (25 mL) was transferred to this mixture under argon pressure. After warming to RT, stirring was continued for 24 h. THF was evaporated and replaced by CH₂Cl₂ (250 mL), water was added (20 mL), and the solution was neutralized with a cooled solution of 2% HCl.
- 5 The organic layer was washed with H₂O (20 mL), 5% aqueous NaHCO₃ (20 mL), H₂O to neutrality, and brine (10 mL). After drying (Na₂SO₄), the solvent was evaporated *in vacuo* to give the crude compound, which was chromatographed on a silica gel column. Elution with light petroleum ether:EtOAc / 7:3 afforded pure 2'-deoxy-2'-methylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-N-(4-*t*-butylbenzoyl)-adenosine 29 (3.86 g, 5.8 mmol, 79%).
- 10

Example 78: 2'-Deoxy-2'-Methylene-6-N-(4-*t*-Butylbenzoyl)-Adenosine

- 2'-Deoxy-2'-methylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-N-(4-*t*-butylbenzoyl)-adenosine (3.86 g, 5.8 mmol) dissolved in THF (30 mL) was treated with 1 M TBAF in THF (15 mL) for 20 m and concentrated *in vacuo*. The residue was triturated with petroleum ether and chromatographed on a silica gel column. 2'-Deoxy-2'-methylene-6-N-(4-*t*-butylbenzoyl)-adenosine (1.8 g, 4.3 mmol, 74%) was eluted with 10% MeOH in CH₂Cl₂.
- 15

20 **Example 79: 5'-O-DMT-2'-Deoxy-2'-Methylene-6-N-(4-*t*-Butylbenzoyl)-Adenosine (29)**

- 2'-Deoxy-2'-methylene-6-N-(4-*t*-butylbenzoyl)-adenosine (0.75 g, 1.77 mmol) was dissolved in pyridine (10 mL) and a solution of DMT-Cl (0.66 g, 1.98 mmol) in pyridine (10 mL) was added dropwise over 15 m.
- 25 The resulting mixture was stirred at RT for 12 h and MeOH (2 mL) was added to quench the reaction. The mixture was concentrated *in vacuo* and the residue taken up in CH₂Cl₂ (100 mL) and washed with sat. NaHCO₃, water and brine. The organic extracts were dried over MgSO₄, concentrated *in vacuo* and purified over a silica gel column using 50% EtOAc:hexanes as an eluant to yield 29 (0.81 g, 1.1 mmol, 62%).
- 30

Example 80: 5'-O-DMT-2'-Deoxy-2'-Methylene-6-N-(4-*t*-Butylbenzoyl)-Adenosine 3'-(2-Cyanoethyl *N,N*-diisopropylphosphoramidite) (31)

1-(2'-Deoxy-2'-methylene-5'-O-dimethoxytrityl-β-D-ribofuranosyl)-6-N-(4-*t*-butylbenzoyl)-adenine 29 dissolved in dry CH₂Cl₂ (15 mL) was placed

in a round bottom flask under Ar. Diisopropylethylamine was added, followed by the dropwise addition of 2-cyanoethyl *N,N*-diisopropylchlorophosphoramidite. The reaction mixture was stirred 2 h at RT and quenched with ethanol (1 mL). After 10 m the mixture was
5 evaporated to a syrup *in vacuo* (40 °C). The product was purified by flash chromatography over silica gel using 30-50% EtOAc gradient in hexanes, containing 1% triethylamine, as eluant (0.7 g, 0.76 mmol, 68%). *R*_f 0.45 (CH₂Cl₂: MeOH / 20:1)

10 Example 81: 2'-Deoxy-2'-Difluoromethylene-3',5'-O-(Tetraisopropylidisiloxane-1,3-diyl)-6-*N*-(4-*t*-Butylbenzoyl)-Adenosine

2'-Keto-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-*N*-(4-*t*-butylbenzoyl)-adenosine 28 (6.7 g, 10 mmol) and triphenylphosphine (2.9 g, 11 mmol) were dissolved in diglyme (20 mL), and heated to a bath temperature of 160 °C. A warm (60 °C) solution of sodium
15 chlorodifluoroacetate (2.3 g, 15 mmol) in diglyme (50 mL) was added (dropwise from an equilibrating dropping funnel) over a period of ~1 h. The resulting mixture was further stirred for 2 h and concentrated *in vacuo*. The residue was dissolved in CH₂Cl₂ and chromatographed over silica gel. 2'-Deoxy-2'-difluoromethylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-*N*-(4-*t*-butylbenzoyl)-adenosine (4.1g, 6.4 mmol, 64%) eluted with 15%
20 hexanes in EtOAc.

Example 82: 2'-Deoxy-2'-Difluoromethylene-6-*N*-(4-*t*-Butylbenzoyl)-Adenosine

2'-Deoxy-2'-difluoromethylene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-6-*N*-(4-*t*-butylbenzoyl)-adenosine (4.1 g, 6.4 mmol) dissolved in THF
25 (20 mL) was treated with 1 M TBAF in THF (10 mL) for 20 m and concentrated *in vacuo*. The residue was triturated with petroleum ether and chromatographed on a silica gel column. 2'-Deoxy-2'-difluoromethylene-6-*N*-(4-*t*-butylbenzoyl)-adenosine (2.3 g, 4.9 mmol, 77%) was eluted
30 with 20% MeOH in CH₂Cl₂.

Example 83: 5'-O-DMT-2'-Deoxy-2'-Difluoromethylene-6-*N*-(4-*t*-Butylbenzoyl)-Adenosine (30)

2'-Deoxy-2'-difluoromethylene-6-*N*-(4-*t*-butylbenzoyl)-adenosine (2.3 g, 4.9 mmol) was dissolved in pyridine (10 mL) and a solution of DMT-Cl in

pyridine (10 mL) was added dropwise over 15 m. The resulting mixture was stirred at RT for 12 h and MeOH (2 mL) was added to quench the reaction. The mixture was concentrated *in vacuo* and the residue taken up in CH₂Cl₂ (100 mL) and washed with sat. NaHCO₃, water and brine. The organic extracts were dried over MgSO₄, concentrated *in vacuo* and purified over a silica gel column using 50% EtOAc:hexanes as eluant to yield 30 (2.6 g, 3.41 mmol, 69%).

10 Example 84: 5'-O-DMT-2'-Deoxy-2'-Difluoromethylene-6-N-(4-*t*-Butylbenzoyl)-Adenosine 3'-(2-Cyanoethyl *N,N*-diisopropylphosphoramidite) (32)

15 1-(2'-Deoxy-2'-difluoromethylene-5'-*O*-dimethoxytrityl-β-D-ribofuransyl)-6-*N*-(4-*t*-butylbenzoyl)-adenine 30 (2.6 g, 3.4 mmol) dissolved in dry CH₂Cl₂ (25 mL) was placed in a round bottom flask under Ar. Diisopropylethylamine (1.2 mL, 6.8 mmol) was added, followed by the dropwise addition of 2-cyanoethyl *N,N*-diisopropylchlorophosphoramidite (1.06 mL, 4.76 mmol). The reaction mixture was stirred 2 h at RT and quenched with ethanol (1 mL). After 10 m the mixture evaporated to a syrup *in vacuo* (40 °C). 32 (2.3 g, 2.4 mmol, 70%) was purified by flash column chromatography over silica gel using 20-50% EtOAc gradient in hexanes, containing 1% triethylamine, as eluant. R_f 0.52 (CH₂Cl₂: MeOH / 15:1).

Example 85: 2'-Deoxy-2'-Methoxycarbonylmethylidene-3',5'-*O*-(Tetraisopropylidisiloxane-1,3-diyl)-Uridine (33)

25 Methyl(triphenylphosphoranylidene)acetate (5.4 g, 16 mmol) was added to a solution of 2'-keto-3',5'-*O*-(tetraisopropyl disiloxane-1,3-diyl)-uridine 14 in CH₂Cl₂ under argon. The mixture was left to stir at RT for 30 h. CH₂Cl₂ (100 mL) and water were added (20 mL), and the solution was neutralized with a cooled solution of 2% HCl. The organic layer was washed with H₂O (20 mL), 5% aq. NaHCO₃ (20 mL), H₂O to neutrality, and brine (10 mL). After drying (Na₂SO₄), the solvent was evaporated *in vacuo* to give crude product, that was chromatographed on a silica gel column. Elution with light petroleum ether:EtOAc / 7:3 afforded pure 2'-deoxy-2'-methoxycarbonylmethylidene-3',5'-*O*-(tetraisopropylidisiloxane-1,3-diyl)-uridine 33 (5.8 g, 10.8 mmol, 67.5%).

Example 86: 2'-Deoxy-2'-Methoxycarbonylmethylidene-Uridine (34)

Et₃N•3 HF (3 mL) was added to a solution of 2'-deoxy-2'-methoxycarbonylmethylidene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-uridine 33 (5 g, 9.3 mmol) dissolved in CH₂Cl₂ (20 mL) and Et₃N (15 mL). The resulting mixture was evaporated *in vacuo* after 1 h and chromatographed on a silica gel column eluting 2'-deoxy-2'-methoxycarbonylmethylidene-uridine 34 (2.4 g, 8 mmol, 86%) with THF:CH₂Cl₂ / 4:1.

Example 87: 5'-O-DMT-2'-Deoxy-2'-Methoxycarbonylmethylidene-Uridine (35)

2'-Deoxy-2'-methoxycarbonylmethylidene-uridine 34 (1.2 g, 4.02 mmol) was dissolved in pyridine (20 mL). A solution of DMT-Cl (1.5 g, 4.42 mmol) in pyridine (10 mL) was added dropwise over 15 m. The resulting mixture was stirred at RT for 12 h and MeOH (2 mL) was added to quench the reaction. The mixture was concentrated *in vacuo* and the residue taken up in CH₂Cl₂ (100 mL) and washed with sat. NaHCO₃, water and brine. The organic extracts were dried over MgSO₄, concentrated *in vacuo* and purified over a silica gel column using 2-5% MeOH in CH₂Cl₂ as an eluant to yield 5'-O-DMT-2'-deoxy-2'-methoxycarbonylmethylidene-uridine 35 (2.03 g, 3.46 mmol, 86%).

Example 88: 5'-O-DMT-2'-Deoxy-2'-Methoxycarbonylmethylidene-Uridine 3'-(2-cyanoethyl-N,N-diisopropylphosphoramidite) (36)

1-(2'-Deoxy-2'-2'-methoxycarbonylmethylidene-5'-O-dimethoxytrityl-β-D-ribofuranosyl)-uridine 35 (2.0 g, 3.4 mmol) dissolved in dry CH₂Cl₂ (10 mL) was placed in a round-bottom flask under Ar. Diisopropylethylamine (1.2 mL, 6.8 mmol) was added, followed by the dropwise addition of 2-cyanoethyl N,N-diisopropylchlorophosphoramidite (0.91 mL, 4.08 mmol). The reaction mixture was stirred 2 h at RT and quenched with ethanol (1 mL). After 10 m the mixture was evaporated to a syrup *in vacuo* (40 °C). 5'-O-DMT-2'-deoxy-2'-methoxycarbonylmethylidene-uridine 3'-(2-cyanoethyl-N,N-diisopropylphosphoramidite) 36 (1.8 g, 2.3 mmol, 67%) was purified by flash column chromatography over silica gel using a 30-60% EtOAc gradient in hexanes, containing 1% triethylamine, as eluant. R_f 0.44 (CH₂Cl₂:MeOH / 9.5:0.5).

Example 89: 2'-Deoxy-2'-Carboxymethylidene-3',5'-O-(Tetraisopropylidisiloxane-1,3-diyl)-Uridine 37

2'-Deoxy-2'-methoxycarbonylmethylidene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-uridine **33** (5.0 g, 10.8 mmol) was dissolved in MeOH (50 mL) and 1 N NaOH solution (50 mL) was added to the stirred solution at RT. The mixture was stirred for 2 h and MeOH removed *in vacuo*. The pH of the aqueous layer was adjusted to 4.5 with 1N HCl solution, extracted with EtOAc (2 x 100 mL), washed with brine, dried over MgSO₄ and concentrated *in vacuo* to yield the crude acid. 2'-Deoxy-2'-carboxymethylidene-3',5'-O-(tetraisopropylidisiloxane-1,3-diyl)-uridine **37** (4.2 g, 7.8 mmol, 73%) was purified on a silica gel column using a gradient of 10-15% MeOH in CH₂Cl₂.

The alkyl substituted nucleotides of this invention can be used to form stable oligonucleotides as discussed above for use in enzymatic cleavage or antisense situations. Such oligonucleotides can be formed enzymatically using triphosphate forms by standard procedure. Administration of such oligonucleotides is by standard procedure. See Sullivan *et al.* PCT WO 94/02595.

Oligonucleotides with 3' and/or 5' Dihalophosphonate

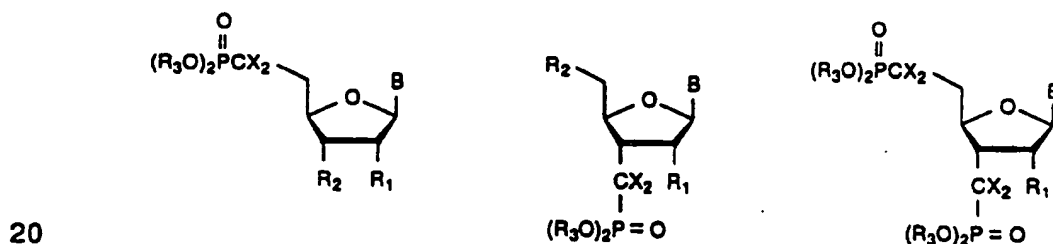
This invention synthesis and uses 3' and/or 5' dihalophosphonate-, e.g., 3' or 5'-CF₂-phosphonate-, substituted nucleotides that maintain or enhance the catalytic activity and/or nuclease resistance of an enzymatic or antisense molecule.

As the term is used in this application, 5'- and/or 3'-dihalophosphonate nucleotide containing ribozymes, deoxyribozymes (see Usman *et al.*, PCT/US94/11649, incorporated by reference herein), and chimeras of nucleotides, are catalytic nucleic molecules that contain 5'- and/or 3'-dihalophosphonate nucleotide components replacing, but not limited to, double-stranded stems, single-stranded "catalytic core" sequences, single-stranded loops or single-stranded recognition sequences. These molecules are able to cleave (preferably, repeatedly cleave) separate RNA or DNA molecules in a nucleotide base sequence specific manner. Such catalytic nucleic acids can also act to cleave intramolecularly if that is desired. Such enzymatic molecules can be targeted to virtually any RNA or DNA transcript. This invention concerns

nucleic acids formed of standard nucleotides or modified nucleotides, which also contain at least one 5'-dihalophosphonate and/or one 3'-dihalophosphonate group.

The synthesis of 1-O-Ac-2,3-di-O-Bz-D-ribofuranose 5-d-
 5-dihalomethylphosphonate in three steps from 1-O-methyl-2,3-O-
 isopropylidene-β-D-ribofuranose 5-deoxy-5-dihalomethylphosphonate is
 described (e.g., for the difluoro, in Figure 87). Condensation of this suitably
 derivatized sugar with silylated pyrimidines and purines affords novel
 nucleoside 5'-deoxy-5'-dihalomethylphosphonates. These intermediates
 may be incorporated into catalytic or antisense nucleic acids by either
 chemical (conversion of the nucleoside 5'-deoxy-5'-
 dihalomethylphosphonates into suitably protected phosphoramidites 12a
 or solid supports 12b, e.g., Figure 88) or enzymatic means (conversion of
 the nucleoside 5'-deoxy-5'-dihalomethylphosphonates into their
 triphosphates, e.g., 14 Figure 89, for T7 transcription).

Thus, in one aspect the invention features 5' and/or 3'-
 dihalonucleotides and nucleic acids containing such 5' and/or 3'-
 dihalonucleotides. The general structure of such molecules is shown
 below.



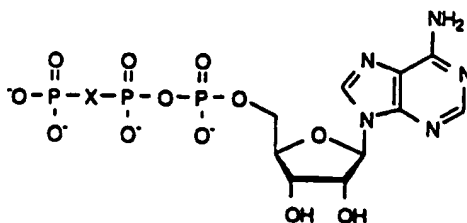
where R₁ is H, OH, or R, where R is a hydroxyl protecting group, e.g.,
 acyl, alkylsilyl, or carbonate; each R₂ is separately H, OH, or R; each R₃ is
 separately a phosphate protecting group, e.g., methyl, ethyl, cyanoethyl, p-
 nitrophenyl, or chlorophenyl; each X is separately any halogen; and each B
 is any nucleotide base.

The invention in particular features nucleic acid molecules having
 such modified nucleotides and enzymatic activity. In a related aspect the
 invention features a method for synthesis of such nucleoside 5'-deoxy-5'-
 dihalo and/or 3'-deoxy-3'-dihalophosphonates by condensing a

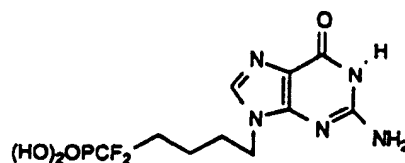
dihalophosphonate-containing sugar with a pyrimidine or a purine under conditions suitable to form a nucleoside 5'-deoxy-5'-dihalophosphonate and/or a 3'-deoxy-3'-dihalophosphonate.

Phosphonic acids may exhibit important biological properties
5 because of their similarity to phosphates (Engel, *Chem. Rev.* 1977, 77, 349-367). Blackburn and Kent (*J. Chem. Soc., Perkin Trans.* 1986, 913-917) indicate that based on electronic and steric considerations α -fluoro and α,α -difluoromethylphosphonates might mimic phosphate esters better than the corresponding phosphonates. Analogues of pyro- and
10 triphosphates 1, where the bridging oxygen atoms are replaced by a difluoromethylene group, have been employed as substrates in enzymatic processes (Blackburn *et al.*, *Nucleosides & Nucleotides* 1985, 4, 165-167; Blackburn *et al.*, *Chem. Scr.* 1986, 26, 21-24). 9-(5,5-Difluoro-5-phosphonopentyl)guanine (2) has been utilized as a multisubstrate
15 analogue inhibitor of purine nucleoside phosphorylase (Halazy *et al.*, *J. Am. Chem. Soc.* 1991, 113, 315-317). Oligonucleotides containing methylene groups in place of phosphodiester 5'-oxygens are resistant toward nucleases that cleave phosphodiester linkages between phosphorus and the 5'-oxygen (Breaker *et al.*, *Biochemistry* 1993, 32, 9125-9128), but can still form stable complexes with complementary
20 sequences. Heinemann *et al.* (*Nucleic Acids Res.* 1991, 19, 427-433) found that a single 3'-methylenephosphonate linkage had a minor influence on the conformation of a DNA octamer double helix.

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1



2



3

One common synthetic approach to α,α -difluoro-alkylphosphonates features the displacement of a leaving group from a suitable reactive substrate by diethyl (lithiodifluoromethyl)phosphonate (3) (Obayashi *et al.*, *Tetrahedron Lett.* 1982, 23, 2323-2326). However, our attempts to synthesize nucleoside 5'-deoxy-5'-difluoro-methylphosphonates from 5'-deoxy-5'-iodonucleosides using 3 were unsuccessful, *i.e.* starting compounds were quantitatively recovered. The reaction of nucleoside 5'-aldehydes with 3, according to the procedure of Martin *et al.* (Martin *et al.*, *Tetrahedron Lett.* 1992, 33, 1839-1842), led to a complex mixture of products. Recently, the synthesis of sugar α,α -difluoroalkylphosphonates from primary sugar triflates using 3 was described (Berkowitz *et al.*, *J. Org. Chem.* 1993, 58, 6174-6176). Unfortunately, our experience is that nucleoside 5'-triflates are too unstable to be used in these syntheses.

The following are non-limiting examples showing the synthesis of nucleoside 5'-deoxy-5'-difluoromethyl-phosphonates. Those in the art will recognize that equivalent methods can be readily devised based upon

these examples. These examples demonstrate that it is possible to achieve synthesis of 5'-deoxy-5'-difluoro derivatives in good yield and thus guide those in the art to such equivalent methods. The examples also indicate utility of such synthesis to provide useful oligonucleotides as described above.

Those in the art will recognize that useful modified enzymatic nucleic acids can now be designed, much as described by Draper et al., PCT/US94/13129 hereby incorporated by reference herein (including drawings).

10 Example 90: Synthesis of Nucleoside 5'-Deoxy-5'-difluoromethylphosphonates

Referring to Fig. 87, we synthesized a suitable glycosylating agent from the known D-ribose α,α -difluoromethylphosphonate (4) (Martin et al., *Tetrahedron Lett.* 1992, 33, 1839-1842) which served as a key intermediate for the synthesis of nucleoside 5'-difluoromethylphosphonates.

Methyl 2,3-O-isopropylidene- β -D-ribofuranose α,α -difluoromethylphosphonate (4) was synthesized from the 5-aldehyde according to the procedure of Martin et al. (*Tetrahedron Lett.* 1992, 33, 1839-1842) (Figure 87). Removal of the isopropylidene group was accomplished under mild conditions (I_2 -MeOH, reflux, 18 h (Szarek et al., *Tetrahedron Lett.* 1986, 27, 3827) or Dowex 50 WX8 (H^+), MeOH, RT (about 20-25°C), 3 days) in 72% yield. The anomeric mixture thus obtained was benzoylated with benzoyl chloride/pyridine to afford the 2,3-di-O-benzoyl derivative, which was subjected to mild acetolysis conditions (Walczak et al., *Synthesis*, 1993, 790-792) (Ac_2O , AcOH, H_2SO_4 , EtOAc, 0°C). The desired 1-O-acetyl-2,3-di-O-benzoyl-D-ribofuranose difluoromethylphosphonate (5) was obtained in quantitative yield as an anomeric mixture. These derivatives were used for selective glycosylation of silylated uracil and N^4 -acetylcytosine under Vorbrüggen conditions (Vorbrüggen, *Nucleoside Analogs. Chemistry, Biology and Medical Applications*, NATO ASI Series A, 26, Plenum Press, New York, London, 1980; pp. 35-69. The use of $F_3CSO_2OSi(CH_3)_3$ as a glycosylation catalyst is precluded because it is expected to lead to the undesired 1-ethyluracil or 9-ethyladenine byproducts: Podyukova, et al., *Tetrahedron*

Lett. 1987, 28, 3623-3626 and references cited therein) (SnCl_4 as a catalyst, boiling acetonitrile) to yield β -nucleosides (62% **6a**, 75% **6b**). Glycosylation of silylated N^6 -benzoyladenine under the same conditions yielded a mixture of N-9 isomer **6c** and N-7 isomer **7** in 34% and 15% yield, respectively. The above nucleotides were successfully deprotected using trimethylsilylbromide for the cleavage of the ethyl groups, followed by treatment with ammonia-methanol to remove the acyl protecting groups. Nucleoside 5'-deoxy-5'-difluoromethylphosphonates **8** were finally purified on a DEAE Sephadex A-25 (HCO_3^-) column using a 0.01-0.25 M TEAB gradient for elution and obtained as their sodium salts (82% **8a**; 87% **8b**; 82% **8c**).

Selected analytical data: ^{31}P -NMR (^{31}P) and ^1H -NMR (^1H) were recorded on a Varian Gemini 400. Chemical shifts in ppm refer to H_3PO_4 and TMS, respectively. Solvent was CDCl_3 unless otherwise noted. **5**: ^1H δ 8.07-7.28 (m, Bz), 6.66 (d, $J_{1,2}$ 4.5, $\alpha\text{H}1$), 6.42 (s, $\beta\text{H}1$), 5.74 (d, $J_{2,3}$ 4.9, $\beta\text{H}2$), 5.67 (dd, $J_{3,2}$ 4.9, $J_{3,4}$ 6.6, $\beta\text{H}3$), 5.63 (dd, $J_{3,2}$ 6.7, $J_{3,4}$ 3.6, $\alpha\text{H}3$), 5.57 (dd, $J_{2,1}$ 4.5, $J_{2,3}$ 6.7, $\alpha\text{H}2$), 4.91 (m, $\text{H}4$), 4.30 (m, CH_2CH_3), 2.64 (m, CH_2CF_2), 2.18 (s, βAc), 2.12 (s, αAc), 1.39 (m, CH_2CH_3). ^{31}P δ 7.82 (t, $J_{\text{P},\text{F}}$ 105.2), 7.67 (t, $J_{\text{P},\text{F}}$ 106.5). **6a**: ^1H δ 9.11 (s, 1H, NH), 8.01 (m, 11H, Bz, H6), 5.94 (d, $J_{1',2'}$ 4.1, 1H, $\text{H}1'$), 5.83 (dd, $J_{5,6}$ 8.1, 1H, $\text{H}5$), 5.79 (dd, $J_{2',1'}$ 4.1, $J_{2',3'}$ 6.5, 1H, $\text{H}2'$), 5.71 (dd, $J_{3',2'}$ 6.5, $J_{3',4'}$ 6.4, 1H, $\text{H}3'$), 4.79 (dd, $J_{4',3'}$ 6.4, $J_{4',\text{F}}$ 11.6, 1H, $\text{H}4'$), 4.31 (m, 4H, CH_2CH_3), 2.75 (tq, $J_{\text{H},\text{F}}$ 19.6, 2H, CH_2CF_2), 1.40 (m, 6H, CH_2CH_3). ^{31}P δ 7.77 (t, $J_{\text{P},\text{F}}$ 104.0). **8c**: ^{31}P (vs DSS) (D_2O) δ 5.71 (t, $J_{\text{P},\text{F}}$ 87.9).

25 Compound **7** was deacylated with methanolic ammonia yielding the product that showed λ_{max} (H_2O) 271 nm and λ_{min} 233 nm, confirming that the site of glycosylation was N-7.

Example 91: Synthesis of Nucleic Acids Containing Modified Nucleotide Containing Cores

30 The method of synthesis used follows the procedure for normal RNA synthesis as described in Usman *et al.*, *J. Am. Chem. Soc.* 1987, 109, 7845-7854 and in Scaringe *et al.*, *Nucleic Acids Res.* 1990, 18, 5433-5441 and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end **35** (Figure 88 and Janda *et al.*, *Science* 1989, 244:437-440.). These

nucleoside 5'-deoxy-5'-difluoromethylphosphonates may be incorporated not only into hammerhead ribozymes, but also into hairpin, hepatitis delta virus, Group 1 or Group 2 introns, or into antisense oligonucleotides. They are, therefore, of general use in any nucleic acid structure.

5 **Example 92: Synthesis of Modified Triphosphate**

The triphosphate derivatives of the above nucleotides can be formed as shown in Fig. 89, according to known procedures. *Nucleic Acid Chem.*, Leroy B. Townsend, John Wiley & Sons, New York 1991, pp. 337-340; *Nucleotide Analogs*, Karl Heinz Scheit; John Wiley & Sons New York 1980, pp. 211-218.

Equivalent synthetic schemes for 3' dihalophosphonates are shown in Figures 90 and 91 using art recognized nomenclature. The conditions can be optimized by standard procedures.

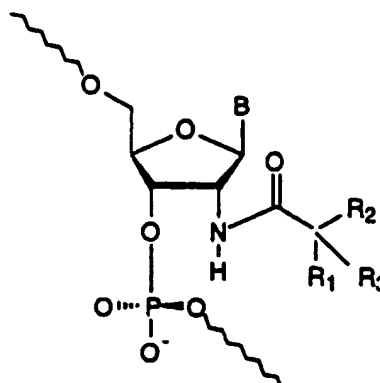
15 The nucleoside dihalophosphonates described herein are advantageous as modified nucleotides in any nucleic acid structure, e.g., catalytic or antisense, since they are resistant to exo- and endonucleases that normally degrade unmodified nucleic acids *in vivo*. They also do not perturb the normal structure of the nucleic acid in which they are incorporated thereby maintaining any activity associated with that structure.

20 These compounds may also be of use as monomers as antiviral and/or antitumor drugs.

Oligonucleotides with Amido or Peptido Modification

This invention replaces 2'-hydroxyl group of a ribonucleotide moiety with a 2'-amido or 2'-peptido moiety. In other embodiments, the 3' and 5' portions of the sugar of a nucleotide may be substituted, or the phosphate group may be substituted with amido or peptido moieties. Generally, such a nucleotide has the general structure shown in Formula I below:

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FORMULA I

The base (B) is any one of the standard bases or is a modified nucleotide base known to those in the art, or can be a hydrogen group. In addition, either R₁ or R₂ is H or an alkyl, alkene or alkyne group containing between 2 and 10 carbon atoms, or hydrogen, an amine (primary, secondary or tertiary, e.g., R₃NR₄ where each R₃ and R₄ independently is hydrogen or an alkyl, alkene or alkyne having between 2 and 10 carbon atoms, or is a residue of an amino acid, i.e., an amide), an alkyl group, or an amino acid (D or L forms) or peptide containing between 2 and 5 amino acids. The zigzag lines represent hydrogen, or a bond to another base or other chemical moiety known in the art. Preferably, one of R₁, R₂ and R₃ is an H, and the other is an amino acid or peptide.

Applicant has recognized that RNA can assume a much more complex structural form than DNA because of the presence of the 2'-hydroxyl group in RNA. This group is able to provide additional hydrogen bonding with other hydrogen donors, acceptors and metal ions within the RNA molecule. Applicant now provides molecules which have a modified amine group at the 2' position, such that significantly more complex structures can be formed by the modified oligonucleotide. Such modification with a 2'-amido or peptido group leads to expansion and enrichment of the side-chain hydrogen bonding network. The amide and peptide moieties are responsible for complex structural formation of the oligonucleotide and can form strong complexes with other bases, and interfere with standard base pairing interactions. Such interference will allow the formation of a complex nucleic acid and protein conglomerate.

Oligonucleotides of this invention are significantly more stable than existing oligonucleotides and can potentially form biologically active bioconjugates not previously possible for oligonucleotides. They may also be used for *in vitro* selection of unique aptamers, that is, randomly generated oligonucleotides which can be folded into an effective ligand for a target protein, nucleic acid or polysaccharide.

Thus, in one aspect, the invention features an oligonucleotide containing the modified base shown in Formula I, above.

In other aspects, the oligonucleotide may include a 3' or 5' nucleotide having a 3' or 5' located amino acid or aminoacyl group. In all these aspects, as well as the 2'-modified nucleotide, it will be evident that various standard modifications can be made. For example, an "O" may be replaced with an S, the sugar may lack a base (i.e., abasic) and the phosphate moiety may be modified to include other substitutions (see Sproat, supra).

Example 93: General procedure for the preparation of 2'-aminoacyl-2'-deoxy-2'-aminonucleoside conjugates.

Referring to Fig. 92, to the solution of 2'-deoxy-2'-amino nucleoside (1 mmol) and N-Fmoc L- (or D-) amino acid (1 mmol) in methanol [dimethylformamide (DMF) and tetrahydrofuran (THF) can also be used], 1-ethoxycarbonyl-2-ethoxy-1,2-dihydroquinoline (EEDQ) [or 1-isobutyloxycarbonyl-2-isobutyloxy-1,2-dihydroquinoline (IIDQ)] (2 mmol) is added and the reaction mixture is stirred at room temperature or up to 50 °C from 3-48 hours. Solvents are removed under reduced pressure and the residual syrup is chromatographed on the column of silica-gel using 1-10 % methanol in dichloromethane. Fractions containing the product are concentrated yielding a white foam with yields ranging from 85 to 95 %. Structures are confirmed by ¹H NMR spectra of conjugates which show correct chemical shifts for nucleoside and aminoacyl part of the molecule. Further proofs of the structures are obtained by cleaving the aminoacyl protecting groups under appropriate conditions and assigning ¹H NMR resonances for the fully deprotected conjugate.

Partially protected conjugates described above are converted into their 5'-O-dimethoxytrityl derivatives and into 3'-phosphoramidites using standard procedures (Oligonucleotide Synthesis: A Practical Approach,

M.J. Gait ed.; IRL Press, Oxford, 1984). Incorporation of these phosphoramidites into RNA was performed using standard protocols (Usman *et al.*, 1987 *supra*).

5 A general deprotection protocol for oligonucleotides of the present invention is described in Fig. 93.

The scheme shows synthesis of conjugate of 2'-d-2'-aminouridine. This is meant to be a non-limiting example, and those skilled in the art will recognize that, variations to the synthesis protocol can be readily generated to synthesize other nucleotides (e.g., adenosine, cytidine,
10 guanosine) and/or abasic moieties.

Example 94: RNA cleavage by hammerhead ribozymes containing 2'-aminoacyl modifications.

Hammerhead ribozymes targeted to site N (see Fig. 94) are synthesized using solid-phase synthesis, as described above. U4 and U7
15 positions are modified, individually or in combination, with either 2'-NH-alanine or 2'-NH-lysine.

RNA cleavage assay *in vitro*: Substrate RNA is 5' end-labeled using [γ -³²P] ATP and T4 polynucleotide kinase (US Biochemicals). Cleavage reactions were carried out under ribozyme "excess" conditions. Trace
20 amount (≤ 1 nM) of 5' end-labeled substrate and 40 nM unlabeled ribozyme are denatured and renatured separately by heating to 90°C for 2 min and snap-cooling on ice for 10 -15 min. The ribozyme and substrate are incubated, separately, at 37°C for 10 min in a buffer containing 50 mM Tris-HCl and 10 mM MgCl₂. The reaction is initiated by mixing the
25 ribozyme and substrate solutions and incubating at 37°C. Aliquots of 5 μ l are taken at regular intervals of time and the reaction is quenched by mixing with equal volume of 2X formamide stop mix. The samples are resolved on 20 % denaturing polyacrylamide gels. The results are quantified and percentage of target RNA cleaved is plotted as a function of
30 time.

Referring to Fig. 95, hammerhead ribozymes containing 2'-NH-alanine or 2'-NH-lysine modifications at U4 and U7 positions cleave the target RNA efficiently.

Sequences listed in Figure 94 and the modifications described in Figure 95 are meant to be non-limiting examples. Those skilled in the art will recognize that variants (base-substitutions, deletions, insertions, mutations, chemical modifications) of the ribozyme and RNA containing other 2'-hydroxyl group modifications, including but not limited to amino acids, peptides and cholesterol, can be readily generated using techniques known in the art, and are within the scope of the present invention.

Example 95: Aminoacylation of 3'-ends of RNA

I. Referring to Fig. 96, 3'-OH group of the nucleotide is converted to succinate as described by Gait, *supra*. This can be linked with amino-alkyl solid support (for example: CpG). Zig-zag line indicates linkage of 3'OH group with the solid support.

II. Preparation of aminoacyl-derivatized solid support

A) Synthesis of O-Dimethoxytrityl (O-DMT) amino acids

Referring to Fig. 97, to a solution of L- (or D-) serine, tyrosine or threonine (2 mmol) in dry pyridine (15 ml) 4,4'-dimethoxytrityl chloride (3 mmol) is added and the reaction mixture is stirred at RT (about 20-25°C) for 16 h. Methanol (10 ml) is then added and the solution evaporated under reduced pressure. The residual syrup was partitioned between 5% aq. NaHCO₃ and dichloromethane, organic layer was washed with brine, dried (Na₂SO₄) and concentrated *in vacuo*. The residue is purified by flash silicagel column chromatography using 2-10% methanol in dichloromethane (containing 0.5 % pyridine). Fractions containing product are combined and concentrated *in vacuo* to yield white foam (75-85 % yield).

B) Preparation of the solid support and its derivatization with amino acids

Referring to Fig. 97, the modified solid support (has an OH group instead of the standard NH₂ end group) was prepared according to Haralambidis et al., Tetrahedron Lett. 1987, 28, 5199, (P denotes aminopropyl CPG or polystyrene type support). O-DMT or NH-monomethoxytrityl (NH-MMT amino acid was attached to the above solid support using standard procedures for derivatization of the solid support (Gait, 1984, *supra*) creating a base-labile ester bond between amino acids

and the support. This support is suitable for the construction of RNA/DNA chain using suitably protected nucleoside phosphoramidites.

Example 96: Aminoacylation of 5'-ends of RNA

- I. Referring to Fig. 98, 5'-amino-containing sugar moiety was synthesized as described (Mag and Engels, 1989 *Nucleic Acids Res.* 17, 5973). Aminoacylation of the 5'-end of the monomer was achieved as described above and RNA phosphoramidite of the 5'-aminoacylated monomer was prepared as described by Usman *et al.*, 1987 *supra*. The phosphoramidite was then incorporated at the 5'-end of the oligonucleotide using standard solid-phase synthesis protocols described above.
- II. Referring to Fig. 99, aminoacyl group(s) is attached to the phosphate group at the 5'-end of the RNA using standard procedures described above.

VII. Reversing Genetic Mutations

- Modification of existing nucleic acid sequences can be achieved by homologous recombination. In this process a transfected sequence recombines with homologous chromosomal sequences and can replace the endogenous cellular sequence. Boggs, 8 *International J. Cell Cloning* 80, 1990, describes targeted gene modification. It reviews the use of homologous DNA recombination to correct genetic defects. Banga and Boyd, 89 *Proc. Natl. Acad. Sci. U.S.A.* 1735, 1992, describe a specific example of *in vivo* site-directed mutagenesis using a 50 base oligonucleotide. In this methodology a gene or gene segment is essentially replaced by the oligonucleotide used.
- This invention uses a complementary oligonucleotide to position a nucleotide base changing activity at a particular site on a gene (RNA or genomic DNA), such that the nucleotide modifying activity will change (or revert) a mutation to wild-type, or its equivalent. By reversion or change of a mutation, we refer to reversion in a broad sense, such as when a mutation at a second site which leads to functional reversion to a wild type phenotype. Also, due to the degeneracy of the genetic code, a revertant may be achieved by changing any one of the three codon positions. Additionally, creation of a stop codon in a deleterious gene (or transcript) is defined here as reverting a mutant phenotype to wild-type. An example of

this type of reversion is creating a stop codon in a critical HIV proviral gene in a human.

Referring to Figures 100 and 101, broadly there are two approaches to causing a site directed change in order to revert a mutation to wild-type.

5 In one (Fig. 100) the oligonucleotide is used to target RNA specifically. RNA is provided with a complementary (Watson-crick) oligonucleotide sequence to that in the target molecule. In this case the sequence modifying oligonucleotide would (analogously to an antisense oligonucleotide or ribozyme) have to be continuously present to revert the
10 RNA as it is made by the cell. Such a reversion would be transient and would potentially require continuous addition of more sequence modifying oligonucleotide. The transient nature of this approach is an advantage, in that treatment could be stopped by simply removing the sequence modifying oligonucleotide (as with a traditional drug).

15 A second approach targets DNA (Fig. 101) and has the advantage that changes may be permanently encoded in the target cell's genetic code. Thus, a single course (or several courses) of treatment may lead to permanent reversion of the genetic disease. If inadvertent chromosomal mutations are introduced this may cause cancer, mutate other genes, or
20 cause genetic changes in the germ-line (in patients of reproductive age). However, if the base changing activity is a specific methylation that may modulate gene expression it would not necessarily lead to germ-line transmission. See Lewin, Genes, 1983 John Wiley & Sons, Inc. NY pp 493-496.

25 Complementary base pairing to single-stranded DNA or RNA is one method of directing an oligonucleotide to a particular site of DNA. This could occur by a strand displacement mechanism or by targeting DNA when it is single-stranded (such as during replication, or transcription). Another method is using triple-strand binding (triplex formation) to double-
30 stranded DNA, which is an established technique for binding polypyrimidine tracts, and can be extended to recognize all 4 nucleotides. See Povsic, T., Strobel, S., & Dervan, P. (1992). Sequence-specific double-strand alkylation and cleavage of DNA mediated by triple-helix formation. J. Am. Chem. Soc. **114**, 5934-5944 (1992). Knorre, D.G., Valentin, V.V.,
35 Valentina, F.Z., Lebedev, A.V. & Federova, O.S. *Design and targeted reactions of oligonucleotide derivatives* 1-366 (CRC Press, Novosibirsk,

1993) describe conjugation of reactive groups or enzyme to oligonucleotides and can be used in the methods described herein.

5 Recently, antisense oligonucleotides have been used to redirect an incorrect splice into order to obtain correct splicing of a splice mutant globin gene *in vitro*. Dominski Z; Kole R (1993) Restoration of correct splicing in thalassemia pre-mRNA by antisense oligonucleotides. Proc Natl Acad Sci U S A 90:8673-7. Analogously, in one preferred embodiment of this invention a complementary oligomer is used to correct an existing mutant RNA, instead of the traditional approach of inhibiting that RNA by
10 antisense.

In either the RNA or DNA mode, after binding to a particular site on the RNA or DNA the oligonucleotide will modify the nucleic acid sequence. This can be accomplished by activating an endogenous enzyme (see Figure 102), by appropriate positioning of an enzyme (or ribozyme)
15 conjugated (or activated by the duplex) to the oligonucleotide, or by appropriate positioning of a chemical mutagen. Specific mutagens, such as nitrous acid which deaminates C to U, are most useful, but others can also be used if inactivation of a harmful RNA is desired.

RNA editing is an naturally occurring event in mammalian cells in
20 which a sequence modifying activity edits a RNA to its proper sequence post-transcriptionally. Higuchi, M., Single, F., Kohler, M., Sommer, B., and Seeburg, P. (1993) RNA Editing of AMPA Receptor Subunit GluR-B: A base-paired intron-exon structure determines position and efficiency Cell 75:1361-1370. The machinery involved in RNA editing can be co-opted by
25 a suitable oligonucleotide in order to promote chemical modification.

The changes in the base created by the methods of this invention cause a change in the nucleotide sequence, either directly, or after DNA repair by normal cellular mechanisms. These changes functionally correct a genetic defect or introduce a stop codon. Thus, the invention is distinct
30 from techniques in which an active chemical group (e.g., an alkylator) is attached to an antisense or triple strand oligonucleotide in order to chemically inactivate the target RNA or DNA.

Thus, this invention creates an alteration to an existing base in a nucleic acid molecule so that the base is read *in vivo* as a different base.

This includes correcting a sequence instead of inactivating a gene but can also include inactivating a deleterious gene.

Thus, in one aspect, the invention features a method for altering in vivo the nucleotide base sequence of a naturally occurring mutant nucleic acid molecule. The method includes contacting the nucleic acid molecule in vivo with an oligonucleotide or peptide nucleic acid or other sequence specific binding molecules able to form a duplex or triplex molecule with the nucleic acid molecule. After formation of the duplex or triplex molecule a base modifying activity chemically or enzymatically alters the targeted base directly, or after nucleic acid repair *in vivo*. This results in the functional alteration of the nucleic acid sequence.

By "alter", as it is used in this context, is meant that one or more chemical moieties in a targeted base, or bases, is altered so that the mutant nucleic acid will be functionally different. Thus, this is distinct from prior methods of correcting defects in DNA, such as homologous recombination, in which an entire segment of the targeted sequence is replaced with a segment of DNA from the transfected nucleic acid. This is also distinct from other methods that use reactive groups to inactivate a RNA or DNA target, in that this method functionally corrects the sequence of the target, instead of merely damaging it, by causing it to be read by a polymerase as a different base from the original base. As noted above, the naturally occurring enzymes in a cell can be utilized to cause the chemical alteration, examples of which are provided below.

By "functionally alter" is meant that the ability of the target nucleic acid to perform its normal function (*i.e.*, transcription or translation control) is changed. For example, an RNA molecule may be altered so that it can cause production of a desired protein, or a DNA molecule can be altered so that upon DNA repair, the DNA sequence is changed.

By "mutant" it is meant a nucleic acid molecule which is altered in some way compared to equivalent molecules present in a normal individual. Such mutants may be well known in the art, and include, molecules present in individuals with known genetic deficiencies, such as muscular dystrophy, or diabetes and the like. It also includes individuals with diseases or conditions characterized by abnormal expression of a gene, such as cancer, thalassemia's and sickle cell anemia, and cystic

fibrosis. It allows modulation of lipid metabolism to reduce artery disease, treatment of integrated AIDS genomes, and AIDS RNA, and Alzheimer's disease. Thus, this invention concerns alteration of a base in a mutant to provide a "wild type" phenotype and/or genotype. For deleterious conditions this involves altering a base to allow expression or prevent expression as is necessary. When treating an infection, such as HIV, it concerns inactivation of a gene in the HIV RNA by mutation of the mutant (*i.e.*, non-human gene) to a wild type (*i.e.*, no production of a non-human protein). Such modification is performed *in trans* rather than *in cis* as in prior methods.

In preferred embodiments, the oligonucleotide is of a length (at least 12 bases, preferably 17 - 22) sufficient to activate dsRNA deaminase *in vivo* to cause conversion of an adenine base to inosine; the oligonucleotide is an enzymatic nucleic acid molecule that is active to chemically modify a base (see below); the nucleic acid molecule is DNA or RNA; the oligonucleotide includes a chemical mutagen, *e.g.*, the mutagen is nitrous acid; and the oligonucleotide causes deamination of 5-methylcytosine to thymidine, cytosine to uracil, or adenine to inosine, or methylation of cytosine to 5-methylcytosine.

In a most preferred embodiment, the invention features correction of a mutation, rather than inactivation of a target by causing a mutation.

Using *in vitro* directed evolution, it is possible to screen for ribozymes with catalytic activities different than RNA cleavage. Bartel, D. and Szostak, J. (1993) Isolation of new ribozymes from a large pool of random sequences. Science 261:1411-1418. Using these methods of *in vitro* directed evolution, an enzymatic nucleic acid molecule, or ribozyme that mutates bases, instead of cleaving the phosphodiester backbone can be selected. This is a convenient method of obtaining an enzyme with the appropriate base sequence modifying activities for use in the present invention.

Sequence modifying activities can change one nucleotide to another (or modify a nucleotide so that it will be repaired by the cellular machinery to another nucleotide). Sequence modifying activities could also delete or add one or more nucleotides to a sequence. A specific embodiment of adding sequences is described by Sullenger and Cech, PCT/US94/12976

hereby incorporated by reference herein), in which entire exons with wild-type sequence are spliced into a mutant transcript. The present invention features only the addition of a few bases (1 - 3).

Thus, in another aspect, the invention features ribozymes or enzymatic nucleic acid molecules active to change the chemical structure of an existing base in a separate nucleic acid molecule. Applicant is the first to determine that such molecules would be useful, and to provide a description of how such molecules might be isolated.

Molecules used to achieve *in situ* reversion can be delivered using the existing means employed for delivering antisense molecules and ribozymes, including liposomes and cationic lipid complexes. If the *in situ* reverting molecule is composed only of RNA, then expression vectors can be used in a gene therapy protocol to produce the reverting molecules endogenously, analogously to antisense or ribozymes expression vectors. There are several advantages of using such an expression vector, rather than simply replacing the gene through standard gene therapy. Firstly, this approach would limit the production of the corrected gene to cells that already express that gene. Furthermore, the corrected gene would be properly regulated by its natural transcriptional promoter. Lastly, reversion can be used when the mutant RNA creates a dominant gain of function protein (e.g., in sickle cell anemia), where correction of the mutant RNA is necessary to stop the production of the deleterious mutant protein, and allow production of the corrected protein.

Endogenous Mammalian RNA Editing System

It was observed in the mid-1980s that the sequence of certain cellular RNAs were different from the DNA sequence that encodes them. By a process called RNA editing, cellular RNA are post-transcriptionally modified to a) create a translation initiation and termination codons, b) enable tRNA and rRNA to fold into a functional conformation (for a review see Bass, B. L. (1993) In The RNA World, R. Gesteland, R. and Atkins, J. eds. (Cold Spring Harbor, New York; CSH Lab. Press) pp. 383-418). The process of RNA editing includes base modification, deletion and insertion of nucleotides.

Although, the RNA editing process is widespread among lower eukaryotes, very few RNAs (four) have been reported to undergo editing in

mammals (Bass, *supra*). The predominant mode of RNA editing in mammalian system is base modification ($C \rightarrow U$ and $A \rightarrow G$). The mechanism of RNA editing in the mammalian system is postulated to be that $C \rightarrow U$ conversion is catalyzed by cytidine deaminase. The mechanism of conversion of $A \rightarrow G$ has recently been reported for glutamate receptor B subunit (gluR-B) in rat PC12 cells (Higuchi, M. et al. (1993) Cell 75, 1361-1370). According to Higuchi gluR-B mRNA precursor attains a structure such that intron 11 and exon 11 can form a stable stem-loop structure. This stem-loop structure is a substrate for a nuclear double strand-specific adenosine deaminase enzyme. The deamination will result in the conversion of $A \rightarrow I$. Reverse transcription followed by double strand synthesis will result in the incorporation of G in place of A.

In the present invention, the endogenous deaminase activity or other such activities can be utilized to achieve targeted base modification.

The following are examples of the invention to illustrate different methods by which *in vivo* conversion of a base can be achieved. These are provided only to clarify specific embodiments of the invention and are not limiting to the invention. Those in the art will recognize that equivalent methods can be readily devised within the scope of the claims.

Example 97: Exploiting cellular dsRNA dependent Adenine to Inosine converter:

An endogenous activity in most mammalian cells and *Xenopus* oocytes converts about 50% of adenines to inosines in double stranded RNA. (Bass, B. L., & Weintraub, H. (1988). An unwinding activity that covalently modifies it double-stranded RNA substrate. Cell, 55, 1089-1098.). This activity can be used to cause an *in situ* reversion of a mutation at the RNA level. Referring to Figures 102 and 104, for demonstration purposes a stop codon is incorporated into the coding region of dystrophin, which is fused to the reporter gene luciferase. This stop codon can be reverted by targeting an antisense RNA which is long enough to activate the dsRNA deaminase, which converts Adenines to Inosines. The A to I transition will be read by the ribosome as an A to G transition in some cases and will thereby functionally revert the stop codon. While other A's in this region may be converted to I's and read as G, converting an A to I (G) cannot create a stop codon. The A to I transitions

in the region surrounding the target mutation will create some point mutations, however, the function of the dystrophin protein is rarely inactivated by point mutations.

5 The reverted mRNA was then translated in a cell lysate and assayed for luciferase activity. As evidenced by the dramatic increase in luciferase counts in the graph in figure 103, the A to I transition was read by the ribosome as an A to G transition and the stop codon has successfully been reverted with the lysate treated complex. As a control, an irrelevant non-complementary RNA oligonucleotide was added to the
10 dystrophin/luciferase mRNA. As expected, in this case no translation (luciferase activity) is observed because of the stop codon. As an additional control, the hybrid was not treated with extract, and again no translation (luciferase activity) is observed (Figure 103).

15 While other A's in the targeted region may have been converted to I's and read as G, converting an A to I (G) cannot create a stop codon, so the ribosome will still read through the region. Dystrophin is not generally sensitive to point mutations if the open reading frame is maintained, so a dystrophin protein made from an mRNA reverted by this method should retain full activity.

20 The following detail specifics of the methodology: RNA oligonucleotides were synthesized on a 394 (ABI) synthesizer using phosphoramidite chemistry. The sequence of the synthetic complementary RNA that binds to the mutant dystrophin sequence is as follows (5' to 3'):

25 CCCGCGGTAGATCTTTCTGGAGGCTTACAGTTTTCTACAAACCTCC
CTTCAA (Seq. ID No. 1)

Referring to Figure 104, fifty-nine base pairs of a human dystrophin mutant sequence containing a stop codon was fused in frame to the luciferase coding region using standard cloning technology, into the *Hind* III and *Not* I sites of pRC-CMV (Invitrogen, San Diego, CA). The AUG of
30 luciferase was deleted. The sequences of the insert from the *Hind* III site to the start of the luciferase coding region is (5' to 3'):

GCCCCTGAGGAGCGATGGAGGCCTGAAGGGAGGTTTGTGGAAAA
CTGTAAGCCTCCAGAAAGATCTACCGCGG (Seq ID No. 2)

This corresponds to base pairs 3649-3708 of normal dystrophin (Entrez ID # 311627) with a *Sac* II site at the 3' end. This plasmid was used as a template for *in vitro* transcription of mRNA using T7 polymerase with the manufacturers protocol (Promega, Madison, WI).

- 5 *Xenopus* nuclear extracts were prepared in 0.5X TGKED buffer (0.5X= 25mM Tris (pH 7.9), 12.5% glycerol, 25 mM KCl, 0.25mM DTT and 0.05mM EDTA), by vortexing nuclei and resuspended in a volume of 0.5X TGKED equal to total cytoplasm volume of the oocytes. Bass, B.L. & Weintraub, H. *Cell* 55, 1089-1098 (1988).
- 10 The target mRNA at 500ng/ul was pre-annealed to 1 micromolar complementary or irrelevant RNA oligonucleotide by heating to 70°C, and allowing it to slowly cool to 37°C over 30 minutes. Fifty nanograms of mRNA pre-annealed to the RNA oligonucleotides was added to 7ul of nuclear extracts containing 1mM ATP, 15mM EDTA, 1600un/ml RNasin and 12.5mM Tris pH 8 to a total volume of 12ul. Bass, B.L. & Weintraub, H. *supra*. This mixture, which contains the dsRNA deaminase activity, was incubated for 30 minutes at 25°C. Next, 1.5ul of this mixture was added to a rabbit reticulocyte lysate *in vitro* translation mixture and translated for two hours according to the manufacturers protocol (Life Technologies, Gaithersburg, MD), except that an additional 1.3 mM magnesium acetate was added to compensate for the EDTA carried through from the nuclear extract mixture. Luciferase assays were performed on 15ul of extract with the Promega luciferase assay system (Promega, Madison, WI), and luminescence was detected with a 96 well luminometer, and the results are displayed in the graph in figure 102.
- 25

Example 98: Base changing activities

- The chemical synthesis of antisense and triple-strand forming oligomers conjugated to reactive groups is well studied and characterized (Knorre, D.G., Valentin, V.V., Valentina, F.Z., Lebedev, A.V. & Federova, O.S. *Design and targeted reactions of oligonucleotide derivatives* 1-366 (CRC Press, Novosibirsk, 1993) and Povsic, T., Strobel, S. & Dervan, P. Sequence-specific double-strand alkylation and cleavage of DNA mediated by triple-helix formation *J. Am. Chem. Soc.* 114, 5934-5944 (1992). Reactive groups such as alkylators that can modify nucleotide bases in targeted RNA or DNA have been conjugated to oligonucleotides.
- 30
- 35

Additionally enzymes that modify nucleic acids have been conjugated to oligonucleotides. (Knorre, D.G., Valentin, V.V., Valentina, F.Z., Lebedev, A.V. & Federova, O.S. *Design and targeted reactions of oligonucleotide derivatives* 1-366 (CRC Press, Novosibirsk, 1993). In the past these
5 conjugated chemical groups or enzymes have been used to inactivate DNA or RNA that is specifically targeted by antisense or triple-strand interactions. Below is a list of useful base changing activities that could be used to change the sequence of DNA or RNA targeted by antisense or triple strand interactions, in order to achieve *in situ* reversion of mutations,
10 as described herein (see figure 100-104).

1. Deamination of 5-methylcytosine to create thymidine (performed by the enzyme cytidine deaminase (Bass, B.L. in *The RNA World* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1993). Also, nitrous acid or related compounds promote oxidative deamination of
15 C to be read at T (Microbial Genetics, David Freifelder, Jones and Bartlett Publishers, Inc., Boston, 1987, PP.226-230.). Additionally hydroxylamine or related compounds can transform C to be read at T (Microbial Genetics, David Freifelder, Jones and Bartlett Publishers, Inc., Boston, 1987, PP.226-230.)

20 2. Deamination of cytosine to create uracil (performed by the enzyme cytidine deaminase (Bass, B.L. in *The RNA World* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1993) or by chemical groups similar to nitrous acid that promote oxidative deamination (Microbial Genetics, David Freifelder, Jones and Bartlett Publishers, Inc.,
25 Boston, 1987, PP.226-230.)

3. Deamination of Adenine to be read like G (Inosine) (as done by the adenosine deaminase, AMP deaminase or the dsRNA deaminating activity (Bass, B.L. in *The RNA World* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1993).

30 4. Methylation of cytosine to 5-methylcytosine

5. Transforming thymidine (or uracil) to O²-methyl thymidine (or O²-methyl uracil), to be read as cytosine by alkynitrosoureas (Xu, and Swann, *Tetrahedron Letters* 35:303-306 (1994)).

6. Transforming guanine to 6-O-methyl (or other alkyls) to be read as adenine (Mehta and Ludlum, *Biochimica et Biophysica Acta*, 521:770-778 (1978) which can be done with the mutagen ethyl methane sulfonate (EMS) Microbial Genetics, David Freifelder, Jones and Bartlett
5 Publishers, Inc., Boston, 1987, PP.226-230.

7. Amination of uracil to cytosine (as performed by the cellular enzyme CTP synthetase (Bass, B.L. in *The RNA World* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1993).

10 The following are examples of useful chemical modifications that can be utilized in the present invention. There are a few preferred straightforward chemical modifications that can change one base to another base. Appropriate mutagenic chemicals are placed on the targetting oligonucleotide, e.g., nitrous acid, or a suitable protein with such activity. Such chemicals and proteins can be attached by standard
15 procedures. These include molecules which introduce fundamental chemical changes, that would be useful independent of the particular technical approach. See Lewin, Genes, 1983 John Wiley & Sons, Inc. NY pp 42-48.

20 The following matrix shows that the chemical modifications noted can cause transversion reversions (pyrimidine to pyrimidine, or purine to purine) in RNA or DNA. The transversions (pyrimidine to purine, or purine to pyrimidine) are not preferred because these are more difficult chemical transformations. The footnotes refer to the specific desired chemical transformations. The bold footnotes refer to the reaction on the opposite
25 DNA strand. For example, if one desires to change an A to a G, this can be accomplished at the DNA level by using reaction #5 to change a T to a C in the opposing strand. In this example an A/T base pair goes to A/C, then when the DNA is replicated, or mismatch repair occurs this can become G/C, thus the original A has been converted to a G.

30

ISR matrix**Reverted Base**

Mutant base	A	T(U)	C	G
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161

A	-	Transversion	Transversion	DNA ^{5,3} /RNA ³
T(U)	Transversion	-	DNA ⁵ /RNA ⁷	Transversion
C	Transversion	RNA ² /DNA ⁶	-	Transversion
G	DNA ⁶ /RNA ⁶	Transversion	Transversion	-

- 1 Deamination of 5-methylcytosine to create thymidine.
- 2 Deamination of cytosine to create uracil.
- 3 Deamination of Adenine to be read like G (Inosine).
- 5 4 Methylation of cytosine to 5-methylcytosine.
- 5 5 Transforming thymidine (or uracil) to O²-methyl thymidine (or O²-methyl uracil), to be read as cytosine (Xu, and Swann, Tetrahedron Letters 35:303-306 (1994)).
- 10 6 Transforming guanine to 6-O-methyl (or other alkyls) to be read as adenine (Mehta and Ludlum, Biochimica et Biophysica Acta, 521:770-778 (1978)).
7. 7. Amination of uracil to cytosine. Bass *supra*. fig. 6c.

In Vitro Selection Strategy

- Referring to Figure 105, there is provided a schematic describing an approach to selecting for a ribozyme with such base changing activity. An RNA is designed that folds back on itself (this is similar to approaches already used to select for RNA ligases, Bartel, D. and Szostak, J. (1993) Isolation of new ribozymes from a large pool of random sequences. Science 261:1411-1418). A degenerate loop opposing the base to be modified provides for diversity. After incubating this library of molecules in a buffer, the RNA is reverse transcribed into DNA (that is, using standard *in vitro* evolution protocol. Tuerk and Gold, 249 Science 505, 1990) , and then the DNA is selected for having a base change. A restriction enzyme cleavage and size selection or its equivalent is used to isolate the fraction of DNAs with the appropriate base change. The cycle could then be repeated many times.

The *in vitro* selection (evolution) strategy is similar to approaches developed by Joyce (Beaudry, A. A. and Joyce, G.F. (1992) Science 257, 635-641; Joyce, G. F. (1992) Scientific American 267, 90-97) and Szostak (Bartel, D. and Szostak, J. (1993) Science 261:1411-1418; Szostak, J. W. (1993) TIBS 17, 89-93). Briefly, a random pool of nucleic acids is synthesized wherein, each member contains two domains: a) one domain consists of a region with defined (known) nucleotide sequence; b) the second domain consists of a region with degenerate (random) sequence. The known nucleotide sequence domain enables: 1) the nucleic acid to bind to its target (the region flanking the mutant nucleotide), 2) complimentary DNA (cDNA) synthesis and PCR amplification of molecules selected for their base modifying activity, 3) introduction of restriction endonuclease site for the purpose of cloning. The degenerate domain can be created to be completely random (each of the four nucleotides represented at every position within the random region) or the degeneracy can be partial (Beaudry, A. A. and Joyce, G.F. (1992) Science 257, 635-641). In this invention, the degenerate domain is flanked by regions containing known sequences (see Figure 105), such that the degenerate domain is placed across from the mutant base (the base that is targeted for modification). This random library of nucleic acids is incubated under conditions that ensure folding of the nucleic acids into conformations that facilitate the catalysis of base modification (the reaction protocol may also include certain cofactors like ATP or GTP or an S-adenosyl-methionine (if methylation is desired) in order to make the selection more stringent). Following incubation, nucleic acids are converted into complimentary DNA (if the starting pool of nucleic acids is RNA). Nucleic acids with base modification (at the mutant base position) can be separated from rest of the population of nucleic acids by using a variety of methods. For example, a restriction endonuclease cleavage site can either be created or abolished as a result of base modification. If a restriction endonuclease site is created as a result of base modification, then the library can be digested with the restriction endonuclease (RE). The fraction of the population that is cleaved by the RE is the population that has been able to catalyze the base modification reaction (active pool). A new piece of DNA (containing oligonucleotide primer binding sites for PCR and RE sites for cloning) is ligated to the termini of the active pool to facilitate PCR amplification and subsequent cycles (if necessary) of selection. The final pool of nucleic acids with the best base modifying activity is cloned in to a plasmid vector

and transformed into bacterial hosts. Recombinant plasmids can then be isolated from transformed bacteria and the identity of clones can be determined using DNA sequencing techniques.

5 Base modifying enzymatic nucleic acids (identified via in vitro selection) can be used to cause the chemical modification *in vivo*.

In addition, the ribozyme could be evolved to specifically bind a protein having an enzymatic base changing activity.

10 Such ribozymes can be used to cause the above chemical modifications *in vivo*. The ribozymes or above noted antisense-type molecules can be administered by methods discussed in the above referenced art.

VIII. Administration of Nucleic Acids

15 Applicant has determined that double-stranded nucleic acid lacking a transcription termination signal can be used for continuous expression of the encoded RNA. This is achieved by use of an R-loop, *i.e.*, an RNA molecule non-covalently associated with the double-stranded nucleic acid and which causes localized denaturation ("bubble" formation) within the double stranded nucleic acid (Thomas et al., 1976 Proc. Natl. Acad. Sci. USA 73, 2294). In addition, applicant has determined that that the RNA
20 portion of the R-loop can be used to target the whole R-loop complex to a desirable intracellular or cellular site, and aid in cellular uptake of the complex. Further, applicant indicates that expression of enzymatically active RNA or ribozymes can be significantly enhanced by use of such R-loop complexes.

25 Thus, in one aspect, the invention features a method for introduction of enzymatic nucleic acid into a cell or tissue. A complex of a first nucleic acid encoding the enzymatic nucleic acid and a second nucleic acid molecule is provided. The second nucleic acid molecule has sufficient complementarity with the first nucleic acid to be able to form an R-loop
30 base pair structure under physiological conditions. The R-loop is formed in a region of the first nucleic acid molecule which promotes expression of RNA from the first nucleic acid under physiological conditions. The method further includes contacting the complex with a cell or tissue under

conditions in which the enzymatic nucleic acid is produced within the cell or tissue.

By "complex" is simply meant that the two nucleic acid molecules interact by intermolecular bond formation (such as by hydrogen bonding) between two complementary base-paired sequences. The complex will generally be stable under physiological condition such that it is able to cause initiation of transcription from the first nucleic acid molecule.

The first and second nucleic acid molecules may be formed from any desired nucleotide bases, either those naturally occurring (such as adenine, guanine, thymine and cytosine), or other bases well known in the art, or may have modifications at the sugar or phosphate moieties to allow greater stability or greater complex formation to be achieved. In addition, such molecules may contain non-nucleotides in place of nucleotides. Such modifications are well known in the art, see e.g., Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 Nature 344, 565; Pieken *et al.*, 1991 Science, 253, 314; Usman and Cedergren, 1992 Trends in Biochem. Sci. 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication No. WO 91/03162, as well as Sproat, B. *European Patent Application* 92110298.4 which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules. All these publications are hereby incorporated by reference herein.

By "sufficient complementarity" is meant that sufficient base pairing occurs so that the R-loop base pair structure can be formed under the appropriate conditions to cause transcription of the enzymatic nucleic acid. Those in the art will recognize routine tests by which such sufficient base pairs can be determined. In general, between about 15 - 80 bases is sufficient in this invention.

By "physiological condition" is meant the condition in the cell or tissue to be targeted by the first nucleic acid molecule, although the R-loop complex may be formed under many other conditions. One example is use of a standard physiological saline at 37°C, but it is simply desirable in this invention that the R-loop structure exists to some extent at the site of action so that the expression of the desired nucleic acid will be achieved at that site of action. While it is preferred that the R-loop structure be stable under

those conditions, even a minimal amount of formation of the R-loop structure to cause expression will be sufficient. Those in the art will recognize that measurement of such expression is readily achieved, especially in the absence of any promoter or leader sequence on the first nucleic acid molecule (Daube and von Hippel, 1992 Science 258, 1320).
5 Such expression can thus only be achieved if an R-loop structure is truly formed with the second nucleic acid. If a promoter or leader sequence is provided, then it is preferred that the R-loop be formed at a site distant from those regions so that transcription is enhanced.

10 In a related aspect, the invention features a method for introduction of ribonucleic acid within a cell or tissue by forming an R-loop base-paired structure (as described above) with the first nucleic acid molecule lacking any promoter region or transcription termination signal such that once expression is initiated it will continue until the first nucleic acid is degraded.

15 In another related aspect, the invention features a method in which the second nucleic acid is provided with a localization factor, such as a protein, *e.g.*, an antibody, transferrin, a nuclear localization peptide, or folate, or other such compounds well known in the art, which will aid in targeting the R-loop complex to a desired cell or tissue.

20 In preferred embodiments, the first nucleic acid is a plasmid, *e.g.*, one without a promoter or a transcription termination signal; the second nucleic acid is of length between about 40-200 bases and is formed of ribonucleotides at a majority of positions; and the second nucleic is covalently bonded with a ligand such as a nucleic acid, protein, peptide,
25 lipid, carbohydrate, cellular receptor, nuclear localization factor, or is attached to maleimide or a thiol group: the first nucleic acid is an expression plasmid lacking a promoter able to express a desired gene, *e.g.*, it is a double-stranded molecule formed with a majority of deoxyribonucleic acids; the R-loop complex is a RNA/DNA heteroduplex;
30 no promoter or leader region is provided in the first nucleic acid; and the R-loop is adapted to prevent nucleosome assembly and is designed to aid recruitment of cellular transcription machinery.

In other preferred embodiments, the first nucleic acid encodes one or more enzymatic nucleic acids, *e.g.*, it is formed with a plurality of

intramolecular and intermolecular cleaving enzymatic nucleic acids to allow release of therapeutic enzymatic nucleic acid *in vivo*.

In a further related aspect, the invention features a complex of the above first nucleic acid molecules and second nucleic acid molecules.

5 R-loop complex

An R-loop complex is designed to provide a non-integrating plasmid so that, when an RNA polymerase binds to the plasmid, transcription is continuous until the plasmid is degraded. This is achieved by hybridizing an RNA molecule, 40 to 200 nucleotides in length, to a DNA expression
10 plasmid resulting in an R-loop structure (see figure 106). This RNA, when conjugated with a ligand that binds to a cell surface receptor, triggers internalization of the plasmid/RNA-ligand complex. Formation of R-loops in general is described by DeWet, 1987 Methods in Enzymol. 145, 235; Neuwald et al., 1977 J. Virol. 21,1019; and Meyer et al., 1986 J. Ult. Mol.
15 Str. Res. 96, 187. Thus, those in the art can readily design complexes of this invention following the teachings of the art.

Promoters placed in retroviral genomes have not always behaved as planned in that the additional promoter will serve as a stop signal or reverses the direction of the polymerase. Applicant was told that creation
20 of an R-loop between the promoter and the reporter gene increased the transfection efficiency. Incubation of an RNA molecule with a double-stranded DNA molecule, containing a region of complementarity with the RNA will result in the formation of a stable RNA-DNA hetroduplex and the DNA strand that has a sequence identical to the RNA will be displaced into
25 a loop-like structure called the R-loop. This displacement of DNA strand occurs because an RNA-DNA duplex is more stable compared to a DNA-DNA duplex. Applicant was also told that an 80 nt long RNA was used to generate a R-loop structure in a plasmid encoding the β -galactosidase gene. The R-loop was initiated either in the promoter region or in the
30 leader sequence. Plasmids containing an R-loop structure were microinjected into the cytoplasm of COS cells and the gene expression was assayed. R-loop formation in the promoter region of the plasmid inhibited expression of the gene. RNA that hybridized to the leader sequence between the promoter and the gene, or directly to the first 80
35 nucleotides of the mRNA increased the expression levels 8-10 fold. The

proposed mechanism is that R-loop formation prevents nucleosome assembly, thus making the DNA more accessible for transcription. Alternatively, the R-loop may resemble a RNA primer promoting either DNA replication or transcription (Daube and von Hippel, 1992, supra).

- 5 One of the salient features of this invention is to generate R-loops in expression vectors of choice and introduce them into cells to achieve enhanced expression from the expression vector. The presence of an R-loop may aid in the recruitment of cellular transcription machinery. Once an RNA polymerase binds to the plasmid and initiates transcription, the
10 process will continue until a termination signal is reached, or the plasmid is degraded.

- This invention will increase the expression of ribozymes inside a cell. The idea is to construct a plasmid with no transcription termination signal, such that a transcript-containing multiple ribozyme units can be
15 generated. In order to liberate unit length ribozymes, self-processing ribozymes can be cloned downstream of each therapeutic ribozyme (see figure 107) as described by Draper *supra*.

Ligand Targeting

- Another salient feature of this invention is that the RNA used to
20 generate R-loop structures can be covalently linked to a ligand (nucleic acid, proteins, peptides, lipids, carbohydrates, etc.). Specific ligands can be chosen such that the ligand can bind selectively to a desired cell surface receptor. This ligand-receptor interaction will help internalize a plasmid containing an R-loop. Thus, RNA is used to attach the ligand to the
25 DNA such that localization of the gene to certain regions of the cell is achieved. One of several methods can be used to attach a ligand to RNA. This includes the incorporation of deoxythymidine containing a 6 carbon spacer having a terminal primary amine into the RNA (see figure 108). This amino group can be directly derivatized with the ligand, such as folate (Lee and Low, 1994 J. Biol. Chem. 269, 3198-3204). The RNA containing a 6
30 carbon spacer with a terminal amine group is mixed with folate and the mixture is reacted with activators like 1-(3-Dimethylaminopropyl)-3-ethylcarbodiimide hydrochloride (EDC). This reaction should be carried out in the presence of 1-Hydroxybenzotriazole hydrate (HOBt) to prevent
35 any undesirable side reactions.

The RNA can also be derivatized with a heterobifunctional crosslinking agent (or linker) like succinimidyl 4-(p-maleimidophenyl)butyrate (SMPB). The SMPB introduces a maleimide into the RNA. This maleimide can then react with a thiol moiety either in a peptide or in a protein. Thiols can also be introduced into proteins or peptides that lack naturally occurring thiols using succinylacetylthioacetate. The amino linker can be attached at the 5' end or 3' end of the RNA. The RNA can also contain a series of nucleotides that do not hybridize to the DNA and extend the linker away from the RNA/DNA complex, thus increasing the accessibility of the ligand for its receptor and not interfering with the hybridization. These techniques can be used to link peptides such as nuclear localization signal (NLS) peptides (Lanford et al., 1984 Cell 37, 801-813; Kalderon et al., 1984 Cell 39, 499-509; Goldfarb et al., 1986 Nature 322, 641-644) and/or proteins like the transferrin (Curiel et al., 1991 Proc. Natl. Acad. Sci. USA 88, 8850-8854; Wagner et al., 1992 Proc. Natl. Acad. Sci. USA 89, 6099-6103; Giulio et al., 1994 Cell. Signal. 6, 83-90) to the ends of R-loop forming RNA in order to facilitate the uptake and localization of the R-loop-DNA complex. To link a protein to the ends of R-loop forming RNA, an intrinsic thiol can be used to react with the maleimide or the thiols can be introduced into the protein itself using either iminothiolate or succinimidyl acetyl thioacetate (SATA; Duncan et al., 1983 Anal. Biochem 132, 68). The SATA requires an additional deprotection step using 0.5 M hydroxylamine.

In addition liposomes can be used to cause an R-loop complex to be delivered to an appropriate intracellular site by techniques well known in the art. For example, pH-sensitive liposomes (Connor and Huang, 1986 Cancer Res. 46, 3431-3435) can be used to facilitate DNA transfection.

Calcium phosphate mediated or electroporation-mediated delivery of the R-loop complex in to desired cells can also be readily accomplished.

In vitro Selection

In vitro selection strategies can be used to select nucleic acids that a) can form stable R-loops b) selectively bind to specific cell surface receptors. These nucleic acids can then be covalently linked to each other. This will help internalize the R-loop-containing plasmid efficiently using receptor-mediated endocytosis. The *in vitro* selection (evolution) strategy is

similar to approaches developed by Joyce (Beaudry and Joyce, 1992 Science 257, 635-641; Joyce, 1992 Scientific American 267, 90-97) and Szostak (Bartel and Szostak, 1993 Science 261:1411-1418; Szostak, 1993 TIBS 17, 89-93). Briefly, a random pool of nucleic acids is synthesized wherein each member contains two domains: a) one domain consists of a region with defined (known) nucleotide sequence; b) the second domain consists of a region with degenerate (random) sequence. The known nucleotide sequence domain enables: 1) the nucleic acid to bind to its target (a specific region of the double strand DNA), 2) complimentary DNA (cDNA) synthesis and PCR amplification of molecules selected for their affinity to form R-loop and/or their ability to bind to a specific receptor, 3) introduction of a restriction endonuclease site for the purpose of cloning. The degenerate domain can be created to be completely random (each of the four nucleotides represented at every position within the random region) or the degeneracy can be partial (Beaudry and Joyce, 1992 Science 257, 635-641). In this invention, the degenerate domain is flanked by regions containing known sequences. This random library of nucleic acids is incubated under conditions that ensure equilibrium binding to either double-stranded DNA or cell surface receptor. Following incubation, nucleic acids are converted into complementary DNA (if the starting pool of nucleic acids is RNA). Nucleic acids with desired characteristics can be separated from the rest of the population of nucleic acids by using a variety of methods (Joyce, 1992 supra). The desired pool of nucleic acids can then be carried through subsequent rounds of selection to enrich the population with the most desired traits. These molecules are then cloned in to appropriate vectors. Recombinant plasmids can then be isolated from transformed bacteria and the identity of clones can be determined using DNA sequencing techniques.

Other embodiments are within the following claims.

TABLE I**Characteristics of Ribozymes****Group I Introns**

Size: ~200 to >1000 nucleotides.

Requires a U in the target sequence immediately 5' of the cleavage site.

Binds 4-6 nucleotides at 5' side of cleavage site.

Over 75 known members of this class. Found in *Tetrahymena thermophila* rRNA, fungal mitochondria, chloroplasts, phage T4, blue-green algae, and others.

RNaseP RNA (M1 RNA)

Size: ~290 to 400 nucleotides.

RNA portion of a ribonucleoprotein enzyme. Cleaves tRNA precursors to form mature tRNA.

Roughly 10 known members of this group all are bacterial in origin.

Hammerhead Ribozyme

Size: ~13 to 40 nucleotides.

Requires the target sequence UH immediately 5' of the cleavage site.

Binds a variable number nucleotides on both sides of the cleavage site.

14 known members of this class. Found in a number of plant pathogens (virusoids) that use RNA as the infectious agent (Figures 1 and 2)

Hairpin Ribozyme

Size: ~50 nucleotides.

Requires the target sequence GUC immediately 3' of the cleavage site.

Binds 4-6 nucleotides at 5' side of the cleavage site and a variable number to the 3' side of the cleavage site.

Only 3 known member of this class. Found in three plant pathogen (satellite RNAs of the tobacco ringspot virus, arabis mosaic virus and chicory yellow mottle virus) which uses RNA as the infectious agent (Figure 3).

Hepatitis Delta Virus (HDV) Ribozyme

Size: 50 - 60 nucleotides (at present).

Cleavage of target RNAs recently demonstrated.

Sequence requirements not fully determined.

Binding sites and structural requirements not fully determined, although no sequences 5' of cleavage site are required.

Only 1 known member of this class. Found in human HDV (Figure 4).

***Neurospora* VS RNA Ribozyme**

Size: ~144 nucleotides (at present)

Cleavage of target RNAs recently demonstrated.
Sequence requirements not fully determined.
Binding sites and structural requirements not fully determined. Only 1
known member of this class. Found in *Neurospora* VS RNA (Figure 5).

Table 2
Human ICAM HH Target sequence

nt. Position	Target Sequences	nt. Position	Target Sequences
11	CCCCAGU C GACGCTG	386	ACCGUGU A CUGGACU
23	CUGAGCU C CUCUGCU	394	CUGGACU C CAGAACG
26	AGCUCU C UGCUACT	420	CACCCU C CUCUCU
31	CUCUGCU A CUCAGAG	425	CUCUCU C UUGGACG
34	UGCUACT C AGAGUUG	427	CCCTUCU U GGCAGCC
40	UCAGAGU U GCAACCU	450	AGAACCU U ACCCUAC
48	GCAACCU C AGCCUCG	451	GAACCUU A CUCUACG
54	UCAGCCU C GCUADGG	456	UUACCUU A CGCUGCC
58	CCUCGCU A UGGCUC	495	CCAACCU C ACCGUGG
64	UADGGCU C CCAGCAG	510	UGCUGCU C CGUGGGG
96	CCGCACU C CUGGUCC	564	CUGAGGU C ACCACCA
102	UCCUGGU C CUGCUCG	592	GAGAGAU C ACCAUGG
108	UCCUGCU C GGGGCTC	607	AGCCAAU U UUCUGUG
115	CGGGGCU C UGUUCCC	608	GCCAAU U CUCUGGC
119	GCUCUGU U CCCAGGA	609	CCAATUU C UCGUGCC
120	CUCUGUU C CCAGGAC	611	AAUUUCU C GUGCCGC
146	CAGACAU C UGUGUCC	656	GAGCUGU U UGAGAAC
152	UCUGUGU C CCCCUCA	657	AGCUGUU U GAGAACA
158	UCCCCCU C AAAAGUC	668	AACACCU C GGGCCCC
165	CAAAAGU C AUCCUGC	677	GGCCCCU A CCAGCUC
168	AAGUCAU C CUGCCCC	684	ACCAGCU C CAGACCU
185	GGAGGCU C CGUGCUG	692	CAGACCU U UGUCCUG
209	AGCAACU C CUGUGAC	693	AGACCUU U GUCCUGC
227	CCCAAGU U GUUGGGC	696	CCUUUGU C CUGCCAG
230	AAGUUGU U GGGCAUA	709	AGCGACU C CCCCACA
237	UGGGCAU A GAGACCC	720	CACAACU U GUCAGCC
248	ACCCCGU U GCCUAAA	723	AACUUGU C AGCCCCC
253	GUUGCCU A AAAAGGA	735	CCCGGGU C CUGAGAG
263	AAGGAGU U GCUCCTG	738	GGGUCCU A GAGGUGG
267	AGUUGCU C CUGCCTG	765	CCGUGGU C UGUUCCC
293	AAGGUGU A UGAACUG	769	GGUCUGU U CCCUGGA
319	AGAAGAU A GCCAACC	770	GUCUGUU C CCUGGAC
335	AUGUGCU A UUCAAC	785	GGGUGU U CCCAGUC
337	GUGCUAU U CAACTUG	786	GGCUGUU C CCAGUCU
338	UGCUAUU C AAACUGC	792	UCCAGU C UCGGAGG
359	GGGCAGU C AACAGCU	794	CCAGUCU C GGAGGCC
367	AACAGCU A AAACCUU	807	CCCAGGU C CACTUGG
374	AAAACCU U CUCACCC	833	CAGAGGU U GAACCCC
375	AAACCUU C CUCACCG	846	CCACAGU C ACCUAUG
378	CCUUCU C ACCGUGU	851	GUCACCU A UGGCAAC

863	AACGACT C CUCUUG	1408	UCGAGAU C UUGAGGG
866	GACUCCU U CUCGGCC	1410	GAGAUUU U GAGGGCA
867	ACUCCUU C UGGGCCA	1421	GGCACTU A CCUCUGU
869	UCCUUCU C GGCCAAG	1425	CCUACCU C UGUCGGG
881	AAGGCTU C AGUCAGU	1429	CTUCUGU C GGGCCAG
885	CCUCAGU C AGGUGA	1444	GAGCACT C AAGGGGA
933	GUGCAGU A AUACUGG	1455	GGGAGGU C ACCCGCG
936	CAGUAAU A CUGGGGA	1482	AUGUGCU C UCCCCCC
978	UGACCAU C UACAGCU	1484	GUGUCU C CCCCCGG
980	ACCAUCC A CAGCUUU	1493	CCCCGGU A UGAGAUU
986	UACAGCU U UCCGGCG	1500	AUGAGAU U GUCAUCA
987	ACAGCUU U CCGGCGC	1503	AGAUGU C AUCAUCA
988	CAGCUUU C CGGCGCC	1506	UUGUCAU C AUCAUCG
1005	ACGGGAU U CUGACGA	1509	UCAUCAU C ACUGUGG
1006	CGUGAUU C UGACGAA	1518	CUGUGGU A GCAGCCG
1023	CAGAGGU C UCAGAAG	1530	CCGCAGU C AUAAUGG
1025	GAGGUUU C AGAAGGG	1533	CAGUCAU A AUGGGCA
1066	CCACCCU A GAGCCAA	1551	CAGGCTU C AGCAAGU
1092	AUGGGGU U CCAGCCC	1559	AGCAGU A CCUCUAU
1093	UGGGGUU C CAGCCCA	1563	CGUACCU C UAUAAAC
1125	CCCAGCU C CUGCUGA	1565	UACCTUC A UAACCGC
1163	CGCAGCU U CUCGCGC	1567	CCUUAU A ACCGCCA
1164	GCAGCUU C UCCUGCU	1584	GGAAGAU C AAGAAAU
1166	AGCUUCU C CUGCUCU	1592	AAGAAAU A CAGACTA
1172	UCCUGCU C UGCAACC	1599	ACAGACT A CAACAGG
1200	GCCAGCU U AUACACA	1651	CACGCTU C CCUGAAC
1201	CCAGCUU A UACACAA	1661	UGAACCU A UCCCCGG
1203	AGCUUAU A CACAAGA	1663	AACCUAU C CCGGGAC
1227	GGGAGCU U CGUGUCC	1678	AGGGCCU C UUCUUGG
1228	GGAGCUU C GUGUCCU	1680	GGCCUCU U CCUCGGC
1233	UUCGUGU C CUGUADG	1681	GCCUCUU C CUCGGCC
1238	GUCCUGU A UGGCCCC	1684	UCUUCUU C GGCCUUC
1264	GAGGGAU U GUCCGGG	1690	UCGGCCU U CCCAUUU
1267	GGAUUGU C CGGGAAA	1691	CGGCCUU C CCAUAUU
1294	AGAAAAU U CCAGACA	1696	UUCCCAU A UUGGUGG
1295	GAAAAUU C CCAGCAG	1698	CCCAUAU U GGUGGCA
1306	GCAGACT C CAADGUG	1737	AAGACAU A UGCCAUG
1321	CCAGGCU U GGGGGAA	1750	UGCAGCU A CACCUAC
1334	AACCCAU U GCCCGAG	1756	UACACCU A CCGGCCC
1344	CCGAGCU C AAGUGUC	1787	AGGGCAU U GUCCUCA
1351	CAAGUGU C UAAAGGA	1790	GCAUUGU C CUCAGUC
1353	AGUGUCU A AAGGADG	1793	UUGUCCU C AGUCAGA
1366	UGGCACU U UCCCACT	1797	CCUCAGU C AGAUACA
1367	GGCACTU U CCCACUG	1802	GUCAUAU A CAACAGC
1368	GCACUUU C CCACUGC	1812	ACAGCAU U UGGGGCC
1380	UGCCCAU C GGGGAUU	1813	CAGCAUU U GGGGCCA
1388	GGGGAAU C AGUGACT	1825	CCAUUGU A CCUGCAC
1398	UGACUGU C ACUCGAG	1837	CACACTU A AAACACT
1402	UGUCACU C GAGAUUU	1845	AAACACT A GGCCACG

1856	CACGCAU C UGAUCUG	2189	UAUUUAU U GAGUGUC
1861	AUCUGAU C UGUAGUC	2196	UGAGUGU C UUUUAUG
1865	GAUCUGU A GUCACAU	2198	AGUGUCU U UUAUGUA
1868	CUGUAGU C ACAUGAC	2199	GUGUCUU U UAUGUAG
1877	CAUGACU A AGCCAAG	2200	UGUCUUU U AUGUAGG
1901	CAAGACU C AAGACAU	2201	GUCUUUU A UGUAGGC
1912	ACADGAU U GADGGAU	2205	UUUAUGU A GGUUAAA
1922	UGGADGU U AAAGOCU	2210	GUGGCUU A AAUGAAC
1923	GGAUGUU A AAGUCUA	2220	UGAACAU A GGUUCUU
1928	UUAAAGU C UAGCCUG	2224	CAUAGGU C UCUGGCC
1930	AAAGCCU A GCUUGAU	2226	UAGGUCU C UGGCCUC
1964	GAGACAU A GCCCCAC	2233	CUGGCCU C ACGGAGC
1983	AGGACAU A CACUGG	2242	CGGAGCU C CCAGUCC
1996	GGGAAAU A CUGAAC	2248	UCCAGU C CADGUCA
2005	UGAAACTU U GCUGCCU	2254	UCCAGU C ACAUCCA
2013	GCUGCCU A UUGGGUA	2259	GUCACAU U CAAGGUC
2015	UGCCUAU U GGUUAUG	2260	UCACAUU C AAGGUCA
2020	AUUGGGU A UGCUGAG	2266	UCAAGGU C ACCAGGU
2039	ACAGACU U ACAGAAG	2274	ACCAGGU A CAGUUGU
2040	CAGACUU A CAGAAGA	2279	GUACAGU U GUACAGG
2057	UGGCCCU C CAUAGAC	2282	CAGUUGU A CAGGUUG
2061	CCUCCAU A GACADGU	2288	UACAGGU U GUACACU
2071	CAUGUGU A GCADCAA	2291	AGGUUGU A CACUGCA
2076	GUAGCAU C AAAACAC	2321	AAAAGAU C AAUUGGG
2097	CCACACU U CUGACCG	2338	UGGGACU U CUCAUUG
2098	CACACUU C CUGACGG	2339	GGGACUU C UCAUUGG
2115	GCCAGCU U GGGCACU	2341	GACUUUU C AUUGGCC
2128	CUUGUGU C UACUGAC	2344	UUUCUAU U GGCCAAC
2130	GUUGUCU A CUGACCC	2358	CUUGCCU U UCCCCAG
2145	CAACCCU U GADGAUA	2359	CUGCCUU U CCCAGAA
2152	UGAUGAU A UGUUUUU	2360	UGCCUUU C CCCAGAA
2156	GAUAGGU A UUUUAUC	2376	GAGUGAU U UUUUAU
2158	UAUGUAU U UAUUCAU	2377	AGUGAUU U UUUUAUC
2159	ADGUUAU U AUUCAUU	2378	GUGAUUU U UCUADCG
2160	UGUAUUU A UUCAUUU	2379	UGAUUUU U CUADCGG
2162	UAUUUAU U CAUUGU	2380	GAUUUUU C UADCGGC
2163	AUUUAUU C AUUGUU	2382	UUUUUUU A UCGGCAC
2166	UAUUCAU U UGUUAUU	2384	UUUCUAU C GGCACAA
2167	AUUCAUU U GUUAUUU	2399	AAGCAU A UAGGGAC
2170	CAUUGU U AUUUUAC	2401	GCACUAU A UGGACUG
2171	AUUUGUU A UUUUACC	2411	GACUGGU A AUGGUUC
2173	UUGUUUAU U UUACCAG	2417	UAUUGGU U CACAGGU
2174	UGUUUAU U UACCAGC	2418	AAUGGUU C ACAGGUU
2175	GUUAUUU U ACCAGCU	2425	CACAGGU U CAGAGAU
2176	UUUUUUU A CCAGCUA	2426	ACAGGUU C AGAGAUU
2183	ACCAGCU A UUUUAUG	2433	CAGAGAU U ACCAGU
2185	CAGCUAU U UAUGAG	2434	AGAGAUU A CCCAGUG
2186	AGCUAUU U AUUGAGU	2448	GAGGCCU U AUUCCUC
2187	GCUAUUU A UUGAGUG	2449	AGGCCUU A UUCUCC

2451	GCCUUAU U CCUCCCU	2750	UAUGGUGU A GACAAGC
2452	CCUUAUU C CUCUCCU	2759	ACAAGCU C UCCGUCU
2455	UAUUCUU C CCUCCCC	2761	AAGCUCU C GCUCUGU
2459	CCUCCCU U CCCCCCA	2765	UCUCGCU C UGUCACC
2460	CUCCCUU C CCCCCAA	2769	GCUCUGU C ACCCAGG
2479	GACACCU U UGUUAGC	2797	GUGCAAU C AUGGUUC
2480	ACACCUU U GUUAGCC	2803	UCAUGGU U CACUGCA
2483	CCUUGU U AGCCACC	2804	CAUGGUU C ACUGCAG
2484	CUUUGUU A GCCACCU	2813	CUGCAGU C UUGACCU
2492	GCCACCU C CCCACCC	2815	GCAGUCU U GACCUUU
2504	CCCACAU A CAUUUCU	2821	UUGACCU U UUGGGCU
2508	CAUACAU U UCUGCCA	2822	UGACCUU U UGGGCUC
2509	AUACAUU U CUGCCAG	2823	GACCUUU U GGGCUCA
2510	UAUAUUU C UGCCAGU	2829	UUGGGCU C AAGUGAU
2520	CCAGUGU U CACAAUG	2837	AAGUGAU C CUCCAC
2521	CAGUGUU C ACAADGA	2840	UGAUCCU C CCACUUC
2533	UGACACU C AGCGGUC	2847	CCCACCU C AGCCTCC
2540	CAGCGGU C AUGUCUG	2853	UCAGCCU C CUGAGUA
2545	GUCAUGU C UGGACAU	2860	CCUGAGU A GCUUGGA
2568	AGGGAAU A UGCCCCA	2872	GGACCAU A GGCUCAC
2579	CCAAGCU A UGCCUUG	2877	AUAGGCU C ACAACAC
2585	UAUGCCU U GUCCUCU	2899	GGCAAU U UGAUUUU
2588	GCCUUGU C CUCUUGU	2900	GCAAUUU U GAUUUUU
2591	UUGGCCU C UUGUCCU	2904	AUUUGAU U UUUUUUU
2593	GUCCUCU U GUCCUGU	2905	UUUGAUU U UUUUUUU
2596	CUCUUGU C CUGUUUG	2906	UUGAUUU U UUUUUUU
2601	GUCCUGU U UGCAUUU	2907	UGAUUUU U UUUUUUU
2602	UCCUGUU U GCAUUUC	2908	GAUUUUU U UUUUUUU
2607	UUUGCAU U UCAUGGG	2909	AUUUUUU U UUUUUUU
2608	UUGCAUU U CACUGGG	2910	UUUUUUU U UUUUUUU
2609	UGCAUUU C ACUGGGA	2911	UUUUUUU U UUUUUUU
2620	GGGAGCU U GCACUAU	2912	UUUUUUU U UUUUUUC
2626	UUGCAU A UUGCAGC	2913	UUUUUUU U UUUUUCA
2628	GCACUAU U GCAGCUC	2914	UUUUUUU U UUUUCAG
2635	UGCAGCU C CAGUUUC	2915	UUUUUUU U UUUUCAG
2640	CUCCAGU U UCCUGCA	2916	UUUUUUU U UUCAGAG
2641	UCCAGUU U CUGCAG	2917	UUUUUUU U UCAGAGA
2642	CCAGUUU C CUGCAGU	2918	UUUUUUU U CAGAGAC
2653	CAGUGAU C AGGGUCC	2919	UUUUUUU C AGAGACG
2659	UCAGGGU C CUGCAAG	2931	ACGGGGU C UCGCAAC
2689	CCAAGGU A UUGGAGG	2933	GGGGUCU C GCAACAU
2691	AAGGUAU U GGAGGAC	2941	GCAACAU U GCCCAGA
2700	GAGGACU C CCUCCCA	2951	CCAGACU U CCUUGU
2704	ACUCCCU C CCAGCUU	2952	CAGACUU C CUUUGUG
2711	CCCAGCU U UGGAAGG	2955	ACUUCUU U UGUGUUA
2712	CCAGCUU U GGAAGGG	2956	CUUCCUU U GUGUAG
2721	GAAGGGU C AUCCGCG	2961	UUUGUGU U AGUUAUU
2724	GGGUCAU C CGCGUGU	2962	UUGUGUU A GUUAUA
2744	UGUGUGU A UGUGUAG	2965	UGUUAU U AAUAAAG

2966	GUUAGUU	A	AUAAGC
2969	AGUUAUU	A	AAGCUUU
2975	UAAAGCU	U	UCUCAAC
2976	AAAGCUU	U	CUCAACT
2977	AAGCUUU	C	UCAACUG
2979	GUUUUCU	C	AACUGCC

Table 3

Mouse ICAM HH Target Sequence

nt. Position	Target Sequence	nt. Position	Target Sequence
11	CCCUGGU C accGUUG	367	AAUGGCU u cAAACCcg
23	CaGuGgU u CUCUGCU	374	gAAgCCU U CCUGcCC
26	uGgUuCU C UGCUcCU	375	AAgCCU C CUgcCCc
31	CUCUGCU c CUCcaca	378	CuacCaU C ACCGUGU
34	UuCUcaU a AGgGUcG	386	ACCGUGU A uUcGuuU
40	gCAcAcU U GuAgCCU	394	CcGGACU u ucGAuCu
48	aggAOCU C AGCCUgG	420	CACaCuU C CCCcCcg
54	UggGCCU C GuGADGG	425	CaCCCCU C ccaGCAG
58	CaUgcCU u UaGCUCC	427	CagCCU C aGCAGug
64	cAcceCU C CCAGCAG	450	AGgACCU c ACCCUgC
96	CuCuGCU C CUGGcCC	451	GAAaCcU u uCCUuuG
102	UgCcaGU a CUGCUgG	456	UUAOCU c aGCCaCu
108	cuCUGCU C cuGGCcC	495	CuAcCaU C ACCGUGu
115	uGGuuCU C UGcUCCu	510	UGCUUGCU C CGUGGGG
119	GgaauGU c aCCAGGA	564	CUcAGGU a uCcAuCc
120	CUCUGcU C CugGccC	592	GAaAGAU C ACaugGG
146	CAGuGgU C cGcuUCC	607	AGCCAAU U UCUCaUG
152	UCUGUGU C agCCaCu	608	GCCAAU U CUCaUGC
158	UCCuguU u AAAAaCC	609	CCAAU U C UCaUGCC
165	CAGAAGU u gUuuUGC	611	AAUUCU C aUGCCGC
168	AAgCcUu C CUGCCCC	656	aAGCCGU U UGAGcug
185	GGuGGgU C CGUGCaG	657	AGCTGUU U GAGcugA
209	gcCAcuU C CUcUGgC	668	cgagCCU a GGCCaCC
227	CagAAGU U GUUuuGC	677	GaCCuCU A CCAGCcu
230	AAGUUGU U uuGCucc	684	uuCAGCU C CgGuCCU
237	UGuGcuU u GAGaCu	692	CgGACuU U cGauCUu
248	AaCCCaU c uCCUAAA	693	AGgaCcU c acCCUGC
253	ccUGCCU A AggAaGA	696	CCUgUuU C CUGCCuc
263	AgGGuuU c uCUaCUG	709	gGCGgCU C CaCCuCA
267	AGggGCU C CUGCCUa	720	uACAACU U uUCAGCu
293	AAGcUGU u UGAGCUG	723	AACTUuU C AGCuCCg
319	AGgAGAU A cuGAgCC	735	aCCaGaU C CUGGAGa
335	cUGUGCU u UgagAAC	738	uGGgCCU c GuGaUGG
337	GUcCaAU U CAcACUG	765	CaGUcGU C cGcUuCC
338	aGCUgUu u gAgCUGa	769	GGcCUGU U uCCUGcc
359	GuGCAGU C guCcGCU	770	uUuUGcU C CCUGGAa
785	GGcCUGU U uCCuGcC	1353	AGUGggU c gAaGgUG
786	GcCUGUU u CCuGcCU	1366	UaaCAgU c UaCaACU
792	UggagGU C UCGGAaG	1367	aGCACcU c CCCACcu
794	CuGgGU u GGAGaCu	1368	GuACTgU a CCACUcu
807	CuGgGaU a uACCUGG	1380	UGCCCAU C GGGGugg
833	CAaAGcU c GAcaCCC	1388	GGaGAcU C AGUGgCU
846	CCcuGgU C ACCguUG	1398	UGgCUGU C ACagaAc
851	GagACCU c UacCAGc	1402	UGUGcUu u GAGaACU

863	AgCcACU u CcUCUgG	1408	gCGAGAU C ggGgaGG
866	GAagCCU U CcuGcCC	1410	GAGgUTCU c GgaAGgg
867	AuUCgUU u cCGGagA	1421	ccCACCU A CuUuUGU
869	UCuUcCU C augCAAG	1425	aCUGCCU u gGUaGaG
881	AuGGCuU C AacCcGU	1429	uCUUUAU u GccCCuG
885	CCUugGU a gagGUGA	1444	GAaggCU C AgGaGGA
933	cUauAaU c ADuCUgg	1455	GGaAuGU C ACCaGga
936	uAaUcAU u CUgGuGc	1482	AgUUGuU u UgCuCCC
978	UaACagU C UACaACU	1484	cUGuUTCU u CCuCaUG
980	ACagUCU A CAaCUUU	1493	CugUGcU u UGAGAac
986	UACaACU U UuCaGCU	1500	AUGAaAU c aUggUCc
987	ACaACUU U uCaGCUc	1503	gGAaUaU a AUCAUuc
988	CAaCUUU u CaGCUCC	1506	UUaUguU u AUaACcG
1005	ACcaGAU c CUggaGA	1509	cuAcCAU C ACCGUGu
1006	uGaGAgU c UGggGAA	1518	ucaUGGU c cCAGgCG
1023	ugGAGGU C UCgGAAG	1530	CuauAaU C AUucUGG
1025	GAGGUUU C gGAAGGG	1533	ugGUCAU u gUGGGCc
1066	CCACuCU c aAaauAA	1551	CAuGCCU u AGCAgcU
1092	AcuGGaU c uCAGgCC	1559	AGCACcU c CCcaccU
1093	UGGaccU u CAGCCaA	1563	CuUaugU u UAUaACC
1125	CCCAaCU C uUcuUGA	1565	UAUGuU A UAACCGC
1163	CGaAGCU U CUuuUGC	1567	ugUuUAU A ACCGCCA
1164	GaAGCUU C UuuUGCU	1584	GaAAGAU C AgGAuAU
1166	AGCUUCU u uUGCUCU	1592	AgGAuAU A CAaguUA
1172	UCCUGuU u aaaAAcC	1599	ACAaguU A CAgaAGG
1200	cuCuGCU c cUcCACA	1651	CcCaCCU C CCTUGaC
1201	gCuGCUU u UgaACAg	1661	gaAACCU u UCCuuUG
1203	AcuUUuU u CACcAGu	1663	AACCUuU C CUuuGAA
1227	GUuAcaU a CGUGUGC	1678	AGGaCCU C agCCUgG
1228	GaAGCUU C uUuUgCU	1680	agCCaCU U CCUCuGg
1233	UUCGUuU C CgGagaG	1681	GCCaCUU C CUcuGgC
1238	GUgCUGU A UGUuCCu	1684	aCUUCCU C uGgCUgu
1264	GAaGGgU c GUgCaAG	1690	cCGGaCU U UCgAUcU
1267	uGAgagU C uGGGgAA	1691	CGGaCUU u CgAUcUU
1294	AGgAgAU a CugAGCc	1696	UgCCCAU c ggGGUGG
1295	GAggggU c uCAGCAG	1698	CggAUAU a ccUGGag
1306	GCAGACU C ugAaaUG	1737	gAGACcU c UaCCAgc
1321	gaAGGCU c aGGaGgA	1750	gGCgGCU c CACCUca
1334	AACCCAU c uCCuaAa	1756	gAagCCU u CCuGCCC
1344	auGAGCU C gAGaGUg	1787	gaGaCAU U GUCCcCA
1351	ugAaUGU a UAAguuA	1790	GCAUUGU u CUcuauu
1793	UgGUCCU C gGcuGGA	2173	UUagagU U UUAACAG
1797	CacCAGU C AcAUaAa	2174	UagagUU U UAACCAGC
1802	acCAGAU c CuggAGa	2175	agagUUU U ACCAGCU
1812	ACuGgAU c UcaGGCC	2176	gagUUUU A CCAGCUA
1813	CAGCAU U acccuCA	2183	ACCAGCU A UUAUUG
1825	CCAcGcU A CUcugC	2185	CAGCUAU U UAUUGAG
1837	CAugCCU u uAgCuCc	2186	AGCUAUU U AUUGAGU
1845	cgAgcCU A GGCACc	2187	GCUAUUU A UUGAGUa

1856	CggaCuU u cGAUCUu	2189	UAUUUAU U GAGUacc
1861	AcaUGAU a UccAGUa	2196	caAcUcU u cUUGAUG
1865	cAcuUGU A GcCuCAg	2198	gcaGcCU c UUAUGUu
1868	CaccAGU C ACAUaAa	2199	GccUCCU a UgUuUAu
1877	CAUGcCU u AGCagcu	2200	UcUuccU c ADGcAaG
1901	uAAaACTU C AAGggAc	2201	aagUUUU A UGUcGGC
1912	luADagU a GAUcagU	2205	UUUAUGU c GGCCugA
1922	UGaADGU a uAAGUua	2210	GgAGaCU c AgUGgcu
1923	uGAUGcU c AgGUaUc	2220	cuGGCAU u GuUCCUCU
1928	UUAgaGU u UuaCCaG	2224	CucAGGU a UCCauCC
1930	AgAGUuU u aCCaGcU	2226	UgGaUcU C aGGCCGc
1964	GAGACAU u GuCCCa	2233	CGaCCU C cuGGAGg
1983	AGGAuAU A CAAGUua	2242	uGGAGCU a gCgGaCC
1996	aGGAgAU A CUGAgcC	2248	UauCcaU C CAUccCA
2005	UGgAgCU a GCgGaCc	2254	UCCAauU C ACaCUga
2013	GUauuuU A UUGaGUA	2259	aUCACAU U CAcGGUg
2015	UGCCcAU c GGGgugG	2260	UCACAUU C AcGGUgc
2020	ggUGGuU c UuCCGAG	2266	ggAAuGU C ACCAGGa
2039	gCuGgCU a gCAGAgG	2274	ACCAGaU c CuGgaGa
2040	CuGACCcU c CuGgAGg	2279	GaAggGU c GUgCAaG
2057	UGcuCCU C CAcAuCC	2282	aAGcUGU u ugaGcUG
2061	CuaCCAU c acCgUGU	2288	UauAaGU U aUggcCU
2071	CAcuUGU A GCcCCAg	2291	caGUgGU u CuUUGCu
2076	GUAGCcU C AgAgCUa	2321	gAAAGAU C AcAUGGG
2097	CaACuCU U CuUGAuG	2338	UGaGACU c UGgccUG
2098	CACACUU C CcccCcG	2339	GaaACcU u UCCUUuG
2115	GCCAGCU c GGaggaU	2341	GACcUcU a ccaGcCu
2128	CaGCUaU u UAUUGAg	2344	UUuegAU c uuCCAAGc
2130	cCUGUuU c CUGcCuC	2358	CCcagCU c UCagCAG
2145	CAACuCU U cuUGAUg	2359	CUGCuUU U gaaCAGA
2152	UauUaAU u UagAgUU	2360	aaCTUUU C CUuuGAA
2156	uugAUGU A UUUUAUa	2376	agGUGgU U cUUCUga
2158	gAUUGAU U UAUUAU	2377	gGUGgUU c UUCUgag
2159	AUGUAUU U AUUAUUU	2378	agGgUUU c UCUAcuG
2160	UGUAUUU A UUAUUUU	2379	UGcUUUU c ucAUaaG
2162	UAUUUAU U aAUUag	2380	aAgUUUU a UgUCGGC
2163	AUgUAUU u AUUaaUU	2382	aUUcUcU A UuGcCcC
2166	acUUCAU U cucUAUU	2384	aUcCagU a GaCACAA
2167	AUguAUU U aUUAAUU	2399	AAaCACTU A UgUGGAC
2170	uAUUUaU U AaUUUAg	2401	aagCUgU u UGagCUG
2171	AgUUGUU u UgcUcCC	2411	uACUGGU c AgGaUgC
2417	gAADGGU a CAuAcGU	2691	AAuGUcU c cGAGGcC
2418	AcUGGaU C uCAGGcc	2700	GAAgCCU u CCUgCCC
2425	CAugGGU c gAGgGuU	2704	gacCuCU a CCAGCcU
2426	luuaaUU u AGAGuUU	2711	CCcAGCU c UcagcaG
2433	uAGAGuU U uaCCAGc	2712	gagGucU c GGAAGGG
2434	AGAGuUU u aCCAGcu	2721	GAAGGGU C gUgCaAG
2448	GAAGCCU U ccUgCcC	2724	GGuaCAU a CGUGUGc
2449	AAGCCUU c cUgCcCC	2744	gGUGgGU c cGUGcAG

2451	GCCUGuU U CCUGCCU	2750	UAAUUAU u GAguAcC
2452	CCUGuUU C CUgCCUc	2759	cCggaCU u UCGaUTC
2455	gAagCCU u CCUGCCC	2761	AgGacCU C aCcCUGc
2459	CCaCaCU U CCCCCc	2765	UUUUUCU C UGCcGu
2460	CaCaCUU C CCCCCcg	2769	agUCUGU C AaaCAGG
2479	GAgACCU c UaccAGC	2797	aUGaAAU C AUGGUcC
2480	uCAACgU U GUgAuCC	2803	UCADGGU c CcagGCg
2483	CCaaUGU c AGCCACC	2804	ggUGGgU C cgUGCAG
2484	CUUUUUU c aCCAguc	2813	CUcCgGU C cUGACCc
2492	agCACCU C CCCACCu	2815	aCAGUCU a cAACTUU
2504	CCCACcU A CUUUUGU	2821	cUGACCU c cUGGagg
2508	uAUcCAU c caUcCCA	2822	gAgGcCU c cGgaCUu
2509	uUAgAgU U uUaCCAG	2823	ugCCUUU a GcuCcCA
2510	UAgAgUU u UaCCAGc	2829	cUGGaCU a uAaUcAU
2520	CUuuUGU U CcCAADG	2837	AgUGGgU u CUuCuGa
2521	CAGcaUU u ACccUcA	2840	UGAgacU C CugCCUG
2533	UGAugCU C AGguaUC	2847	CCaAugU C AGCCaCC
2540	CAGCaGU C cgcUGUG	2853	gCAGCCU C uUauGUu
2545	GUgcUGU a UGGuCCU	2860	gCcaAGU A aCTUGaA
2568	guGaAgU c UGuCaAA	2872	GGACCUU c aGCcaAg
2579	auAAGuU A UGgCcUG	2877	uUccGCU a cCAuCAC
2585	cugGCaU U GUuCUUU	2899	cGgAcuU U cGAUcUU
2588	GCaUUGU u CUUaaU	2900	uuAAuUU a GAgUUUU
2591	UgGUuCU C UgcUCCU	2904	AcUUcAU U cUcUaUU
2593	cUUUUUU U GcuCUGc	2905	cUUcAUU c UcUaUUg
2596	CUuUUUGU u CccaaUG	2906	UUGAUgU a UUUaUUa
2601	acCgUGU a UUcGUUU	2907	UGuaUUU a UUaaUUU
2602	UCCaGcU a cCAUccC	2908	GAagcUU c UUUUgcU
2607	cUcGgAU a UaccUGG	2909	AgcUUcU U UUgcUcU
2608	caGCAgU c CgCUGuG	2910	UgUaUUU a UUaaUUU
2609	gGaAUgU C ACcaGGA	2911	UgUaUUU a UUaaUUU
2620	aGGAcCU c aCcCUGc	2912	UUgUUcU c UaaUgUC
2626	UUuCGaU c UUcCAGC	2913	UUUcUcU a cUggUCA
2628	GCACacU U GuAGCcu	2914	UgcUUUU c UcaUaAG
2635	UUcAGCU C CgGUccu	2915	aUUUaUU a aUUuAGA
2640	ggCCuGU U UCCUGCc	2916	UaUUcgU U UcCgGAG
2641	cCCAGcU c uCaGCAG	2917	aUUcgUU U cCgGAGA
2642	CCuGUUU C CUGCcuc	2918	UUcgUUU c CgGAGAg
2653	uAcUGgU C AGGaUgC	2919	UUcUcaU a AGGGuCG
2659	gaAGGGU C gUGCAAG	2931	ugGaGGU C UCGgAAG
2689	CUAAuGU c UccGAGG	2933	GaGGUCU C GgAaggg
2941	GagACAU U GuCCcCA		
2951	CCAagCU a CCUcUGc		
2952	CAGcagU C CgcUGUG		
2955	AgUgaCU c UGUUcAA		
2956	uUUCCUU U GaaUcAA		
2961	UcUGUGU c AGccAcU		
2962	aUGUaUU u aUUAAUu		
2965	UUUGAaU c AAUAAG		

2966	GcUgGcU	A	gcAgAGg
2969	LaUcAAU	A	AAGuUUU
2975	UAgAGuU	U	UacCAgC
2976	gAgGgUU	U	CUcUACU
2977	AAGCUgU	u	UgAgCUG
2979	uCaUUUU	C	uAuUGCC

Table 4
Human ICAM HH Ribozyme Sequences

nt. Position Ribozyme Sequence

11	CAGCGUC	CUGAUGAGGCCGAAAGGCCGAA	ACUGGGG
23	AGCAGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUCAG
26	AGUAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCU
31	CUCUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
34	CACTUCU	CUGAUGAGGCCGAAAGGCCGAA	AGUAGCA
40	AGGUUGC	CUGAUGAGGCCGAAAGGCCGAA	ACUCUGA
48	CGAGGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUUGC
54	CCAUAGC	CUGAUGAGGCCGAAAGGCCGAA	AGGUCGA
58	GGAGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGCGAGG
64	CTGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGCCATA
96	GGACCAG	CUGAUGAGGCCGAAAGGCCGAA	AGUGCGG
102	CGAGCAG	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGA
108	GAGCCCC	CUGAUGAGGCCGAAAGGCCGAA	AGCAGGA
115	GGGAACA	CUGAUGAGGCCGAAAGGCCGAA	AGCCCCG
119	UCCUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGAGC
120	GUCCUGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGAG
146	GGACACA	CUGAUGAGGCCGAAAGGCCGAA	AUGUCUG
152	UGAGGGG	CUGAUGAGGCCGAAAGGCCGAA	ACACAGA
158	GACUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGGGGGA
165	GCAGGAU	CUGAUGAGGCCGAAAGGCCGAA	ACUUUUG
168	GGGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AUGACUU
185	CAGCACG	CUGAUGAGGCCGAAAGGCCGAA	AGCCUCC
209	GUCACAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGCU
227	GCCCCAAC	CUGAUGAGGCCGAAAGGCCGAA	ACUUGGG
230	UAUGCCC	CUGAUGAGGCCGAAAGGCCGAA	ACAACUU
237	GGGUCUC	CUGAUGAGGCCGAAAGGCCGAA	AUGCCCC
248	UUUAGGC	CUGAUGAGGCCGAAAGGCCGAA	ACGGGGU
253	UCCUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCAAC
263	CAGGAGC	CUGAUGAGGCCGAAAGGCCGAA	ACUCCUU
267	CAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAACU
293	CAGUUCA	CUGAUGAGGCCGAAAGGCCGAA	ACAACUU
319	GGUUGGC	CUGAUGAGGCCGAAAGGCCGAA	AUCUUUU
335	GUUUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGCACAU
337	CAGUUUG	CUGAUGAGGCCGAAAGGCCGAA	AUAGCAC
338	GCAGUUU	CUGAUGAGGCCGAAAGGCCGAA	AADAGCA
359	AGCUGUU	CUGAUGAGGCCGAAAGGCCGAA	ACUGCCC
367	AAGGUUU	CUGAUGAGGCCGAAAGGCCGAA	AGCUGUU
374	GGUGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUUUU
375	CGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGUUU
378	ACACGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGG
386	AGUCCAG	CUGAUGAGGCCGAAAGGCCGAA	ACACGGU
394	CGUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCAG
420	AAGAGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUG
425	CUGCCAA	CUGAUGAGGCCGAAAGGCCGAA	AGGGGAG

427	GGCUGCC	CUGAUGAGGCCGAAAGGCCGAA	AGAGGGG
450	GUAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCU
451	CGUAGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGGUUC
456	GGCAGCG	CUGAUGAGGCCGAAAGGCCGAA	AGGGUAA
495	CCACGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUUGG
510	CCCCACG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGCA
564	UGGUCCU	CUGAUGAGGCCGAAAGGCCGAA	ACCUCCG
592	CCAUGGU	CUGAUGAGGCCGAAAGGCCGAA	AUCUCUC
607	CACGAGA	CUGAUGAGGCCGAAAGGCCGAA	AUUGGCU
608	GCAAGAG	CUGAUGAGGCCGAAAGGCCGAA	AAUUGGC
609	GGCAGCA	CUGAUGAGGCCGAAAGGCCGAA	AAAUUGG
611	GCGGCAC	CUGAUGAGGCCGAAAGGCCGAA	AGAAAUU
656	GUUUCUA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCUC
657	UGUUCUC	CUGAUGAGGCCGAAAGGCCGAA	AACAGCU
668	GGGGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGUUUU
677	GAGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGGC
684	AGGUCUG	CUGAUGAGGCCGAAAGGCCGAA	AGCUUGU
692	CAGGACA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCG
693	GCAGGAC	CUGAUGAGGCCGAAAGGCCGAA	AAGGUUC
696	CUGGCAG	CUGAUGAGGCCGAAAGGCCGAA	ACAAAGG
709	UGUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGUCGCU
720	GGCUGAC	CUGAUGAGGCCGAAAGGCCGAA	AGUUGUG
723	GGGGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACAAAGU
735	CCUCUAG	CUGAUGAGGCCGAAAGGCCGAA	ACCGGGG
738	CCACCTC	CUGAUGAGGCCGAAAGGCCGAA	AGGACCC
765	GGGAACA	CUGAUGAGGCCGAAAGGCCGAA	ACCACGG
769	UCCAGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGACC
770	GUCCAGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGAC
785	GACTUGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGCCC
786	AGACTUG	CUGAUGAGGCCGAAAGGCCGAA	AACAGCC
792	CCUCCGA	CUGAUGAGGCCGAAAGGCCGAA	ACUGGGA
794	GGCCUCC	CUGAUGAGGCCGAAAGGCCGAA	AGACTUG
807	CCAGGUG	CUGAUGAGGCCGAAAGGCCGAA	ACCUGGG
833	GGGGUUC	CUGAUGAGGCCGAAAGGCCGAA	ACCUUCG
846	CAUAGGU	CUGAUGAGGCCGAAAGGCCGAA	ACUGUGG
851	GUUGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGGUGAC
863	CGAGAAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCGUU
866	GGCCGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGUC
867	UGGCCGA	CUGAUGAGGCCGAAAGGCCGAA	AAGGAGU
869	CUUGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGAAGGA
881	ACTUGACU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUU
885	UCACACU	CUGAUGAGGCCGAAAGGCCGAA	ACUGAGG
933	CCAGUAT	CUGAUGAGGCCGAAAGGCCGAA	ACTGCAC
936	UCCCCAG	CUGAUGAGGCCGAAAGGCCGAA	AUUACUG
978	AGCUGUA	CUGAUGAGGCCGAAAGGCCGAA	AUGGUCA
980	AAAGCTG	CUGAUGAGGCCGAAAGGCCGAA	AGAUGGU
986	CGCCGGA	CUGAUGAGGCCGAAAGGCCGAA	AGCUGUA
987	GCGCCGG	CUGAUGAGGCCGAAAGGCCGAA	AAGCUGU
988	GGCCCGG	CUGAUGAGGCCGAAAGGCCGAA	AAAGCTG

1005	UCCUCAG	CUGAUGAGGCCGAAAGGCCGAA	AUCACGU
1006	UUCGUCA	CUGAUGAGGCCGAAAGGCCGAA	AAUCACG
1023	CUUCUGA	CUGAUGAGGCCGAAAGGCCGAA	ACUCUCG
1025	CCCUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGACCCU
1066	UUGGCTC	CUGAUGAGGCCGAAAGGCCGAA	AGGGUGG
1092	GGGCTUG	CUGAUGAGGCCGAAAGGCCGAA	ACCCCAU
1093	UGGGCTG	CUGAUGAGGCCGAAAGGCCGAA	AAACCCA
1125	UCAGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGG
1163	GCAGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGCG
1154	AGCAGGA	CUGAUGAGGCCGAAAGGCCGAA	AAGCTGC
1156	AGAGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCT
1172	GGUUGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCAGGA
1200	UGUGUAU	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGC
1201	UUGUGUA	CUGAUGAGGCCGAAAGGCCGAA	AAGCTUG
1203	UCUUGUG	CUGAUGAGGCCGAAAGGCCGAA	AUAAGCT
1227	GGACACG	CUGAUGAGGCCGAAAGGCCGAA	AGCUCCC
1228	AGGACAC	CUGAUGAGGCCGAAAGGCCGAA	AAGCTCC
1233	CAUACAG	CUGAUGAGGCCGAAAGGCCGAA	ACACGAA
1238	GGGGCCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGGAC
1264	CCCGGAC	CUGAUGAGGCCGAAAGGCCGAA	AUCCCTC
1267	UUUCCCG	CUGAUGAGGCCGAAAGGCCGAA	ACAADCC
1294	UGCUGGG	CUGAUGAGGCCGAAAGGCCGAA	AUUUUCU
1295	CUCUGGG	CUGAUGAGGCCGAAAGGCCGAA	AAUUUUC
1306	CACAUUG	CUGAUGAGGCCGAAAGGCCGAA	AGUCUGC
1321	UUCCCCC	CUGAUGAGGCCGAAAGGCCGAA	AGCCTUG
1334	CUCCGGC	CUGAUGAGGCCGAAAGGCCGAA	AUGGGUU
1344	GACACUU	CUGAUGAGGCCGAAAGGCCGAA	AGCUCGG
1351	UCCUUUA	CUGAUGAGGCCGAAAGGCCGAA	ACACTUG
1353	CAUCCUU	CUGAUGAGGCCGAAAGGCCGAA	AGACACT
1366	AGUGGGA	CUGAUGAGGCCGAAAGGCCGAA	AGUGCCA
1367	CAGUGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGCC
1368	GCAGUGG	CUGAUGAGGCCGAAAGGCCGAA	AAAGUGC
1380	AUUCCCC	CUGAUGAGGCCGAAAGGCCGAA	AUGGGCA
1388	AGUCACU	CUGAUGAGGCCGAAAGGCCGAA	AUUCCCC
1398	CUCGAGU	CUGAUGAGGCCGAAAGGCCGAA	ACAGUCA
1402	AGAUCUC	CUGAUGAGGCCGAAAGGCCGAA	AGUGACA
1408	CCUCUAA	CUGAUGAGGCCGAAAGGCCGAA	ADUCUGA
1410	UGCCCTC	CUGAUGAGGCCGAAAGGCCGAA	AGAUCUC
1421	ACAGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGCC
1425	CCCGACA	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGG
1429	CUGGCCC	CUGAUGAGGCCGAAAGGCCGAA	ACAGAGG
1444	UCCCTUU	CUGAUGAGGCCGAAAGGCCGAA	AGUGCTC
1455	CGCGGGU	CUGAUGAGGCCGAAAGGCCGAA	ACCTCCC
1482	GGGGGGA	CUGAUGAGGCCGAAAGGCCGAA	AGCACAU
1484	CCGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGAGCAC
1493	AAUCUCA	CUGAUGAGGCCGAAAGGCCGAA	ACCGGGG
1500	UGAUGAC	CUGAUGAGGCCGAAAGGCCGAA	AUTCACU
1503	UGAUGAU	CUGAUGAGGCCGAAAGGCCGAA	ACAADCU
1506	CAGUGAU	CUGAUGAGGCCGAAAGGCCGAA	AUGACAA

1509	CCACAGU	CUGADGAGGCCGAAAGGCCGAA	AUGAUGA
1518	CGGUGC	CUGADGAGGCCGAAAGGCCGAA	ACCACAG
1530	CCAUUAU	CUGADGAGGCCGAAAGGCCGAA	ACUGCGG
1533	UGCCCAU	CUGADGAGGCCGAAAGGCCGAA	AUGACUG
1551	ACGUGCU	CUGADGAGGCCGAAAGGCCGAA	AGGCCUG
1559	AUAGAGG	CUGADGAGGCCGAAAGGCCGAA	ACGUGCU
1563	GGUUAUA	CUGADGAGGCCGAAAGGCCGAA	AGGUACG
1565	GCGGUUA	CUGADGAGGCCGAAAGGCCGAA	AGAGGUA
1567	UGGCGGU	CUGADGAGGCCGAAAGGCCGAA	AUAGAGG
1584	AUUUCUU	CUGADGAGGCCGAAAGGCCGAA	AUCUCC
1592	UAGUCUG	CUGADGAGGCCGAAAGGCCGAA	AUUUCUU
1599	CCUGUUG	CUGADGAGGCCGAAAGGCCGAA	AGUCUGU
1651	GUUCAGG	CUGADGAGGCCGAAAGGCCGAA	AGGCGUG
1661	CCCGGA	CUGADGAGGCCGAAAGGCCGAA	AGGUUCA
1663	GUCCCGG	CUGADGAGGCCGAAAGGCCGAA	AUAGGUU
1678	CGAGGAA	CUGADGAGGCCGAAAGGCCGAA	AGGCCCU
1680	GCCGAGG	CUGADGAGGCCGAAAGGCCGAA	AGAGGCC
1681	GGCCGAG	CUGADGAGGCCGAAAGGCCGAA	AAGAGGC
1684	GAAGGCC	CUGADGAGGCCGAAAGGCCGAA	AGGAAGA
1690	AUAUGGG	CUGADGAGGCCGAAAGGCCGAA	AGGCCGA
1691	AUAUGG	CUGADGAGGCCGAAAGGCCGAA	AAGGCCG
1696	CCACCAA	CUGADGAGGCCGAAAGGCCGAA	AUGGGAA
1698	UGCCACC	CUGADGAGGCCGAAAGGCCGAA	AUAUGGG
1737	CAUGGCA	CUGADGAGGCCGAAAGGCCGAA	AUGUCUU
1750	GUAGGUG	CUGADGAGGCCGAAAGGCCGAA	AGCUGCA
1756	GGGCCGG	CUGADGAGGCCGAAAGGCCGAA	AGGUGUA
1787	UGAGGAC	CUGADGAGGCCGAAAGGCCGAA	AUGCCCU
1790	GACUGAG	CUGADGAGGCCGAAAGGCCGAA	ACAAUGC
1793	UCUGACU	CUGADGAGGCCGAAAGGCCGAA	AGGACAA
1797	UGUAUCU	CUGADGAGGCCGAAAGGCCGAA	ACTGAGG
1802	GCUGUUG	CUGADGAGGCCGAAAGGCCGAA	AUCUGAC
1812	GGCCCCA	CUGADGAGGCCGAAAGGCCGAA	AUGCUGU
1813	UGGCCCC	CUGADGAGGCCGAAAGGCCGAA	A AUGCUG
1825	GUGCAGG	CUGADGAGGCCGAAAGGCCGAA	ACCADGG
1837	AGUGUUU	CUGADGAGGCCGAAAGGCCGAA	AGGUGUG
1845	CGUGGCC	CUGADGAGGCCGAAAGGCCGAA	AGUGUUU
1856	CAGAUCA	CUGADGAGGCCGAAAGGCCGAA	AUGCGUG
1861	GACUACA	CUGADGAGGCCGAAAGGCCGAA	AUCAGAU
1865	AUGUGAC	CUGADGAGGCCGAAAGGCCGAA	ACAGAUC
1868	GUCAUGU	CUGADGAGGCCGAAAGGCCGAA	ACTACAG
1877	CUUGGCU	CUGADGAGGCCGAAAGGCCGAA	AGUCAUG
1901	AUGUCUU	CUGADGAGGCCGAAAGGCCGAA	AGUCUUG
1912	AUCCADC	CUGADGAGGCCGAAAGGCCGAA	AUCAUGU
1922	AGACTUU	CUGADGAGGCCGAAAGGCCGAA	ACADCCA
1923	UAGACUU	CUGADGAGGCCGAAAGGCCGAA	AACADCC
1928	CAGGCUA	CUGADGAGGCCGAAAGGCCGAA	ACTUUA
1930	AUCAGGC	CUGADGAGGCCGAAAGGCCGAA	AGACTUU
1964	GUGGGGC	CUGADGAGGCCGAAAGGCCGAA	AUGUCUC
1983	CCAGUUG	CUGADGAGGCCGAAAGGCCGAA	AUGCCCU

1996	GUUUCAG	CUGAUGAGGCCGAAAGGCCGAA	AUUUCCC
2005	AGGCAGC	CUGAUGAGGCCGAAAGGCCGAA	AGUUUCA
2013	UACCCAA	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGC
2015	CAUACCC	CUGAUGAGGCCGAAAGGCCGAA	AUAGGCA
2020	CUCAGCA	CUGAUGAGGCCGAAAGGCCGAA	ACCCAAU
2039	CUUCUGU	CUGAUGAGGCCGAAAGGCCGAA	AGUCUGU
2040	UCUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AAGUCUG
2057	GUTUAUG	CUGAUGAGGCCGAAAGGCCGAA	AGGGCCA
2061	ACAUGUC	CUGAUGAGGCCGAAAGGCCGAA	AUGGAGG
2071	UUGAUGC	CUGAUGAGGCCGAAAGGCCGAA	ACACADG
2076	GUGUUUU	CUGAUGAGGCCGAAAGGCCGAA	AUGCUAC
2097	CSCCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGUGUGG
2098	CCGUCAG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGUG
2115	AGUGCCC	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGC
2128	GUCAGUA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCAG
2130	GGGUCAG	CUGAUGAGGCCGAAAGGCCGAA	AGACAGC
2145	UAUCAUC	CUGAUGAGGCCGAAAGGCCGAA	AGGGUUG
2152	AAAUACA	CUGAUGAGGCCGAAAGGCCGAA	AUCAUCA
2156	GAUAAA	CUGAUGAGGCCGAAAGGCCGAA	ACAUACC
2158	AUGAAUA	CUGAUGAGGCCGAAAGGCCGAA	AUACAUU
2159	AAUGAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
2160	AAAUCAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACA
2162	ACAAADG	CUGAUGAGGCCGAAAGGCCGAA	AUAAUAU
2163	AACAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
2166	AAUAACA	CUGAUGAGGCCGAAAGGCCGAA	AUGAAUA
2167	AAUAAC	CUGAUGAGGCCGAAAGGCCGAA	AAUGAAU
2170	GUAAAAU	CUGAUGAGGCCGAAAGGCCGAA	ACAAADG
2171	GGUAAA	CUGAUGAGGCCGAAAGGCCGAA	AACAAAU
2173	CUGGUAA	CUGAUGAGGCCGAAAGGCCGAA	AUAACAA
2174	GCUGGUA	CUGAUGAGGCCGAAAGGCCGAA	AAUAACA
2175	AGCUGGU	CUGAUGAGGCCGAAAGGCCGAA	AAUAAC
2176	UAGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AAAUAA
2183	CAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGU
2185	CUCAUAU	CUGAUGAGGCCGAAAGGCCGAA	AUAGCUG
2186	ACTCAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAGCU
2187	CACUCAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAGC
2189	GACATUC	CUGAUGAGGCCGAAAGGCCGAA	AUAAUAU
2196	CAUAAAA	CUGAUGAGGCCGAAAGGCCGAA	ACACUCA
2198	UACAUAA	CUGAUGAGGCCGAAAGGCCGAA	AGACACT
2199	CUACAUA	CUGAUGAGGCCGAAAGGCCGAA	AAGACAC
2200	CCUACAU	CUGAUGAGGCCGAAAGGCCGAA	AAAGACA
2201	GCCUACA	CUGAUGAGGCCGAAAGGCCGAA	AAAAGAC
2205	UUUAGCC	CUGAUGAGGCCGAAAGGCCGAA	ACAUAAA
2210	GUUCAUU	CUGAUGAGGCCGAAAGGCCGAA	AGCCUAC
2220	AGAGACC	CUGAUGAGGCCGAAAGGCCGAA	AUGUUCA
2224	GGCCAGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUAUG
2226	GAGGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGACCUA
2233	GCUCCGU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCAG
2242	GGACTUG	CUGAUGAGGCCGAAAGGCCGAA	AGCUCOG

2248	UGACAUG	CUGAUGAGGCCGAAAGGCCGAA	ACUGGGA
2254	UGAUGU	CUGAUGAGGCCGAAAGGCCGAA	ACAUGGA
2259	GACCTUG	CUGAUGAGGCCGAAAGGCCGAA	AUGUGAC
2260	UGACCTU	CUGAUGAGGCCGAAAGGCCGAA	AADUGA
2266	ACCTUGU	CUGAUGAGGCCGAAAGGCCGAA	ACCTUGA
2274	ACAACUG	CUGAUGAGGCCGAAAGGCCGAA	ACCTUGU
2279	CCUGUAC	CUGAUGAGGCCGAAAGGCCGAA	ACUGUAC
2282	CAACCTG	CUGAUGAGGCCGAAAGGCCGAA	ACAACUG
2288	AGUGUAC	CUGAUGAGGCCGAAAGGCCGAA	ACCTUGA
2291	UGCAGUG	CUGAUGAGGCCGAAAGGCCGAA	ACAACCU
2321	CCCAUUU	CUGAUGAGGCCGAAAGGCCGAA	AUCUUUU
2338	CAADGAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCCA
2339	CCAADGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCC
2341	GGCCAAU	CUGAUGAGGCCGAAAGGCCGAA	AGAAGUC
2344	GUUGGCC	CUGAUGAGGCCGAAAGGCCGAA	AUGAGAA
2358	CUGGGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGG
2359	UCUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCAG
2360	UUCUGGG	CUGAUGAGGCCGAAAGGCCGAA	AAAGCCA
2376	AUAGAAA	CUGAUGAGGCCGAAAGGCCGAA	AUCACUC
2377	GADAGAA	CUGAUGAGGCCGAAAGGCCGAA	AADCAU
2378	CGAUAGA	CUGAUGAGGCCGAAAGGCCGAA	AAADCAC
2379	COGAUAG	CUGAUGAGGCCGAAAGGCCGAA	AAAUAUA
2380	GCCGADA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAUA
2382	GUGCCGA	CUGAUGAGGCCGAAAGGCCGAA	AGAAAAA
2384	UUGUGCC	CUGAUGAGGCCGAAAGGCCGAA	AUAGAAA
2399	GUCCAUA	CUGAUGAGGCCGAAAGGCCGAA	AGUGCUU
2401	CAGUCCA	CUGAUGAGGCCGAAAGGCCGAA	AUAGUGC
2411	GAACCAU	CUGAUGAGGCCGAAAGGCCGAA	ACCAGUC
2417	ACCTUGG	CUGAUGAGGCCGAAAGGCCGAA	ACCAUUA
2418	AACCTGU	CUGAUGAGGCCGAAAGGCCGAA	AACCAUU
2425	AUCUCUG	CUGAUGAGGCCGAAAGGCCGAA	ACCTUGG
2426	AAUCUCU	CUGAUGAGGCCGAAAGGCCGAA	AACCTUG
2433	ACUGGGU	CUGAUGAGGCCGAAAGGCCGAA	AUCUCUG
2434	CACUGGG	CUGAUGAGGCCGAAAGGCCGAA	AAUCUCU
2448	GAGGAUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUC
2449	GGAGGAA	CUGAUGAGGCCGAAAGGCCGAA	AAGGCCU
2451	AGGGAGG	CUGAUGAGGCCGAAAGGCCGAA	AUAAGGC
2452	AAGGGAG	CUGAUGAGGCCGAAAGGCCGAA	AAUAAGG
2455	GGGAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGAUAU
2459	UGGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGAGG
2460	UUGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGGGAG
2479	GCTAACA	CUGAUGAGGCCGAAAGGCCGAA	AGGUGUC
2480	GGCTAAC	CUGAUGAGGCCGAAAGGCCGAA	AAGGUGU
2483	GGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACAAAGG
2484	AGGUGGC	CUGAUGAGGCCGAAAGGCCGAA	AACAAAG
2492	GGUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGC
2504	AGAAADG	CUGAUGAGGCCGAAAGGCCGAA	AUGUGGG
2508	UGGCAGA	CUGAUGAGGCCGAAAGGCCGAA	AUGUAUG
2509	COGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAUGUAU

2510	ACUGGCA	CUGAUGAGGCCGAAAGGCCGAA	AAADGUA
2520	CAUUGUG	CUGAUGAGGCCGAAAGGCCGAA	ACACUGG
2521	UCAUUGU	CUGAUGAGGCCGAAAGGCCGAA	AACACUG
2533	GACCGCU	CUGAUGAGGCCGAAAGGCCGAA	AGUGUCA
2540	CAGACAU	CUGAUGAGGCCGAAAGGCCGAA	ACCGCUG
2545	AUGUCCA	CUGAUGAGGCCGAAAGGCCGAA	ACAUGAC
2568	UUGGGCA	CUGAUGAGGCCGAAAGGCCGAA	AUUCCTT
2579	CAAGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCUUGG
2585	AGAGGAC	CUGAUGAGGCCGAAAGGCCGAA	AGGCAUA
2588	ACAAGAG	CUGAUGAGGCCGAAAGGCCGAA	ACAAGGC
2591	AGGACAA	CUGAUGAGGCCGAAAGGCCGAA	AGGACAA
2593	ACAGGAC	CUGAUGAGGCCGAAAGGCCGAA	AGAGGAC
2596	CAAACAG	CUGAUGAGGCCGAAAGGCCGAA	ACAAGAG
2601	AAADGCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGGAC
2602	GAAADGC	CUGAUGAGGCCGAAAGGCCGAA	AACAGGA
2607	CCAGUGA	CUGAUGAGGCCGAAAGGCCGAA	AUGCAAA
2608	CCCAGUG	CUGAUGAGGCCGAAAGGCCGAA	AADGCAA
2609	UCCCAGU	CUGAUGAGGCCGAAAGGCCGAA	AAADGCA
2620	AUAGUGC	CUGAUGAGGCCGAAAGGCCGAA	AGCUCCC
2626	GCUGCAA	CUGAUGAGGCCGAAAGGCCGAA	AGUGCAA
2628	GAGCTGC	CUGAUGAGGCCGAAAGGCCGAA	AUAGUGC
2635	GAAACUG	CUGAUGAGGCCGAAAGGCCGAA	AGCCGCA
2640	UGCAGGA	CUGAUGAGGCCGAAAGGCCGAA	ACUGGAG
2641	CUGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AACUGGA
2642	ACUGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAACUGG
2653	GGACCTU	CUGAUGAGGCCGAAAGGCCGAA	ADCACTG
2659	CUUGCAG	CUGAUGAGGCCGAAAGGCCGAA	ACCCUGA
2689	CCUCCAA	CUGAUGAGGCCGAAAGGCCGAA	ACCUUGG
2691	GUCCUCC	CUGAUGAGGCCGAAAGGCCGAA	ADACCUU
2700	UGGGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCUC
2704	AAGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGAGU
2711	CCUUGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCUUGG
2712	CCCUUCC	CUGAUGAGGCCGAAAGGCCGAA	AAGCUGG
2721	CGCGGAU	CUGAUGAGGCCGAAAGGCCGAA	ACCCUUC
2724	ACACGCG	CUGAUGAGGCCGAAAGGCCGAA	AUGACCC
2744	CUACACA	CUGAUGAGGCCGAAAGGCCGAA	ACACACA
2750	GCUUGUC	CUGAUGAGGCCGAAAGGCCGAA	ACACADA
2759	AGAGCGA	CUGAUGAGGCCGAAAGGCCGAA	AGCUUGU
2761	ACAGAGC	CUGAUGAGGCCGAAAGGCCGAA	AGAGCUU
2765	GGUGACA	CUGAUGAGGCCGAAAGGCCGAA	AGCGAGA
2769	CCUGGGU	CUGAUGAGGCCGAAAGGCCGAA	ACAGAGC
2797	GAACCAU	CUGAUGAGGCCGAAAGGCCGAA	AUUGCAC
2803	UGCAGUG	CUGAUGAGGCCGAAAGGCCGAA	ACCAUGA
2804	CUGCAGU	CUGAUGAGGCCGAAAGGCCGAA	AACCAUG
2813	AGGUCAA	CUGAUGAGGCCGAAAGGCCGAA	ACTUCAG
2815	AAAGGUC	CUGAUGAGGCCGAAAGGCCGAA	AGACUGC
2821	AGCCCAA	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAA
2822	GAGCCCA	CUGAUGAGGCCGAAAGGCCGAA	AAGGUCA
2823	UAGCCC	CUGAUGAGGCCGAAAGGCCGAA	AAAGGUC

2829	ADCACUU	CUGAUGAGGCCGAAAGGCCGAA	AGCCCAA
2837	GUGGGAG	CUGAUGAGGCCGAAAGGCCGAA	AUCACUU
2840	GAGGUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGAUCA
2847	GGAGGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGG
2853	UACUCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGCTGA
2860	UCCAGC	CUGAUGAGGCCGAAAGGCCGAA	ACUCAGG
2872	GUGAGCC	CUGAUGAGGCCGAAAGGCCGAA	AUGGUCC
2877	GUGUUGU	CUGAUGAGGCCGAAAGGCCGAA	AGCCTAU
2899	AAAAUCA	CUGAUGAGGCCGAAAGGCCGAA	AUUUGCC
2900	AAAAAUC	CUGAUGAGGCCGAAAGGCCGAA	AUUUGGC
2904	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AUCAAAU
2905	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAUCAAA
2906	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUCAA
2907	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAUCA
2908	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAUC
2909	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAU
2910	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2911	AAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2912	GAAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2913	UGAAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2914	CUGAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2915	UCUGAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2916	CUCUGAA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2917	UCUCUGA	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2918	GUCUCUG	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2919	CGUCUCU	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAA
2931	GUUGCGA	CUGAUGAGGCCGAAAGGCCGAA	ACCCCGU
2933	AUGUUGC	CUGAUGAGGCCGAAAGGCCGAA	AGACCCC
2941	UCUGGGC	CUGAUGAGGCCGAAAGGCCGAA	AUGUUGC
2951	ACAAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGUCUGG
2952	CACAAAG	CUGAUGAGGCCGAAAGGCCGAA	AAGUCUG
2955	UACACA	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGU
2956	CUAACAC	CUGAUGAGGCCGAAAGGCCGAA	AAGGAAG
2961	AUUAACU	CUGAUGAGGCCGAAAGGCCGAA	ACACAAA
2962	UAUUAAC	CUGAUGAGGCCGAAAGGCCGAA	AACACAA
2965	CUUUAUU	CUGAUGAGGCCGAAAGGCCGAA	ACTUAAC
2966	GCUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AACUAAC
2969	AAAGCTU	CUGAUGAGGCCGAAAGGCCGAA	AUUAACU
2975	GUUGAGA	CUGAUGAGGCCGAAAGGCCGAA	AGCUUUA
2976	AGUUGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGCUUU
2977	CAGUUGA	CUGAUGAGGCCGAAAGGCCGAA	AAAGCTU
2979	GGCAGUU	CUGAUGAGGCCGAAAGGCCGAA	AGAAAGC

Table 5

Mouse ICAM HH Ribozyme Sequence
nt. Position Ribozyme Sequence

11	CAACGGU	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGG
23	AGCAGAG	CUGAUGAGGCCGAAAGGCCGAA	ACCACUG
26	AGGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGAACCA
31	UGUGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
34	CGACCCU	CUGAUGAGGCCGAAAGGCCGAA	AUGAGAA
40	AGGCUAC	CUGAUGAGGCCGAAAGGCCGAA	AGUGUGC
48	CCAGGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCU
54	CCADCAC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCA
58	GGAGCUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCAUG
64	CUGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUG
96	GGGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
102	CCAGCAG	CUGAUGAGGCCGAAAGGCCGAA	ACUGGCA
108	GGGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
115	AGGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGAACCA
119	UCCUGGU	CUGAUGAGGCCGAAAGGCCGAA	ACAUUCC
120	GGGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
146	GGAAGCG	CUGAUGAGGCCGAAAGGCCGAA	ACGACUG
152	AGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACACAGA
158	GGUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AACAGGA
165	GCAAAAC	CUGAUGAGGCCGAAAGGCCGAA	ACUUCUG
168	GGGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCUU
185	CUGCACG	CUGAUGAGGCCGAAAGGCCGAA	ACCCACC
209	GCCAGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGGC
227	GCAAAAC	CUGAUGAGGCCGAAAGGCCGAA	ACUUCUG
230	GGAGCAA	CUGAUGAGGCCGAAAGGCCGAA	ACAACTU
237	AGUUCUC	CUGAUGAGGCCGAAAGGCCGAA	AAGCACA
248	UUUAGGA	CUGAUGAGGCCGAAAGGCCGAA	AUGGGUU
253	UCUCCU	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGG
263	CAGUAGA	CUGAUGAGGCCGAAAGGCCGAA	AAACCCU
267	UAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCCCU
293	CAGCUCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCUU
319	GGCUCAG	CUGAUGAGGCCGAAAGGCCGAA	AUCUCCU
335	GUUCUCA	CUGAUGAGGCCGAAAGGCCGAA	AGCACAG
337	CAGUGUG	CUGAUGAGGCCGAAAGGCCGAA	AUUGGAC
338	UCAGCUC	CUGAUGAGGCCGAAAGGCCGAA	AACAGCU
359	AGCGGAC	CUGAUGAGGCCGAAAGGCCGAA	ACUGCAC
367	CGGGUUG	CUGAUGAGGCCGAAAGGCCGAA	AGCCAUU
374	GGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUC
375	GGGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCUU
378	ACACGGU	CUGAUGAGGCCGAAAGGCCGAA	AUGGUAG
386	AAACGAA	CUGAUGAGGCCGAAAGGCCGAA	ACACGGU
394	AGAUCGA	CUGAUGAGGCCGAAAGGCCGAA	AGUCCGG
420	CGGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGUG
425	CUGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUG

427	CACUGCU	CUGAUGAGGCCGAAAGGCCGAA	AGAGCUG
450	GCAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCU
451	CAAAGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUUC
456	AGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUUAA
495	ACACGGU	CUGAUGAGGCCGAAAGGCCGAA	AUGGUAG
510	CCOCACG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGCA
564	GGAUUGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUAGG
592	CCCAUGU	CUGAUGAGGCCGAAAGGCCGAA	ACCUUUC
607	CAUGAGA	CUGAUGAGGCCGAAAGGCCGAA	AUUGGCU
608	GCAUGAG	CUGAUGAGGCCGAAAGGCCGAA	AAUUGGC
609	GGCAUGA	CUGAUGAGGCCGAAAGGCCGAA	AAAUUGG
611	GCGGCAU	CUGAUGAGGCCGAAAGGCCGAA	AGAAAUU
656	CAGCTCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCTU
657	UCAGTUC	CUGAUGAGGCCGAAAGGCCGAA	AACAGCT
668	GGUGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUG
677	AGGCTUG	CUGAUGAGGCCGAAAGGCCGAA	AGAGGUC
684	AGGACCG	CUGAUGAGGCCGAAAGGCCGAA	AGCTUGA
692	AAGAUCG	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCG
693	GCAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCU
696	GAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAACAGG
709	UGAGGUG	CUGAUGAGGCCGAAAGGCCGAA	AGCCGCC
720	AGCTUGA	CUGAUGAGGCCGAAAGGCCGAA	AGUUGUA
723	CGGAGCU	CUGAUGAGGCCGAAAGGCCGAA	AAAAGUU
735	UCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AUCUGGU
738	CCAUCAC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCA
765	GGAGCGG	CUGAUGAGGCCGAAAGGCCGAA	ACGACUG
769	GGCAGGA	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCC
770	UUCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAA
785	GGCAGGA	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCC
786	AGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGGC
792	CUUCCGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUCCA
794	AGUCUCC	CUGAUGAGGCCGAAAGGCCGAA	AGCCCTAG
807	CCAGGUA	CUGAUGAGGCCGAAAGGCCGAA	AUCCGAG
833	GGGUGUC	CUGAUGAGGCCGAAAGGCCGAA	AGCUUUG
846	CAACGGU	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGG
851	GCTGGUA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUUC
863	CCAGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGUGGCU
866	GGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUC
867	UCTCCGG	CUGAUGAGGCCGAAAGGCCGAA	AACGAUU
869	CUUGCAU	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGA
881	ACGGGUU	CUGAUGAGGCCGAAAGGCCGAA	AAGCCAU
885	UCACCUC	CUGAUGAGGCCGAAAGGCCGAA	ACCAAGG
933	CCAGAAU	CUGAUGAGGCCGAAAGGCCGAA	AUUAUAG
936	GCACCAG	CUGAUGAGGCCGAAAGGCCGAA	AUGAUUA
978	AGUUGUA	CUGAUGAGGCCGAAAGGCCGAA	ACUGUUA
980	AAAGUUG	CUGAUGAGGCCGAAAGGCCGAA	AGACUGU
986	AGCTUGA	CUGAUGAGGCCGAAAGGCCGAA	AGUUGUA
967	GAGCTGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUUGU
968	GGAGCTG	CUGAUGAGGCCGAAAGGCCGAA	AAAGUUG

1005	UCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AUCUGGU
1006	UUCCCCA	CUGAUGAGGCCGAAAGGCCGAA	ACUCUCA
1023	CUUCCGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUCCA
1025	CCCUUCC	CUGAUGAGGCCGAAAGGCCGAA	AGACCTUC
1066	UUUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAGUGG
1092	GGCCUGA	CUGAUGAGGCCGAAAGGCCGAA	AUCCAGU
1093	UUGGCUG	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCA
1125	UCAAGAA	CUGAUGAGGCCGAAAGGCCGAA	AGUUGGG
1163	GCAAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUUCG
1164	AGCAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAGCUUC
1166	AGAGCAA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCU
1172	GGUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AACAGGA
1200	UGUGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
1201	CUGUUCA	CUGAUGAGGCCGAAAGGCCGAA	AAGCAGC
1203	ACUGGUG	CUGAUGAGGCCGAAAGGCCGAA	AAAAAGU
1227	GCACACG	CUGAUGAGGCCGAAAGGCCGAA	AUGUACC
1228	AGCAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAGCUUC
1233	CUUCCCG	CUGAUGAGGCCGAAAGGCCGAA	AAACGAA
1238	AGGACCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCAC
1264	CUUGCAC	CUGAUGAGGCCGAAAGGCCGAA	ACCUUUC
1267	UUCCCCA	CUGAUGAGGCCGAAAGGCCGAA	ACUCUCA
1294	GGUCUAG	CUGAUGAGGCCGAAAGGCCGAA	AUCUCCU
1295	CUGCUGA	CUGAUGAGGCCGAAAGGCCGAA	ACCCUUC
1306	CAUUUCA	CUGAUGAGGCCGAAAGGCCGAA	AGUCUGC
1321	UCCUCCU	CUGAUGAGGCCGAAAGGCCGAA	AGCCUUC
1334	UUUAGGA	CUGAUGAGGCCGAAAGGCCGAA	AUGGGUU
1344	CACUCUC	CUGAUGAGGCCGAAAGGCCGAA	AGCUCAU
1351	UAACUUA	CUGAUGAGGCCGAAAGGCCGAA	ACAUUCA
1353	CACCUUC	CUGAUGAGGCCGAAAGGCCGAA	ACCCACU
1366	AGUUGUA	CUGAUGAGGCCGAAAGGCCGAA	ACUGUUA
1367	AGGUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGCU
1368	AGAGUGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGUAC
1380	CCACCCC	CUGAUGAGGCCGAAAGGCCGAA	AUGGGCA
1388	AGCCACTU	CUGAUGAGGCCGAAAGGCCGAA	AGUCUCC
1398	GUUCUGU	CUGAUGAGGCCGAAAGGCCGAA	ACAGCCA
1402	AGUUCUC	CUGAUGAGGCCGAAAGGCCGAA	AAGCACA
1408	CCUCCCC	CUGAUGAGGCCGAAAGGCCGAA	AUCUCCG
1410	CCCUUCC	CUGAUGAGGCCGAAAGGCCGAA	AGACCTUC
1421	ACAAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGG
1425	CUUACC	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGU
1429	CAGGGGC	CUGAUGAGGCCGAAAGGCCGAA	AUAGAGA
1444	UCCUCCU	CUGAUGAGGCCGAAAGGCCGAA	AGCCUUC
1455	UCCUGGU	CUGAUGAGGCCGAAAGGCCGAA	ACAUCC
1482	GGGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AACAACU
1484	CAUGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGAACAG
1493	GUUCUCA	CUGAUGAGGCCGAAAGGCCGAA	AGCACAG
1500	GGACCAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUCAU
1503	GAAUGAU	CUGAUGAGGCCGAAAGGCCGAA	AUAGUCC
1506	CGGUUAU	CUGAUGAGGCCGAAAGGCCGAA	AACAUA

1509	ACACGGU	CUGAUGAGGCCGAAAGGCCGAA	AUGGUAG
1518	CGCCUGG	CUGAUGAGGCCGAAAGGCCGAA	ACCAUGA
1530	CCAGAAU	CUGAUGAGGCCGAAAGGCCGAA	AUUAUAG
1533	GGCCAC	CUGAUGAGGCCGAAAGGCCGAA	AUGACCA
1551	AGCUGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGCAUG
1559	AGGUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGCU
1563	GGUUAUA	CUGAUGAGGCCGAAAGGCCGAA	ACAUAAG
1565	GCGGUUA	CUGAUGAGGCCGAAAGGCCGAA	AAACAUU
1567	UGGCGGU	CUGAUGAGGCCGAAAGGCCGAA	AUAACA
1584	AUAUCCU	CUGAUGAGGCCGAAAGGCCGAA	AUCUUC
1592	UAACUUG	CUGAUGAGGCCGAAAGGCCGAA	AUAUCCU
1599	CCUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AACUUGU
1651	GCUCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGG
1661	CAAAGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUUC
1663	UUCAAAG	CUGAUGAGGCCGAAAGGCCGAA	AAAGGUU
1678	CCAGGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCU
1680	CCAGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGUGGCU
1681	GCCAGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGGC
1684	ACAGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGU
1690	AGAUCCA	CUGAUGAGGCCGAAAGGCCGAA	AGUCCGG
1691	AAGAUCC	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCG
1696	CCACCC	CUGAUGAGGCCGAAAGGCCGAA	AUGGGCA
1698	CUCCAGG	CUGAUGAGGCCGAAAGGCCGAA	AUAUCCG
1737	GCUGGUA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCU
1750	UGAGGUG	CUGAUGAGGCCGAAAGGCCGAA	AGCCGCC
1756	GGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUC
1787	UGGGGAC	CUGAUGAGGCCGAAAGGCCGAA	AUGUCUC
1790	AUUAAGG	CUGAUGAGGCCGAAAGGCCGAA	ACAADGC
1793	UCCAGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGACCA
1797	UUUAUGU	CUGAUGAGGCCGAAAGGCCGAA	ACUGGUG
1802	UCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AUCUGGU
1812	GGCCUGA	CUGAUGAGGCCGAAAGGCCGAA	AUCCAGU
1813	UGAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AAUGCUG
1825	GCAGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGCGUGG
1837	GGAGCUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCAUG
1845	GGUGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGCUCC
1856	AAGAUCC	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCG
1861	UACUGGA	CUGAUGAGGCCGAAAGGCCGAA	AUCAUGU
1865	UCAGGCC	CUGAUGAGGCCGAAAGGCCGAA	ACAAGUG
1868	UUUAUGU	CUGAUGAGGCCGAAAGGCCGAA	ACUGGUG
1877	AGCUGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGCAUG
1901	GUCCCUU	CUGAUGAGGCCGAAAGGCCGAA	AGUUUUA
1912	ACUGAUC	CUGAUGAGGCCGAAAGGCCGAA	ACTUAUA
1922	UAACUUA	CUGAUGAGGCCGAAAGGCCGAA	ACAUCUA
1923	GAUACCU	CUGAUGAGGCCGAAAGGCCGAA	AGCAUCA
1928	CUGGUAA	CUGAUGAGGCCGAAAGGCCGAA	ACTUUAU
1930	AGCUGGU	CUGAUGAGGCCGAAAGGCCGAA	AAACTUCU
1964	UGGGGAC	CUGAUGAGGCCGAAAGGCCGAA	AUGUCUC
1983	UAACUUG	CUGAUGAGGCCGAAAGGCCGAA	AUAUCCU

1996	GGCUCAG	CUGAUGAGGCCGAAAGGCCGAA	AUTCUCU
2005	GGUCCGC	CUGAUGAGGCCGAAAGGCCGAA	AGCUCCA
2013	UACUCAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAGC
2015	CCACCCC	CUGAUGAGGCCGAAAGGCCGAA	AUGGGCA
2020	CUCAGAA	CUGAUGAGGCCGAAAGGCCGAA	AACCACC
2039	CCUCUGC	CUGAUGAGGCCGAAAGGCCGAA	AGCCAGC
2040	CCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAG
2057	GGADGUG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCA
2061	ACACGGU	CUGAUGAGGCCGAAAGGCCGAA	AUGGUAG
2071	CUGAGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAAGUG
2076	UAGCUCU	CUGAUGAGGCCGAAAGGCCGAA	AGGCUAC
2097	CAUCAAG	CUGAUGAGGCCGAAAGGCCGAA	AGAGUUG
2098	CGGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGUG
2115	AUCCUCC	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGC
2128	CUCAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAGCUG
2130	GAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAACAGG
2145	CAUCAAG	CUGAUGAGGCCGAAAGGCCGAA	AGAGUUG
2152	AACUCUA	CUGAUGAGGCCGAAAGGCCGAA	AUUAUA
2156	UAUAUA	CUGAUGAGGCCGAAAGGCCGAA	ACAUCAA
2158	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUACAU
2159	AAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
2160	AAAUUA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACA
2162	CUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAAUA
2163	AAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUAACAU
2166	AAUAGAG	CUGAUGAGGCCGAAAGGCCGAA	AUGAAGU
2167	AAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
2170	CUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAAUA
2171	GGGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AACAACU
2173	CUGGUAA	CUGAUGAGGCCGAAAGGCCGAA	ACUCUA
2174	GCUGGUA	CUGAUGAGGCCGAAAGGCCGAA	AACUCUA
2175	AGCUGGU	CUGAUGAGGCCGAAAGGCCGAA	AAACUCU
2176	UAGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AAAACUC
2183	CAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGU
2185	CUCAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAGCUG
2186	ACUCAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAGCU
2187	UACUCAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAGC
2189	GGUACUC	CUGAUGAGGCCGAAAGGCCGAA	AUAAUA
2196	CAUCAAG	CUGAUGAGGCCGAAAGGCCGAA	AGAGUUG
2198	AACAUAA	CUGAUGAGGCCGAAAGGCCGAA	AGGUCGC
2199	AUAAACA	CUGAUGAGGCCGAAAGGCCGAA	AAGAGGC
2200	CUUGCAU	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGA
2201	GCCGACA	CUGAUGAGGCCGAAAGGCCGAA	AAAACUU
2205	UCAGGCC	CUGAUGAGGCCGAAAGGCCGAA	ACAUAAA
2210	AGCCACU	CUGAUGAGGCCGAAAGGCCGAA	AGUCUCC
2220	AGAGAAC	CUGAUGAGGCCGAAAGGCCGAA	AUGCCAG
2224	GGAUUGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUAG
2226	GCGGCTU	CUGAUGAGGCCGAAAGGCCGAA	AGAUCCA
2233	CCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAG
2242	GGUCCGC	CUGAUGAGGCCGAAAGGCCGAA	AGCUCCA

2248	UGGGAUG	CUGAUGAGGCCGAAAGGCCGAA	AUGGAUA
2254	UCAGUGU	CUGAUGAGGCCGAAAGGCCGAA	AAUUGGA
2259	CACCGUG	CUGAUGAGGCCGAAAGGCCGAA	AUGUGAU
2260	GCACCGU	CUGAUGAGGCCGAAAGGCCGAA	AAUGUGA
2266	UCCUGGU	CUGAUGAGGCCGAAAGGCCGAA	ACAUTCC
2274	UCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AUCUGGU
2279	CUUGCAC	CUGAUGAGGCCGAAAGGCCGAA	ACCCUUC
2282	CAGCUCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCTU
2288	AGGCCAU	CUGAUGAGGCCGAAAGGCCGAA	ACUUAUA
2291	AGCAGAG	CUGAUGAGGCCGAAAGGCCGAA	ACCACUG
2321	CCCADGU	CUGAUGAGGCCGAAAGGCCGAA	ADCUUUC
2338	CAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUCUA
2339	CAAAGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUUC
2341	AGGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGAGGUC
2344	GCTUGAA	CUGAUGAGGCCGAAAGGCCGAA	ADCGAAA
2358	CUGCTGA	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGG
2359	UCUGUUC	CUGAUGAGGCCGAAAGGCCGAA	AAAGCAG
2360	UUCAAAG	CUGAUGAGGCCGAAAGGCCGAA	AAAGGUU
2376	UCAGAAG	CUGAUGAGGCCGAAAGGCCGAA	ACCACCT
2377	CUCAAG	CUGAUGAGGCCGAAAGGCCGAA	AACCACC
2378	CAGUAGA	CUGAUGAGGCCGAAAGGCCGAA	AAACCTU
2379	CUUADGA	CUGAUGAGGCCGAAAGGCCGAA	AAAAGCA
2380	GCCGACA	CUGAUGAGGCCGAAAGGCCGAA	AAAACUU
2382	GGGGCAA	CUGAUGAGGCCGAAAGGCCGAA	AGAGAAU
2384	UUGUGUC	CUGAUGAGGCCGAAAGGCCGAA	ACUGGAU
2399	GUCCACA	CUGAUGAGGCCGAAAGGCCGAA	AGUGUUU
2401	CAGCTCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCTU
2411	GCAUCCU	CUGAUGAGGCCGAAAGGCCGAA	ACCAGUA
2417	ACGUUUG	CUGAUGAGGCCGAAAGGCCGAA	ACCAUUC
2418	GGCTUGA	CUGAUGAGGCCGAAAGGCCGAA	AUCCAGU
2425	AAACCTC	CUGAUGAGGCCGAAAGGCCGAA	ACCCAUU
2426	AAACUUC	CUGAUGAGGCCGAAAGGCCGAA	AAUUAUU
2433	GCTUGUA	CUGAUGAGGCCGAAAGGCCGAA	AACUCUA
2434	AGCUGGU	CUGAUGAGGCCGAAAGGCCGAA	AAACUUC
2448	GGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUC
2449	GGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCTU
2451	AGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGGC
2452	GAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAACAGG
2455	GGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUC
2459	GGGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGUGUGG
2460	CGGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGUG
2479	GCTUGUA	CUGAUGAGGCCGAAAGGCCGAA	AGGUCUC
2480	GGADCAC	CUGAUGAGGCCGAAAGGCCGAA	ACGGUGA
2483	GGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACAUGGG
2484	GACUGGU	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAG
2492	AGGUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGCU
2504	ACAAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGG
2508	UGGGAUG	CUGAUGAGGCCGAAAGGCCGAA	AUGGAUA
2509	CUUGUAA	CUGAUGAGGCCGAAAGGCCGAA	ACUCUAA

2510	GCUGGUA	CUGAUGAGGCCGAAAGGCCGAA	AACUCTA
2520	CAUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAAAAG
2521	UGAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AAUGCTG
2533	GAUACCU	CUGAUGAGGCCGAAAGGCCGAA	AGCADCA
2540	CACAGCG	CUGAUGAGGCCGAAAGGCCGAA	ACUGCTG
2545	AGGACCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCAC
2568	UUUGACA	CUGAUGAGGCCGAAAGGCCGAA	ACTUCAC
2579	CAGGCCA	CUGAUGAGGCCGAAAGGCCGAA	AACTUAT
2585	AGAGAAC	CUGAUGAGGCCGAAAGGCCGAA	AUGCCAG
2588	AUUAGAG	CUGAUGAGGCCGAAAGGCCGAA	ACAAUGC
2591	AGGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGAACCA
2593	GCAGAGC	CUGAUGAGGCCGAAAGGCCGAA	AAAGNAG
2596	CAUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAAAAG
2601	AAACGAA	CUGAUGAGGCCGAAAGGCCGAA	ACACGGU
2602	GGGADGG	CUGAUGAGGCCGAAAGGCCGAA	AGTUGGA
2607	CCAGGUA	CUGAUGAGGCCGAAAGGCCGAA	ATCCGAG
2608	CACAGCG	CUGAUGAGGCCGAAAGGCCGAA	ACUGCTG
2609	UCCUGGU	CUGAUGAGGCCGAAAGGCCGAA	ACAUTCC
2620	GCAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCT
2626	GCTUGAA	CUGAUGAGGCCGAAAGGCCGAA	AUCGAAA
2628	AGGCUAC	CUGAUGAGGCCGAAAGGCCGAA	AGUGGCG
2635	AGGACCG	CUGAUGAGGCCGAAAGGCCGAA	AGCTGAA
2640	GGCAGGA	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCC
2641	CUGCTGA	CUGAUGAGGCCGAAAGGCCGAA	AGCTUGG
2642	GAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAACAGG
2653	GCAUCCU	CUGAUGAGGCCGAAAGGCCGAA	ACCAGUA
2659	CUUGCAC	CUGAUGAGGCCGAAAGGCCGAA	ACCCUUC
2689	CTCCGGA	CUGAUGAGGCCGAAAGGCCGAA	ACAUTAG
2691	GGCTUCG	CUGAUGAGGCCGAAAGGCCGAA	AGACAUT
2700	GGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCTUC
2704	AGGCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGAGGUC
2711	CUGCTGA	CUGAUGAGGCCGAAAGGCCGAA	AGCTUGG
2712	CCCTUCC	CUGAUGAGGCCGAAAGGCCGAA	AGACCTC
2721	CUUGCAC	CUGAUGAGGCCGAAAGGCCGAA	ACCCUUC
2724	GCACACG	CUGAUGAGGCCGAAAGGCCGAA	AUGUACC
2744	CUGCACG	CUGAUGAGGCCGAAAGGCCGAA	ACCCACC
2750	GGUACTC	CUGAUGAGGCCGAAAGGCCGAA	AUAAATA
2759	AGAUCGA	CUGAUGAGGCCGAAAGGCCGAA	AGUCCGG
2761	GCAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCT
2765	AGCGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAA
2769	CCUGUUU	CUGAUGAGGCCGAAAGGCCGAA	ACAGACT
2797	GGACCAU	CUGAUGAGGCCGAAAGGCCGAA	AUTUCAU
2803	CGCTUGG	CUGAUGAGGCCGAAAGGCCGAA	ACCAUGA
2804	CUGCACG	CUGAUGAGGCCGAAAGGCCGAA	ACCCACC
2813	GGGUCAG	CUGAUGAGGCCGAAAGGCCGAA	ACCGGAG
2815	AAAGUUG	CUGAUGAGGCCGAAAGGCCGAA	AGACTUG
2821	CTUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAG
2822	AAGUCCG	CUGAUGAGGCCGAAAGGCCGAA	AGGCTCC
2823	UGGGAGC	CUGAUGAGGCCGAAAGGCCGAA	AAAGGCA

2829	AUGAUUA	CUGAUGAGGCCGAAAGGCCGAA	AGUCCAG
2837	UCAGAAG	CUGAUGAGGCCGAAAGGCCGAA	ACCACCU
2840	CAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCUCA
2847	GGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACAUGGG
2853	AACAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCTGC
2860	UCACAGU	CUGAUGAGGCCGAAAGGCCGAA	ACTUGGC
2872	CUUGGCU	CUGAUGAGGCCGAAAGGCCGAA	AAGGUCC
2877	GUGAUGG	CUGAUGAGGCCGAAAGGCCGAA	AGCGGAA
2899	AAGAUCG	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCG
2900	AAAACUC	CUGAUGAGGCCGAAAGGCCGAA	AAAUUA
2904	AAUAGAG	CUGAUGAGGCCGAAAGGCCGAA	AUGAAGU
2905	CAUAGA	CUGAUGAGGCCGAAAGGCCGAA	AAUGAAG
2906	UAUAUA	CUGAUGAGGCCGAAAGGCCGAA	ACAUCAA
2907	AAAUUA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACA
2908	AGCAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAGCTUC
2909	AGAGCAA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCU
2910	AAAUUA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACA
2911	AAAUUA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACA
2912	GACAUUA	CUGAUGAGGCCGAAAGGCCGAA	AGAACAA
2913	UGACCAG	CUGAUGAGGCCGAAAGGCCGAA	AGAGAAA
2914	CUUAUGA	CUGAUGAGGCCGAAAGGCCGAA	AAAAGCA
2915	UCUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
2916	CUCCGGA	CUGAUGAGGCCGAAAGGCCGAA	ACGAUAU
2917	UCUCCGG	CUGAUGAGGCCGAAAGGCCGAA	AACGAUU
2918	CUCUCCG	CUGAUGAGGCCGAAAGGCCGAA	AAACGAA
2919	CGACCCU	CUGAUGAGGCCGAAAGGCCGAA	ADGAGAA
2931	CUUCCGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUCCA
2933	CCUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGACCUU
2941	UGGGGAC	CUGAUGAGGCCGAAAGGCCGAA	ADGUCUC
2951	GCAGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGG
2952	CACAGCG	CUGAUGAGGCCGAAAGGCCGAA	ACUGCUG
2953	UGACACA	CUGAUGAGGCCGAAAGGCCGAA	AGUCACU
2956	UUGAUUC	CUGAUGAGGCCGAAAGGCCGAA	AAGGAAA
2961	AGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACACAGA
2962	AAUUAUU	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
2965	CUUUAUU	CUGAUGAGGCCGAAAGGCCGAA	AUUCAAA
2966	CCUUCGC	CUGAUGAGGCCGAAAGGCCGAA	AGCCAGC
2969	AAAACUU	CUGAUGAGGCCGAAAGGCCGAA	AUUGAUU
2975	GCUGGUA	CUGAUGAGGCCGAAAGGCCGAA	AACUUAU
2976	AGUAGAG	CUGAUGAGGCCGAAAGGCCGAA	AACCCUC
2977	CAGCUCA	CUGAUGAGGCCGAAAGGCCGAA	ACAGCUU
2979	GGCAUAU	CUGAUGAGGCCGAAAGGCCGAA	AGAAUGA

Table 6
Human ICAM Hairpin Ribozyme/Substrate Sequences

Position	Hairpin Ribozyme Sequence	Substrate
70	GGGCGGG AGAA GCUG ACCAGAGAAACACACGUGUGGUACAUUACCUUGUA	CAGCA GCC CCGGGCCC
86	GGAGUGCG AGAA GCYC ACCAGAGAAACACACGHIUGIYGGIACAIHACCUUGUA	GGGCU GCC CGCACUCC
343	CCCAUCAG AGAA GUUU ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	AAACU GCC CUGAUGGG
635	GCCCUUGG AGAA GCAG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CUGCG GCC CCNAGGSC
653	UGUUCUCA AGAA GCUC ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	GAGCU GUU UGAGAAACA
782	AGACUGGG AGAA GCCC ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	GGGCU GUU OCCAGUCU
920	CUGCACAC AGAA GCGG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CGGCU GAC GUGUGCAG
1301	ACAUUGGA AGAA GCUG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CAGCA GAC UCCAAUGU
1373	CCCCAUG AGAA GUGG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CCACU GCC CAUCGGGG
1521	AUGACUGC AGAA GCUA ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	UAGCA GCC GCAGUCAU
1594	CUGUUGUA AGAA GUUU ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	AUACA GAC UACAACAG
2008	ACCCAAUA AGAA GCNA ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	UUGCU GCC UAUUGGGU
2034	UUCUGUAA AGAA GUGG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CCACA GAC UUAACAGAA
2125	GGUCAGUA AGAA GCAG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CUGCU GUC UACUGACC
2132	GGGUGGG AGAA GUAG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CUACU GAC CCCAACCC
2276	ACCGUAC AGAA GUAC ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	GUACA GUU GUACAGGU
2810	AAGGUCAA AGAA GCAG ACCAGAGAAACACACCGIUGUGGUACAUUACCUUGUA	CUGCA GUC UUGACCUU

Table 7
Mouse ICAM Hairpin Ribozyme/Substrate Sequences
nt. Hairpin Ribozyme Sequence
Position

Position	nt.	Substrate
76	GGGAUCAC AGAA GUGA ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	UCACC GUU GUGAUCCC
164	UGAGGAAG AGAA GUUC ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	GAACTU GUU CUUCCUCA
252	UCAGGUCA AGAA GCUU ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	AAGCU GUU UGAGCTUGA
284	GCACAGCG AGAA GCUG ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	CAGCA GUC CCUGUGGC
318	AAGCGGAC AGAA GCAC ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	GUGCA GUC GUCCGCUU
447	AGAGCTUG AGAA GCGG ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	CCGCG GAC CCAGCUCU
804	UCUCCUGG AGAA GCAU ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	AUGCC GAC CCAGGAGA
847	UCUACCAA AGAA GUGG ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	CCACU GCC UUGGUAGA
913	AGGAUCUG AGAA GCUA ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	UAGCG GAC CAGAUCCU
946	AAGUGUGA AGAA GUUA ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	UAAAC GUC UACAACTU
1234	CCCAAGCA AGAA GUCU ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	AGACG GAC UGCUIGGG
1275	AUUDCAGA AGAA GCUG ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	CAGCA GAC UCUGAAAU
1325	UGCCUUCG AGAA GCAG ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	CUGCA GAC GGAAGGCA
1350	CCCCGAUG AGAA GCAG ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	CUGCU GCC CAUCGGGG
1534	ACAUAGA AGAA GCCA ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	UGGCA GCC UCUUAUGU
1851	GUCCACCG AGAA GUAG ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	CUACA GCC CGGUGGAC
1880	AGAAUGAA AGAA GCGU ACCAGAGAAACACACGUGUGGUAACAUIUACCUUGUA	ACGCU GAC UUCAUUCU

Table 8
Rat ICAM Hairpin Ribozyme/Substrate Sequences

nt. Position	Hairpin Ribozyme Sequence	Substrate
5	AAAGUGCA AGAA GCAG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CUGCU GCC UGCACUUU
59	GGAGCAGA AGAA GCAU ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	AUGCU GCC UCUGCUCC
84	GGGAUCAC AGAA GCQA ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	UUGCC GUU GUGAUCCC
295	GCACAGUG AGAA GCUG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CAGCA GAC CACUGUCC
329	AAGCCGAG AGAA GCGU ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	ACGCA GUC CUCGGCUU
433	UUCACCCA AGAA GCGC ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	GCGCU GCC UGGUGGAA
626	CAUUCUUG AGAA GUGA ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	UCACU GUU CAAGAAUG
806	UUCUCCAG AGAA GCAU ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	AUGCU GAC CCUGGAGA
849	UCCACUGA AGAA GUGG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CCACU GCC UCAGUGGA
915	AGGCUUUG AGAA GCCA ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	UGGCG GAC CAGACCCU
1182	ACCUCCAA AGAA GCAG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CUGCG GCC UUGGAGGU
1307	AUGUAAGA AGAA GCUG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CAGCA GAC UCUUACAU
1357	UGCUUUCU AGAA GCAG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CUGCA GCC GGAAGCA
1382	UCCCGNUA AGAA GCGG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CUGCU GCC UAUGGGGA
1058	GCCACCA AGAA GUAG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CUACA GCC UGGUGGGC
1887	AGAAGGAA AGAA GCCU ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	AGGCU GAC UUCUUCU
2012	GAGUUGGG AGAA GUGU ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	ACACU GUC CCCAATUC
2303	AGACUCCA AGAA GUGG ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	CCACA GCC UGAGGUCU
2539	CCUCCAC AGAA GCUU ACCAGAGAAACACACGUGUGGUAACAUUACCUGGUA	AAGCU GUU GUGGAGG

Table 9: Rat ICAM HH Ribozyme Target Sequence

nt. Position	HH Target sequence	nt. Position	HH Target Sequence
11	GAUCCAAU U CACACUGA	394	GGGGUGCU U CUGAACAG
23	GCUGACUU C CUUCUCUA	420	GCACCCCU C CCAGCGCA
26	GAACUGCU C UUCUCUU	425	CCUCGGCU U CUGCCACC
31	CCUCUGCU C CUGGUCCU	427	UCCUCGUU U AAAAATCA
34	CUGAAGCU C AGAUUAC	450	AAGAACCU C AUUCUGCG
40	CUCAAGGU A CAAGCCCC	451	GGGUACUU C CCCCAGGC
48	GAGAACCU C GGCCUGGG	456	CUCCGCUU C UGCCACCA
54	CCCCGCUU C CCUGAGCC	495	GCCACCAU C ACUGUGUA
58	CCGUGCUU U UAGCUCC	510	GUGCUGCU C CGUGGGAA
64	CAADGGCU U CAACCCGU	564	GAAGAGU U CCAACCAC
96	CCUCUGCU C CUGGUCCU	592	GGGAGUAT C ACCAGGGA
102	CUCCUGGU C CUGGUCCG	607	GAGCCAAU U UUCUAGC
108	GGACUGCU U GGGGAACU	608	AGCCAAU U CCUAGCUU
115	UCCUACCU U UGUUCCA	609	GCCAAUUU C UCAGUCUU
119	GACACUGU C CCAACUC	611	CAAUUUU C AUGCUUCA
120	GUUGUGAU C CCGGGCC	656	GUACUGU U CAAGAAG
146	CCAGACCU U GGAACUC	657	UCACUGU C AAGAAGU
152	ACCCGGCU C CACUCAA	668	GAACUGCU C UUCUCUU
158	AUUUCUUU C ACGAGUCA	677	GCACCCCU C CCAGCGCA
165	UGAACAGU A CUUCCCC	684	AGGCAGCU C CGGACUUU
168	GAAGCCUU C CUGCCUUG	692	CCAGACCU U GGAACUC
185	GGGUGGAGU C CGUGCAGG	693	CGGACUUU C GADUUC
209	CAGCCCUU A AUCUGACC	696	GCCUGUUU C CCGCCUUU
227	GACCAAGU A ACUGUGAA	709	CAGCAUUU A CCCCUCAC
230	CAAGCUGU U GUGGGAGG	720	CUACAAU U UUCAGUC
237	CUGAAGCU C GACACCCC	723	CAACUUUU C AGCUCCA
248	GGCCCCCU A CCUAGGA	735	CUCCUGGU C CUGGUCCG
253	CACUGCCU C AGUGGAGG	738	UCCUGCCU C GGGUGGA
263	GAGCCAAU U UCUAGUC	765	ACUGUGCU U UGAGAACU
267	GAAGCCUU C CUGCCUUG	769	UCUUGUGU U CCUGGAA
293	GAAGCUCU U CAAGCUGA	770	CUUGUGUU C CCUGGAAG
319	CGGAGGAGU C ACAACGA	785	AGGCCUGU U UCCUGCCU
335	ACUGUGCU U UGAGAAU	786	GGCCUGUU U CCUGCCUC
337	UGUGCUAU A UGUUCCUC	792	CUCCUGGU C CUGGUCCG
338	AAGCUCUU C AAGCUGAG	794	UCCUGCCU C UGAAGCUC
359	CACGCAGU C CUGGGCUU	807	GUACAGAU A UACUUGGA
367	CAUUGGCU U CAACCCGU	833	CCUGGGGU U GGAGACUA
374	UUAACCCU C ACCACCU	846	CUGACAGU U AUUUAUUG
375	AGAAGCCU U CCUGCCUC	851	GUACACCU U UAGCAGCU
378	ACCCACCU C ACAGGGUA	863	CAUUGGCU U CAACCCGU
386	CGCUGUGU U UUGAGCU	866	CCAUGCUU C CUCUGACA

867	GACCACTU C CCCACCTA	1421	GGGUACTU C CCCCAGGC
869	CUCUUCCTU C UUGCGAAG	1425	ACCCACCTU C CUCUGGCU
881	AUUGGCTU C AACCGGUG	1429	ADACTUGU A GCCUCAGG
885	GACCAAGU A ACTUGGAA	1444	AGAAGGCU C AGGAGGAG
933	UGUGUADU C GUUCCCAG	1455	GGGAGUAD C ACCAGGGA
936	GCAGAGAU U UUGUGUCA	1482	AGGGUACTU U CCCCCAGG
978	UUGAGAAU C UACAACUU	1484	ACUGCUCU U CCUCUUGC
980	GAGAADCU A CAACUUUU	1493	CCUGGGGU U GGAGACTA
986	CUACAACU U UUCAGCUC	1500	CGUGAAAU U AUGGUCAA
987	UACAACUU U UCAGCUCU	1503	GAAAADGU U CCAACCAC
988	ACAACUUU U CAGCUUCC	1506	UGGGUCAD A AUUGUUGG
1005	UUUGUGAU C GUGGGGUC	1509	GCCACCAU C ACUGUGUA
1006	GUGGGAGU A UCACCCAGG	1518	GUCCUGGU C GCCGUUGU
1023	CCGGAGGU C UCAGAAGG	1530	ACCUGGGU C ADAAUUGU
1025	GGAGGUCU C AGAAGGGG	1533	CUGAUCAA U GCGGGCUU
1066	CCUACCUU U GUUCCCAA	1551	GUGGGCCU C UGCUCGUA
1092	AGAGGGGU C UCAGCAGA	1559	UGGGAAGU C CCUGUUUA
1093	AGGGGAUU C CAGCCCCU	1563	UCCUACCU U UGUUCCCA
1125	CCCCAACU C UUGUUGAU	1565	UUACACCU A UUACCGCC
1163	ACGACGCU U CUUUUGCU	1567	ACACCUAU U ACCGCCAG
1164	CGACGCUU C UUUUGCUC	1584	AGGAAGAU C AGGAUAUA
1166	ACGCUUCU U UUGCUCUG	1592	CAGGAUAU A CAAGUUAU
1172	CUUUUGCU C UGCGGCCU	1599	UACAAGUU A CAGAAGGC
1200	AUCCAADU C ACACUGAA	1651	CCCCGCCU C CCUGAGCC
1201	UUGGGCTU C UCCACAGG	1661	CUGCACUU U GCCCUGGU
1203	GGGCUUCU C CACAGGUC	1663	GAACAGAU C AADGGACA
1227	UUGGAACU C CADUGUCU	1678	GAGAACTU C GGCCUGGG
1228	GCGGGCTU C GUGADUGU	1680	GGGCUUCU C CACAGGUC
1233	CUCCUGGU C CUGGUGGC	1681	GGCCUGUU U CCUGCCUC
1238	UGUGCUAU A UGGUCUCU	1684	CUGCUUGU A GACUCUCU
1264	GGAAAGAU C AUACGGGU	1690	CCCCACCU A CAUACAUU
1267	GUCAUGU U CAAGAADG	1691	COGGACUU U CGADCUUC
1294	CAGAGADU U UGUGUCAG	1696	CUCCUGGU C CUGGUUGC
1295	AGAGGGGU C UCAGCAGA	1698	UCAGAUAU A CCUGGAGA
1306	AGCAGACU C UUAUUGC	1737	GADCAAU U CACGGUGC
1321	AACAGAGU C UGGGGAAA	1750	GUCCAUUU A CACCUAUU
1334	GUUUGGU U CCAGAGGC	1756	CCUCUGCU C CUGGUCCU
1344	UCGGUGCU C AGGUADCC	1787	GAGAACTU C GGCCUGGG
1351	UCAGGOCU A AGAGGACU	1790	GACACGU C CCCAACUC
1353	UAGCAGCU C AACAAUGG	1793	AUGGUCCU C ACCUGGAC
1366	AGGGUACU U CCCCCAGG	1797	UCCUGUU U AAAAACCA
1367	GGGUACTU C CCCCAGGC	1802	GUUCAGAU A UACCUUGA
1368	GADGGUGU C CCGCUGCC	1812	AACAGAGU C UGGGGAAA
1380	CUGCCUAD C GGAUGGUU	1813	GCGGGCTU C GUGADUGU
1388	UGGAGACTU A ACUGGAUG	1825	GCCACCAU C ACUGUGUA
1398	CUGGCUUU C ACAGGACA	1837	ACCCACCU C ACAGGGUA
1402	CUGUGCUU U GAGAACTG	1845	AGAGGACU C GGAGGGGC
1408	UUGUGAU C GUGGGGUC	1856	CCCCUAUU C UGACCUUC
1410	CGAACTAU C GAGUGGAC	1861	CAUGUGCU A UADGGUCC

1865	UAUCCGGU A GACACAAG	2198	GAADGUCU C CGAGGUCA
1868	UCACGAGU C AUAUAAAU	2199	AGACGCUU A CAUGCCAG
1877	ACAGUACU U CCCCCAGG	2200	GGGUACUU C CCCCAGGC
1901	CUAAAACU C AAGGUACA	2201	GGGCUUCU C CACAGGUC
1912	GAACAGAU C AAUGGACA	2205	UUUUGUGU C AGCCACTG
1922	AUGUAAGU U AUUGGCUA	2210	UGGAGACU A ACUGGADG
1923	UGGACGCU C ACCUUUAG	2220	GAGAACCU C GCGCUGGG
1928	GUCAGAU A UACTUGGA	2224	ACATACAU U CCUACCTU
1930	UGGAGACU A ACUGGADG	2226	CUGGACCU C AGGCCACA
1964	AGAGACUU U GCGUCAGC	2233	UCAUGCUU C ACAGAACTU
1983	GAGAACCU C GCGCUGGG	2242	ACACAGCU C UCAGTAGU
1996	UGGAAGCU C UUCAAGCU	2248	CUCCUGGU C CUGGUCGC
2005	AUGUAAGU U AUUGGCUA	2254	AUCCAATU C ACACUGAA
2013	CUCUGCCU A UCGGADG	2259	GAUCACAU U CACGGGUC
2015	CUGCCUAT C GGGADGGU	2260	AUCACAUU C ACGGUGCU
2020	UAUUGAGU A CCCCUGAC	2266	AUCAGGAU A UACAAGUU
2039	CGGAGGAU C ACAAAACA	2274	GAGCAGGU U AACADGUA
2040	CUUGACCU C CUGGAGGU	2279	GGAAAGAU C AUACGGGU
2057	CUGGUCUU C CAUUGGCU	2282	ACAGUUAU U UAUUGAGU
2061	GCGUCCAU U UACAACUA	2288	GCCCCUGU C CUCCAATG
2071	AUACUUGU A GCGUCAGG	2291	CAGGAUAU A CAAGUAC
2076	UGUAGCCU C AGGCCUAA	2321	GGAAAGAU C AUACGGGU
2097	CCAACUCU U GUUGADGU	2338	UUGGGCUU C UCCACAGG
2098	CUUGACCU C CUGGAGGU	2339	GGGUACUU C CCCCAGGC
2115	UUCCGACU A GGGUCCCG	2341	GGGCCUGU C GGGUCUCA
2128	AGUGCGGU A CCADGADC	2344	CUGGUCGU A GACCUUCU
2130	GCCUGUUU C CUGCCUCU	2358	CCUGCCCU C CUCCACA
2145	CCAACUCU U GUUGADGU	2359	CCADUCCU C CCACAGAA
2152	UUGAGAAU C UACAACUU	2360	CUUGUGUU C CCUGGAAG
2156	UGACAGUU A UUUAUUGA	2376	GAACUGCU C UUCUCUUU
2158	UGAUGUAU U UAUUAUUU	2377	GACUUCUU U CUUAUUUA
2159	GAUGUAUU U AUUAUUUC	2378	GUGUAUUU C UUUCACGA
2160	AUGUAUUU A UUUAUUCA	2379	CUGUCUUU C CUUUGCG
2162	ACAUUCCU A CCUUUGUU	2380	UGAUUUCU U UCAAGAGU
2163	UAUUUAUU A AUUCAGAG	2382	AUUUCUUU C ACGAGUCA
2166	UGADGUUU U UAUUAUUU	2384	UAUCCGGU A GACACAAG
2167	GADGUUUU U AUUAUUUC	2399	UAAAUUACU A UGUGGACG
2170	GUUUUAUU U AAUUCAGA	2401	UGUGCUAU A UGGUCCUC
2171	CAGUUUUU U AUUGAGUA	2411	CAAUUUUU C AUGCUUCA
2173	UGUGCUAU A UGGUCCUC	2417	AUCAGGAU A UACAAGUU
2174	UCUCUAUU A CCCCUGCU	2418	UCAUGCUU C ACAGAACTU
2175	AUUUCUUU C ACGAGUCA	2425	UUAUUAUU U CAGAGUUC
2176	GAAAADGU U CCAACCAC	2426	CCUGGGGU U GGAGACTA
2183	UGACAGUU A UUUAUUGA	2433	UCAGAGUU C UGACAGUU
2185	ACAGUUAU U UAUUGAGU	2434	CGGAGGAU C ACAAAACA
2186	CAGUUAUU U AUUGAGUA	2448	UGAACAGU A CUUCCCCC
2187	AGUUAUUU A UUGAGUAC	2449	GAAGCCUU C CUGCCUCG
2189	UUUUUAUU U GAGUACCC	2451	GGCCUGUU U CCUGCCUC
2196	CUGACAGU U AUUUUAUG	2452	GCCUGUUU C CUGCCUCU

2455	ACAUUCCU A CCUUUGUU	2761	CGGACUUU C GAUCUUCC
2459	CCUUGCCU C CUCCCA	2765	CUUUUGCU C UGCGGCTU
2460	CCUACCUU U GUUCCCA	2769	UUCUUAU U ACCCUCG
2479	UUACACCU A UUAUCCG	2797	CGUGAAU U AUGGUCAA
2480	GUUGCCU U GUGAUCC	2803	CUCAUGCU U CACAGAAC
2483	ACCUUUGU U CCAUUGU	2804	UCAUGCU C ACAGAACTU
2484	CCUUUGUU C CCAUUGU	2813	GCUCCCAU C CUGACCCU
2492	GACCACTU C CCAACCUA	2815	CGGACUUU C GAUCUUCC
2504	ACCUACAU A CAUUCUA	2821	CCUGACCU C CUGGAGGU
2508	ACAUAU U CUUACCUU	2822	UACAACCU U UCAGCUCC
2509	CAUAU U CUUACCUU	2823	CAACUUU C AGCUCCCA
2510	GUCAUUU A CACCUAUU	2829	UGGUGCU C AGGUUCC
2520	ACCUUUGU U CCAUUGU	2837	CACAGGU A CUUCCCC
2521	CCUUUGUU C CCAUUGU	2840	GCACCCU C CAGCGCA
2533	ACAGCAU U ACCCUCA	2847	UUAACCU C ACCACCU
2540	UGGUGCU C AGGUUCC	2853	UUGAUU U CCGACUAG
2545	AGGAGCU C CGGACUUU	2860	UCUUGUU U CCGGAA
2568	CAGAGAU U UGUGCAG	2872	GGGUGCU C GGUGCUA
2579	CCUGACU U UGUGCAG	2877	UGGAGCU C CAGCACC
2585	CUGCUU A GACCUUC	2899	AGGAGCU C CGGACUUU
2588	UGCUU C CCACAGC	2900	GGCUGAU U CCUUCU
2591	CUUUU C UUGGAG	2904	GAACUGCU C UUCUUCU
2593	UCUUAU A CCCCUGU	2905	GGCUGAU U CCUUCU
2596	CUUUGU C CUGGUGC	2906	GUUGAU A UUAUUA
2601	UGUGUAU A UGGUCU	2907	CUUCU C CUUUGC
2602	GUUUGU C GCGUGU	2908	UGAGUAU U UAUUAU
2607	GUGGAGU A UCACAGG	2909	GAACUGCU C UUCUUCU
2608	CUUAGCU C CUGUGGA	2910	ACUUCU C UCUAUAC
2609	UGGAGAU A ACUGGAG	2911	UUCUUCU C UAUUACC
2620	UCAGAGU C UGACAGU	2912	AUGUAU A UUAUUA
2626	CUUAGU A GUGUGCU	2913	UGUGUAU C GUUCCAG
2628	UACAACU U UCAGUCC	2914	GUUAUUAU U AAUUCAGA
2635	UCACAGU C CAUUCAC	2915	UAUUAU A AUUCAGAG
2640	GUCAGGU A UCCAUCA	2916	CUUUCU C UUGGAG
2641	CCCACCU A CAUAUUA	2917	CUUUCU U GCGAGAC
2642	GCCUGUU C CUGCUU	2918	AUUUCUU C AGGAGUA
2653	CCACAGU C AGGUGCU	2919	UUUUGU C AGCCACU
2659	AGAAGGU C CUGCAAG	2931	GAUGGUGU C CCGUGCC
2689	ACUAGGU C CUGAAGU	2933	UGGAGCU C CAGCACC
2691	UCAGGCU A AGAGGACU	2941	CAGUACU C CCGAGGC
2700	AGGUAU U CCCCAGG	2951	ACCAGCU U CUCUGAC
2704	GACCACTU C CCAACCUA	2952	CGGACUU U CGAUUCU
2711	CCUACCU U AGGAAGU	2953	UGCUUCU C UGACUUG
2712	CCUACCU A GGAAGUG	2956	CUUUCU U GAUUAU
2721	GGAAAGU C AUACGGU	2961	UUUUGU C AGCCACU
2724	AAGAU A CCGGUUG	2962	UGUGUAU C GUUCCAG
2744	GGUGGUAU C CUGCAGG	2965	CUUUGAU C AAUAAGU
2750	GUUUCU U UAAAAAC	2966	UGGAAGCU C UUCAAGU
2759	GACGAACU A UCGAGUG	2969	GAUUAU A AAGUUUA

2975	UGGAAGCU C UUCAAGCU
2976	UAUAAGGU C CUCACCUG
2977	GAAGCUCU U CAAGCUGA

Table 10: Rat ICAM HH Ribozyme Sequences

nt. Position	Rat HH Ribozyme Sequence		
11	UCAGGGUG	CUGADGAGGCCGAAAGGCCGAA	AUTGGGATC
23	UAGAGAAG	CUGADGAGGCCGAAAGGCCGAA	AAGUCAGC
26	AAGAGGAA	CUGADGAGGCCGAAAGGCCGAA	AGCAGUUC
31	AGGACCAG	CUGADGAGGCCGAAAGGCCGAA	AGCAGAGG
34	GUADAUCU	CUGADGAGGCCGAAAGGCCGAA	AGCUUCAG
40	GGGGCUUG	CUGADGAGGCCGAAAGGCCGAA	ACCUUGAG
48	CCCAGGCC	CUGADGAGGCCGAAAGGCCGAA	AGGUUCC
54	GGUCAGG	CUGADGAGGCCGAAAGGCCGAA	AGGCGGGG
58	GGGAGCUA	CUGADGAGGCCGAAAGGCCGAA	AGGCAAGG
64	ACGGGUUG	CUGADGAGGCCGAAAGGCCGAA	AGCCAUUG
96	AGGACCAG	CUGADGAGGCCGAAAGGCCGAA	AGCAGAGG
102	GCGACCAG	CUGADGAGGCCGAAAGGCCGAA	ACCAGGAG
108	AGUCCCC	CUGADGAGGCCGAAAGGCCGAA	AGCAGUCC
115	UGGGAACA	CUGADGAGGCCGAAAGGCCGAA	AGGUAGGA
119	GAGUUGG	CUGADGAGGCCGAAAGGCCGAA	ACAGGUC
120	GGCCGGG	CUGADGAGGCCGAAAGGCCGAA	ADCAAC
146	GGAGUUC	CUGADGAGGCCGAAAGGCCGAA	AGGUUUG
152	UUGAGGUG	CUGADGAGGCCGAAAGGCCGAA	AGCGGGU
158	UGACUUGU	CUGADGAGGCCGAAAGGCCGAA	AAAGAAU
165	GGGGGAG	CUGADGAGGCCGAAAGGCCGAA	ACUGUUA
168	CGAGGCAG	CUGADGAGGCCGAAAGGCCGAA	AAGGCUUC
185	CCUGCAG	CUGADGAGGCCGAAAGGCCGAA	ADCCACC
209	GGUCAGAU	CUGADGAGGCCGAAAGGCCGAA	AGGGGUG
227	UUCACAGU	CUGADGAGGCCGAAAGGCCGAA	ACUUGGUC
230	CCUCCAC	CUGADGAGGCCGAAAGGCCGAA	ACAGCUUG
237	GGGUUGUC	CUGADGAGGCCGAAAGGCCGAA	AGCUUCAG
248	UCCUAAGG	CUGADGAGGCCGAAAGGCCGAA	AGGGGGCC
253	CCUCCACTU	CUGADGAGGCCGAAAGGCCGAA	AGGCAGUG
263	GCADGAGA	CUGADGAGGCCGAAAGGCCGAA	AUTGGCUC
267	CGAGGCAG	CUGADGAGGCCGAAAGGCCGAA	AAGGCUUC
293	UCAGCUUG	CUGADGAGGCCGAAAGGCCGAA	AGAGCUUC
319	UCGUUUGU	CUGADGAGGCCGAAAGGCCGAA	ADCCUCCG
335	AGUUCUA	CUGADGAGGCCGAAAGGCCGAA	AGCACAGU
337	GAGGACCA	CUGADGAGGCCGAAAGGCCGAA	ADAGCACA
338	CCAGCTU	CUGADGAGGCCGAAAGGCCGAA	AAGAGCTU
359	AAGCCGAG	CUGADGAGGCCGAAAGGCCGAA	ACUGCGUG
367	ACGGGUUG	CUGADGAGGCCGAAAGGCCGAA	AGCCAUUG
374	AGGUGGGU	CUGADGAGGCCGAAAGGCCGAA	AGGGGUA
375	GAGGCAGG	CUGADGAGGCCGAAAGGCCGAA	AGGCUUCU
378	UACCCUGU	CUGADGAGGCCGAAAGGCCGAA	AGGUUGGU
386	AGCUCCAA	CUGADGAGGCCGAAAGGCCGAA	ACACAGCG

394 CTGUTUCAG CUGAUGAGGCCGAAAGGCCGAA AGCACCCAC
420 UGCGCUGG CUGAUGAGGCCGAAAGGCCGAA AGGGGUGC
425 GGUGGCAG CUGAUGAGGCCGAAAGGCCGAA AGCCGAGG
427 UGGUUTUU CUGAUGAGGCCGAAAGGCCGAA AACAGGGA
450 CGCAGGAT CUGAUGAGGCCGAAAGGCCGAA AGGUUCUU
451 GCCUGGGG CUGAUGAGGCCGAAAGGCCGAA AAGUACCC
456 UGGUGGCA CUGAUGAGGCCGAAAGGCCGAA AAGCCGAG
495 UACACAGU CUGAUGAGGCCGAAAGGCCGAA AUGGUGGC
510 UCCCCACG CUGAUGAGGCCGAAAGGCCGAA AGCAGCAC
564 GUGGUUGG CUGAUGAGGCCGAAAGGCCGAA ACAUUTUC
592 UCCCGUGU CUGAUGAGGCCGAAAGGCCGAA AUAUCCCC
607 GCADGAGA CUGAUGAGGCCGAAAGGCCGAA AUUGGUCU
608 AGCADGAG CUGAUGAGGCCGAAAGGCCGAA AAUUGGCU
609 AAGCAUGA CUGAUGAGGCCGAAAGGCCGAA AAADUGGC
611 UGAAGCAU CUGAUGAGGCCGAAAGGCCGAA AGAAAUUG
656 CAUUCUUG CUGAUGAGGCCGAAAGGCCGAA ACAGUGAC
657 ACAUUCUU CUGAUGAGGCCGAAAGGCCGAA AACAGUGA
668 AAGAGGAA CUGAUGAGGCCGAAAGGCCGAA AGCAGUUC
677 UGCGCUGG CUGAUGAGGCCGAAAGGCCGAA AGGGGUGC
684 AAAGUCCG CUGAUGAGGCCGAAAGGCCGAA AGCUGCCU
692 GGAUUC CUGAUGAGGCCGAAAGGCCGAA AGGUUCUG
693 GGAAGADC CUGAUGAGGCCGAAAGGCCGAA AAAGUCCG
696 AGAGGCAG CUGAUGAGGCCGAAAGGCCGAA AAACAGGC
709 GUGAGGGG CUGAUGAGGCCGAAAGGCCGAA AAADUGCU
720 GAGCUGAA CUGAUGAGGCCGAAAGGCCGAA AGUUGUAG
723 UGGGAGCU CUGAUGAGGCCGAAAGGCCGAA AAAAGUUG
735 GCGACCAG CUGAUGAGGCCGAAAGGCCGAA ACCAGGAG
738 UCCACCCC CUGAUGAGGCCGAAAGGCCGAA AGGCAGGA
765 AGUUCUCA CUGAUGAGGCCGAAAGGCCGAA AGCACAGU
769 UUCAGGG CUGAUGAGGCCGAAAGGCCGAA ACACAAGA
770 CUUCCAGG CUGAUGAGGCCGAAAGGCCGAA AACACAAG
785 AGGCAGGA CUGAUGAGGCCGAAAGGCCGAA ACAGGCCU
786 GAGGCAGG CUGAUGAGGCCGAAAGGCCGAA AACAGGCC
792 GCGACCAG CUGAUGAGGCCGAAAGGCCGAA ACCAGGAG
794 GAGCUUCA CUGAUGAGGCCGAAAGGCCGAA AGGCAGGA
807 UCCAGGUA CUGAUGAGGCCGAAAGGCCGAA AUCUGAGC
833 UAGUCUCC CUGAUGAGGCCGAAAGGCCGAA ACCCCAGG
846 CAADAAAU CUGAUGAGGCCGAAAGGCCGAA ACUGUCAG
851 AGCUGCUA CUGAUGAGGCCGAAAGGCCGAA AGGUGAGC
863 ACGGGUUG CUGAUGAGGCCGAAAGGCCGAA AGCCAUGG
866 UGUCAGAG CUGAUGAGGCCGAAAGGCCGAA AAGCAUGG
867 UAGGUGGG CUGAUGAGGCCGAAAGGCCGAA AGGUGGUC
869 CUUCGCAA CUGAUGAGGCCGAAAGGCCGAA AGGAAGAG
881 CACGGGUU CUGAUGAGGCCGAAAGGCCGAA AAGCCAUU
885 UUCACAGU CUGAUGAGGCCGAAAGGCCGAA ACUUGGUC
933 CUGGGAAC CUGAUGAGGCCGAAAGGCCGAA AADACACA
936 UGACACAA CUGAUGAGGCCGAAAGGCCGAA AUCUCUGC
978 AAGUUGUA CUGAUGAGGCCGAAAGGCCGAA AUCUCUAA
980 AAAAGUUG CUGAUGAGGCCGAAAGGCCGAA AGAUUCUC

986	GAGCUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGUUGUAG
987	GGAGCUGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUUGUA
988	GCGAGCUG	CUGAUGAGGCCGAAAGGCCGAA	AAAGUUGU
1005	GACGCCAC	CUGAUGAGGCCGAAAGGCCGAA	AUCACGAA
1006	CCUGGUGA	CUGAUGAGGCCGAAAGGCCGAA	ACTCCAC
1023	CCUUCUGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUCCG
1025	CCCCUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGACTUC
1066	UUGGAAC	CUGAUGAGGCCGAAAGGCCGAA	AAGGUAGG
1092	UCUGCUGA	CUGAUGAGGCCGAAAGGCCGAA	ACCCUCU
1093	AGGGGCTG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCCU
1125	ACCAACAA	CUGAUGAGGCCGAAAGGCCGAA	AGUUGGG
1163	AGCAAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGCGUCU
1164	GAGCAAAA	CUGAUGAGGCCGAAAGGCCGAA	AAGCGUC
1166	CAGAGCAA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCU
1172	AGGCCGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAAG
1200	UUCAGUGU	CUGAUGAGGCCGAAAGGCCGAA	AADUGAU
1201	CCUGUGGA	CUGAUGAGGCCGAAAGGCCGAA	AAGCCAA
1203	GACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCCC
1227	AGCACAU	CUGAUGAGGCCGAAAGGCCGAA	AGUCCAA
1228	ACGAUCAC	CUGAUGAGGCCGAAAGGCCGAA	AAGCCGC
1233	GCGACCAG	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGAG
1238	GAGGACCA	CUGAUGAGGCCGAAAGGCCGAA	AUAGCACA
1264	ACCCGUAT	CUGAUGAGGCCGAAAGGCCGAA	AUCUUCC
1267	CAUUCUUG	CUGAUGAGGCCGAAAGGCCGAA	ACAGUGAC
1294	CUGACACA	CUGAUGAGGCCGAAAGGCCGAA	AADUCUG
1295	UCUGCUGA	CUGAUGAGGCCGAAAGGCCGAA	ACCCUCU
1306	GCAUGUAA	CUGAUGAGGCCGAAAGGCCGAA	AGUCUCU
1321	UUUCCCCA	CUGAUGAGGCCGAAAGGCCGAA	ACUCUGU
1334	GCUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACGAATAC
1344	GGATACTU	CUGAUGAGGCCGAAAGGCCGAA	AGCACCGA
1351	AGUCCUCU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUGA
1353	CCAUGUUG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGCUA
1366	CCUGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAACCU
1367	GCUUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUACCC
1368	GGCAGCGG	CUGAUGAGGCCGAAAGGCCGAA	ACACCAUC
1380	ACCAUCCC	CUGAUGAGGCCGAAAGGCCGAA	AUAGGCAG
1388	CAUCCAGU	CUGAUGAGGCCGAAAGGCCGAA	AGUCUCCA
1398	UGUCCUGU	CUGAUGAGGCCGAAAGGCCGAA	ACAGCCAG
1402	CAGUUCUC	CUGAUGAGGCCGAAAGGCCGAA	AAGCACAG
1408	GACGCCAC	CUGAUGAGGCCGAAAGGCCGAA	AUCACGAA
1410	GUCCACTC	CUGAUGAGGCCGAAAGGCCGAA	AUAGUUCG
1421	GCCUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUACCC
1425	AGCCAGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGGU
1429	CCUGAGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAAGUAT
1444	CUCUCCU	CUGAUGAGGCCGAAAGGCCGAA	AGCCUUCU
1455	UCCUUGGU	CUGAUGAGGCCGAAAGGCCGAA	AUACUCCC
1482	CCUGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGUACCUU
1484	GCAAGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGAGCAGU
1493	UAGUCUCC	CUGAUGAGGCCGAAAGGCCGAA	ACCCACG

1500	UUGACCAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUCACG
1503	GUGGUUGG	CUGAUGAGGCCGAAAGGCCGAA	ACAUUUUC
1506	CCAACAAT	CUGAUGAGGCCGAAAGGCCGAA	ADGACCCA
1509	UACACAGU	CUGAUGAGGCCGAAAGGCCGAA	ADGGUGGC
1518	ACAACGGC	CUGAUGAGGCCGAAAGGCCGAA	ACCCAGGAC
1530	ACAATUAT	CUGAUGAGGCCGAAAGGCCGAA	ACCCAGGU
1533	AAGCCCGC	CUGAUGAGGCCGAAAGGCCGAA	ADGAUCAG
1551	UACGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGGCCAC
1559	UAAACAGG	CUGAUGAGGCCGAAAGGCCGAA	ACTUCCCA
1563	UGGGAACA	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGGA
1565	GGCGGUA	CUGAUGAGGCCGAAAGGCCGAA	AGGUGUAA
1567	CUGGCGGU	CUGAUGAGGCCGAAAGGCCGAA	AUAGGUGU
1584	UAUAUCCU	CUGAUGAGGCCGAAAGGCCGAA	AUCUUCU
1592	GUAACUUG	CUGAUGAGGCCGAAAGGCCGAA	AUAUCCUG
1599	GCCUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AACUUGUA
1651	GGCUCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCGGGG
1661	ACCAGGGC	CUGAUGAGGCCGAAAGGCCGAA	AAGUGCAG
1663	UUCUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUCUGUUC
1678	CCCAGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCUC
1680	GACCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCCC
1681	GAGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGGCC
1684	GAGAGGUC	CUGAUGAGGCCGAAAGGCCGAA	ACGAGCAG
1690	AADGUADG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGGG
1691	GAAGUUCG	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCGG
1696	GCGACCA	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGAG
1698	UCUCCAGG	CUGAUGAGGCCGAAAGGCCGAA	AUAUCUGA
1737	GCAACGUG	CUGAUGAGGCCGAAAGGCCGAA	ADGUGAUC
1750	AUAAGGUG	CUGAUGAGGCCGAAAGGCCGAA	AAADGGAC
1756	AGGACCA	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAGG
1787	CCCAGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCUC
1790	GAGUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGUGUC
1793	GUCCAGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGACCAU
1797	UGGUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AACAGGGA
1802	UCCAGGUA	CUGAUGAGGCCGAAAGGCCGAA	AUCUGAGC
1812	UUUCCCCA	CUGAUGAGGCCGAAAGGCCGAA	ACUCUGUU
1813	ACGATCAC	CUGAUGAGGCCGAAAGGCCGAA	AAGCCCGC
1825	UACACAGU	CUGAUGAGGCCGAAAGGCCGAA	ADGGUGGC
1837	UACCCUGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGGU
1845	GCCCCUCC	CUGAUGAGGCCGAAAGGCCGAA	AGUCCUCU
1856	GCAGGUCA	CUGAUGAGGCCGAAAGGCCGAA	ADUAGGGG
1861	GGACCAUA	CUGAUGAGGCCGAAAGGCCGAA	AGCACADG
1865	CUUGUGUC	CUGAUGAGGCCGAAAGGCCGAA	ACCGGAUA
1868	AUUUAUAU	CUGAUGAGGCCGAAAGGCCGAA	ACUCUGUA
1877	CCCGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGUACUGU
1901	UGUACCUU	CUGAUGAGGCCGAAAGGCCGAA	AGUUUAG
1912	UGUCCAUU	CUGAUGAGGCCGAAAGGCCGAA	AUCUGUUC
1922	UAGGCAAU	CUGAUGAGGCCGAAAGGCCGAA	ACTUACAU
1923	CUAAAGGU	CUGAUGAGGCCGAAAGGCCGAA	AGCGUCCA
1928	UCCAGGUA	CUGAUGAGGCCGAAAGGCCGAA	AUCUGAGC

1930	CAUCCAGU	CUGAUGAGGCCGAAAGGCCGAA	AGGCUCCA
1964	GCTGACAC	CUGAUGAGGCCGAAAGGCCGAA	AAAUCUCU
1983	CCCAGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCUC
1996	AGCTUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGCTUCCA
2005	UAGGCAAU	CUGAUGAGGCCGAAAGGCCGAA	ACTUACAU
2013	CAUCCCGA	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGCG
2015	ACCAUCCC	CUGAUGAGGCCGAAAGGCCGAA	ADAAGCAG
2020	GUACAGGG	CUGAUGAGGCCGAAAGGCCGAA	ACUCAADA
2039	UGGUUUGU	CUGAUGAGGCCGAAAGGCCGAA	ADCCUCCG
2040	ACCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAGG
2057	AGCCAUUG	CUGAUGAGGCCGAAAGGCCGAA	AGGACCAG
2061	UAGGUGUA	CUGAUGAGGCCGAAAGGCCGAA	ADGGACCC
2071	CCUGAGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAAGUAU
2076	UUAGGCTU	CUGAUGAGGCCGAAAGGCCGAA	AGGCUACA
2097	ACAUCAAC	CUGAUGAGGCCGAAAGGCCGAA	AGAGUUGG
2098	ACCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAGG
2115	CAGGACCC	CUGAUGAGGCCGAAAGGCCGAA	AGUCGGAA
2128	GADCAUGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGCACT
2130	AGAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAACAGGC
2145	ACAUCAAC	CUGAUGAGGCCGAAAGGCCGAA	AGAGUUGG
2152	AAGUUGUA	CUGAUGAGGCCGAAAGGCCGAA	AUUCUCAA
2156	UCAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AACUGUCA
2158	AAUUAADA	CUGAUGAGGCCGAAAGGCCGAA	AUACAUCA
2159	GAADUAAU	CUGAUGAGGCCGAAAGGCCGAA	AATACAUU
2150	UGAADUAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACAU
2162	AACAAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGAAUGU
2163	CUCUGAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUAAUA
2166	AAUUAADA	CUGAUGAGGCCGAAAGGCCGAA	AUACAUCA
2167	GAADUAAU	CUGAUGAGGCCGAAAGGCCGAA	AATACAUU
2170	UCUGAAUU	CUGAUGAGGCCGAAAGGCCGAA	AUAUAAUAC
2171	UACUCAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUACUG
2173	GAGGACCA	CUGAUGAGGCCGAAAGGCCGAA	AUAGCACA
2174	AGCAGGGG	CUGAUGAGGCCGAAAGGCCGAA	AUAGAGA
2175	UGACTUCU	CUGAUGAGGCCGAAAGGCCGAA	AAAGAAAU
2176	GUGGUUGG	CUGAUGAGGCCGAAAGGCCGAA	ACAUUUUC
2183	UCAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AACUGUCA
2185	ACUCAADA	CUGAUGAGGCCGAAAGGCCGAA	AUAACUGU
2186	UACUCAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUACUG
2187	GUACUCAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAACT
2189	GGGUACUC	CUGAUGAGGCCGAAAGGCCGAA	AUAUAAUA
2196	CAAUAAAU	CUGAUGAGGCCGAAAGGCCGAA	ACUGUCAG
2198	UGACCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGACAUUC
2199	CUGGCADG	CUGAUGAGGCCGAAAGGCCGAA	AAGAGUCU
2200	GCCUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUACCC
2201	GACCUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCCC
2205	CAGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACACAAAA
2210	CAUCCAGU	CUGAUGAGGCCGAAAGGCCGAA	AGUCUCCA
2220	CCCAGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCUC
2224	AAGGUAGG	CUGAUGAGGCCGAAAGGCCGAA	AUGUAUGU

2226	UGUGGCTU	CUGAUGAGGCCGAAAGGCCGAA	AGGUCCAG
2233	AGUUCUGU	CUGAUGAGGCCGAAAGGCCGAA	AAGCADGA
2242	ACTACUGA	CUGAUGAGGCCGAAAGGCCGAA	AGCUGUGU
2248	GCGACCAG	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGAG
2254	UUCAGUGU	CUGAUGAGGCCGAAAGGCCGAA	AAUUGGAT
2259	GCACCGUG	CUGAUGAGGCCGAAAGGCCGAA	ADGUGATC
2260	AGCACCGU	CUGAUGAGGCCGAAAGGCCGAA	AADGUGAU
2266	AACUUGUA	CUGAUGAGGCCGAAAGGCCGAA	ADCCUGAU
2274	UACADGUT	CUGAUGAGGCCGAAAGGCCGAA	ACCUCCUC
2279	ACCCGUAU	CUGAUGAGGCCGAAAGGCCGAA	ADCUUUCU
2282	ACUCAADA	CUGAUGAGGCCGAAAGGCCGAA	ADAACTGU
2288	CAUUGGAG	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGGC
2291	GUAACUUG	CUGAUGAGGCCGAAAGGCCGAA	ADAUCCUG
2321	ACCCGUAU	CUGAUGAGGCCGAAAGGCCGAA	ADCUUUCU
2338	CCUGUGGA	CUGAUGAGGCCGAAAGGCCGAA	AAGCCCAA
2339	GCCUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUACCC
2341	UGAGCACC	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCCC
2344	GAGAGGUC	CUGAUGAGGCCGAAAGGCCGAA	ACGAGCAG
2358	UGUGGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGGG
2359	UUCUGUGG	CUGAUGAGGCCGAAAGGCCGAA	ADGGAUGG
2360	CUUCCAGG	CUGAUGAGGCCGAAAGGCCGAA	AACAACAAG
2376	AAGAGGAA	CUGAUGAGGCCGAAAGGCCGAA	AGCAGTUC
2377	UAADAGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGUC
2378	UCGUGAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACAG
2379	CGCAAGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGAGCAG
2380	ACTUGUGA	CUGAUGAGGCCGAAAGGCCGAA	AGAAADCA
2382	UGACUUGU	CUGAUGAGGCCGAAAGGCCGAA	AAAGAAAU
2384	CUUGUGUC	CUGAUGAGGCCGAAAGGCCGAA	ACCCGADA
2399	CGUCCACA	CUGAUGAGGCCGAAAGGCCGAA	AGUADUUA
2401	GAGGACCA	CUGAUGAGGCCGAAAGGCCGAA	ADAGCACA
2411	UGAAGCAU	CUGAUGAGGCCGAAAGGCCGAA	AGAAADUG
2417	AACUUGUA	CUGAUGAGGCCGAAAGGCCGAA	ADCCUGAU
2418	AGUUCUGU	CUGAUGAGGCCGAAAGGCCGAA	AAGCADGA
2425	GAACUUCG	CUGAUGAGGCCGAAAGGCCGAA	ADUAAATA
2426	UAGUCUCC	CUGAUGAGGCCGAAAGGCCGAA	ACCCCAGG
2433	AACUGUCA	CUGAUGAGGCCGAAAGGCCGAA	AACUCUGA
2434	UCGUUUGU	CUGAUGAGGCCGAAAGGCCGAA	ADCCUCCG
2448	GGGGGAAG	CUGAUGAGGCCGAAAGGCCGAA	ACTGUUCA
2449	CGAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCTUC
2451	GAGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGGCC
2452	AGAGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AAACAGGC
2455	AACAAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGAADGU
2459	UGUGGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGGG
2460	UUGGGAAC	CUGAUGAGGCCGAAAGGCCGAA	AAGGUAGG
2479	GGCGGUA	CUGAUGAGGCCGAAAGGCCGAA	AGGUGUA
2480	GGGADCAC	CUGAUGAGGCCGAAAGGCCGAA	ACGGCGAC
2483	ACAUGGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAAAGGU
2484	GACAUUGG	CUGAUGAGGCCGAAAGGCCGAA	AACAAAGG
2492	UAGGUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGUC

2504	UAGGAADG	CUGAUGAGGCCGAAAGGCCGAA	AUGUAGGU
2508	AAAGGUAG	CUGAUGAGGCCGAAAGGCCGAA	AUGUADGU
2509	AAAGGUAG	CUGAUGAGGCCGAAAGGCCGAA	AADGUADG
2510	AADAGGUG	CUGAUGAGGCCGAAAGGCCGAA	AAADGGAC
2520	ACAUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAAAGGU
2521	GACAUUGG	CUGAUGAGGCCGAAAGGCCGAA	AACAAAGG
2533	UGAGGGGU	CUGAUGAGGCCGAAAGGCCGAA	AADGCUGU
2540	GGADACCU	CUGAUGAGGCCGAAAGGCCGAA	AGCACCGA
2545	AAAGUCCG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGCCU
2568	CUGACACA	CUGAUGAGGCCGAAAGGCCGAA	AADUCUG
2579	CCAGGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGUGCAGG
2585	GAGAGGUC	CUGAUGAGGCCGAAAGGCCGAA	ACGAGCAG
2588	GGCUGUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGGCA
2591	CUUGCCAA	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGAG
2593	AGCAGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAUAGAGA
2596	GCGACCA	CUGAUGAGGCCGAAAGGCCGAA	ACCAAGGAG
2601	GAGGACCA	CUGAUGAGGCCGAAAGGCCGAA	AUAGCACA
2602	ACAACGGC	CUGAUGAGGCCGAAAGGCCGAA	ACCAAGGAC
2607	CCUGGUGA	CUGAUGAGGCCGAAAGGCCGAA	ACUCCAC
2608	UCCCAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGCUAAAG
2609	CAUCCAGU	CUGAUGAGGCCGAAAGGCCGAA	AGUCUCCA
2620	AACUGUCA	CUGAUGAGGCCGAAAGGCCGAA	AACUCUGA
2626	AGCAGCAC	CUGAUGAGGCCGAAAGGCCGAA	ACUGAGAG
2628	GGAGCCGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUUGUA
2635	GUGAAUUG	CUGAUGAGGCCGAAAGGCCGAA	AUCUGUGA
2640	UGGADGGA	CUGAUGAGGCCGAAAGGCCGAA	ACCUAGAG
2641	AADGUADG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGGG
2642	AGAAGGAG	CUGAUGAGGCCGAAAGGCCGAA	AAACAGGC
2653	AGCACCCU	CUGAUGAGGCCGAAAGGCCGAA	ACCUUGGG
2659	GCUUGCAG	CUGAUGAGGCCGAAAGGCCGAA	ACCCUUCU
2689	AGCUUCAG	CUGAUGAGGCCGAAAGGCCGAA	ACCCUAGU
2691	AGUCCUCU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUGA
2700	CCUGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAACCU
2704	UAGGUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGUC
2711	ACCUUCCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGGG
2712	CACCUUCC	CUGAUGAGGCCGAAAGGCCGAA	AAGGUAGG
2721	ACCCGUAU	CUGAUGAGGCCGAAAGGCCGAA	AUCUUCU
2724	CAAACCCG	CUGAUGAGGCCGAAAGGCCGAA	AUGADCUU
2744	CCUGCAGG	CUGAUGAGGCCGAAAGGCCGAA	AUCCACCC
2750	GGUUUUUA	CUGAUGAGGCCGAAAGGCCGAA	ACAGGGAC
2759	CCACUCGA	CUGAUGAGGCCGAAAGGCCGAA	AGUUCGUC
2761	GGAAGADC	CUGAUGAGGCCGAAAGGCCGAA	AAAGUCCG
2765	AGGCCGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAAG
2769	GCAGGGGU	CUGAUGAGGCCGAAAGGCCGAA	AUAGAGAA
2797	UUGACCAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUCACG
2803	GUUCUGUG	CUGAUGAGGCCGAAAGGCCGAA	AGCADGAG
2804	AGUUCUGU	CUGAUGAGGCCGAAAGGCCGAA	AAGCADGA
2813	AGGGUCAG	CUGAUGAGGCCGAAAGGCCGAA	AUGGGAGC
2815	GGAGAUUC	CUGAUGAGGCCGAAAGGCCGAA	AAAGUCCG

2821	ACCTCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGTCAGG
2822	GGAGTUGA	CUGAUGAGGCCGAAAGGCCGAA	AAGTUGUA
2823	UGGGAGCU	CUGAUGAGGCCGAAAGGCCGAA	AAAAGTUG
2829	GGATACCU	CUGAUGAGGCCGAAAGGCCGAA	AGCACCGA
2837	GGGGGAAG	CUGAUGAGGCCGAAAGGCCGAA	ACCCUGUG
2840	UGGCTUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUGC
2847	AGGUGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUA
2853	CUAGGCGG	CUGAUGAGGCCGAAAGGCCGAA	AGAUGGAA
2860	UUCGAGGG	CUGAUGAGGCCGAAAGGCCGAA	ACACAAGA
2872	UGAGCACCC	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCCCC
2877	GGUGCTUGG	CUGAUGAGGCCGAAAGGCCGAA	AGACTCCA
2899	AAAGTCCG	CUGAUGAGGCCGAAAGGCCGAA	AGCTGCCU
2900	AGAGAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGUCAGCC
2904	AAGAGGAA	CUGAUGAGGCCGAAAGGCCGAA	AGCAGTUC
2905	AGAGAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGUCAGCC
2906	UUAATAAA	CUGAUGAGGCCGAAAGGCCGAA	ACATCAAC
2907	CGCAAGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGAGCAG
2908	AATUATAA	CUGAUGAGGCCGAAAGGCCGAA	ATACTACA
2909	AAGAGGAA	CUGAUGAGGCCGAAAGGCCGAA	AGCAGTUC
2910	GUAATAGA	CUGAUGAGGCCGAAAGGCCGAA	AAGGAAGT
2911	GGGUAATA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGGAA
2912	UGAATUAA	CUGAUGAGGCCGAAAGGCCGAA	AAATACAU
2913	CTGGGAAC	CUGAUGAGGCCGAAAGGCCGAA	AATACACA
2914	UCUGAAUU	CUGAUGAGGCCGAAAGGCCGAA	ATAAAUAC
2915	CCTUGAAU	CUGAUGAGGCCGAAAGGCCGAA	AATAAATA
2916	CUUCGCAA	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGAG
2917	GUUUUGGC	CUGAUGAGGCCGAAAGGCCGAA	AGAGGAAG
2918	UGACUCGU	CUGAUGAGGCCGAAAGGCCGAA	AAAGAAAU
2919	CAGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACACAAAA
2931	GGCAGCGG	CUGAUGAGGCCGAAAGGCCGAA	ACACCAAC
2933	GGUGCTUGG	CUGAUGAGGCCGAAAGGCCGAA	AGACTCCA
2941	GCTUGGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUACUG
2951	GUCAGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGCAUGGU
2952	GAAGAUUG	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCGG
2955	CCAUGUCA	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGCA
2956	AUUGAUUC	CUGAUGAGGCCGAAAGGCCGAA	AAGGAAAG
2961	CAGUGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACACAAAA
2962	CTGGGAAC	CUGAUGAGGCCGAAAGGCCGAA	AATACACA
2965	ACUUUAUU	CUGAUGAGGCCGAAAGGCCGAA	AUUCAAAG
2966	AGCTUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGCTUCCA
2969	UAAAACTU	CUGAUGAGGCCGAAAGGCCGAA	AUUGAUUC
2975	AGCTUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGCTUCCA
2976	CAGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	ACCAUATA
2977	UCAGCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGAGCTUC

Table 11: Human IL-5 HH Target Sequence

nt. Position	HH Target Sequence	nt. Position	HH Target Sequence
8	AUGCAU U UCUUGC	245	AAGAAU C UUUCAGG
9	UGCAU U CUUGCC	247	GAAAUU U UCAGGA
10	GCACUU C UUUGCA	248	AAAUUU U CAGGAA
12	ACUUUU U UGCCAA	249	AADUUU C AGGAAU
13	CUUUUU U GCCAAG	257	AGGAAU A GGCACAC
36	AGAAGU U UCAGAGC	273	GGAGAU C AAACUU
37	GAAAGU U CAGAGCC	291	AGGGGU A CUUGGA
38	AAGGUU C AGAGCA	305	AAAGAU A UUCAAA
56	GGAGGU U CUGCAU	307	AGAUU U CAAAAAC
57	GAGGUU C UGCAUU	308	GACAUU C AAAAUA
63	UCUGAU U UGAGUU	316	AAAAAU U GUCCUA
64	CUGCAU U GAGUUG	319	AACUUG C CUUAUA
69	UUUGAU U UGUAGC	322	UUGUCCU U AAUAAAG
70	UUGAGU U GUAGCU	323	UGUCCU A AUAAAG
74	GUUUGU A GCUUUG	326	CUUAU A AAGAAU
78	GCUAGU C UUGGAGC	334	AAGAAU A CAUUGAC
80	UAGCUU U GGAGCU	338	AUAUAU U GACGGCC
91	GUUGGU A GUUGAU	380	GGAGAU A AACCAU
97	UAGGUU A UGCCAU	388	AACCAU U CUAGAC
104	AUGCAU C CCCACG	389	ACCAAU C CUAGAU
116	CAGAAU U CCCACA	392	AAUCCU A GACUACC
117	AGAAAU C CCACAG	397	CUAGAU A CCUGCA
130	AGUGAU U GGUGAA	409	CAAGAU U UCUUGU
145	GAGACU U GGCACU	410	AAGAGU U CUUGUG
155	CACUGU U UCUACU	411	AGAGUU C UUGGUG
156	ACUGGU U CUACUA	413	AGUUUU U GGUGUA
157	CUGGUU C UACUAU	419	UUGGUU A AUGACA
159	GCUUUU A CUCAUG	437	AGUGAU A AUGAAA
162	UUCUAU C AUGAAC	440	GGUAU A GAAAGU
165	UACUAU C GAACUU	447	AGAAAU U GAGAU
171	UCGAU C UGCGAU	454	UGAGAU A AACUGU
179	UGCGAU A GCCAUG	462	AACUGU U UGUUGA
192	UGAGAU C UGAGAU	463	ACUGGU U GUUGAG
200	UGAGAU U CCUGUC	466	GGUUUU U GCAGCA
201	GAGGAU C CUGUCC	479	CAAAGU U UUGAGG
206	UCCUGU U CCUGAC	480	AAAGAU U UGAGGA
207	UCCUGU C CUGACA	481	AAGAUU U GGAGAG
212	UCCUGU A CAUAAA	497	AGGACU U UACUGC
216	UGUAU A AAAUCA	498	GGACAU U UACUGA
222	UAAAAU C ACCAAU	499	GACAUU U ACUGAG

500	ACADUUU A CUGCAGU	684	UACUUUU U UCUUUUU
531	AAAGAGU C AGGCCUU	685	ACUUUUU U CUUUUUU
538	CAGGCCU U AAUUUUC	686	CUUUUUU C UUAUUUA
539	AGGCCUU A AUUUUCA	688	UUUUUUU U AUUUUAC
542	CCUUAAU U UUCAATA	689	UUUUUUU A UUUAACU
543	CUUAADU U UCAATAU	691	UUUUUUU U UAACUUA
544	UUAAUUU U CAATAUA	692	UCUUUUU U AACUUAA
545	UAADUUU C AAATAAA	693	CUUAUUU A ACUUUAC
549	UUUCAAU A UAADUUA	697	UUUAACU U AACAUUC
551	UCAATAU A AUUUUAC	698	UUUAACU A ACAUUUC
554	AUAUAUU U UAACUUC	703	UUUAACU U CUGUAAA
555	UAUAUUU U AACUUCA	704	UAACAUU C UGUAAA
556	AUAUUUU A ACUUUCG	708	AUUUUUU A AAADGUC
560	UUUAACU U CAGAGGG	715	AAADGUC C UGUUAC
561	UUUAACU C AGAGGGA	719	UGUUUUU U AACUUAA
573	GGAAAGU A AAUAUUU	720	GUUUUUU A ACUUUAA
577	AGUAAAU A UUUCAGG	724	GUUAACU U AAUAUAU
579	UAUAUUU U UCAGGCA	725	UUUAACU A AAUAUAU
580	AAUAUUU U CAGGCAU	728	ACUUUAA A GUUUUUA
581	AAUAUUU C AGGCATA	731	UAUAUAU A UUUAUGA
588	CAGGCAU A CUGACAC	733	AUAUAUU U UAUGAAA
597	UGACACU U UGUCAGA	734	UAUAUUU U AUUAAAU
598	GACACUU U GUCAGAA	735	AGUAUUU A UGAAADG
611	AAAGCAU A AAADUUC	745	AAADGUC U AUAUUU
616	AUAUAUU U CUUAAA	746	AAADGUC A AGAUUU
617	UAUAUUU C UUAUAU	752	UAUAUUU U UGUAAA
619	AAAUUUU U AAUAUU	753	AUAUUU U GGUAAU
620	AAAUUUU A AAUAUA	757	AUUUUUU A AAUAUU
625	UUUAUUU A UAUUUCA	761	GUUAUUU U AGUAUU
627	AAUAUUU A UUUCAGA	762	GUUAUUU A GUUUUUA
629	AAUAUUU U UCAGATA	765	AAUAUUU A UUUAUUU
630	AUAUAUU U CAGAUUU	767	UAUAUUU U UAUUUAA
631	UAUAUUU C AGAUUUC	768	UAUAUUU U AUUUAAU
636	UUCAGAU A UCAGAUU	769	AGUAUUU A UUUAADG
638	CAGAUUU C AGAUUCA	771	UAUUUUU U UAADGUU
644	UCAGAUU C AUUGAAG	772	AUUUAUU U AAUGUUA
647	GAADCAU U GAAGUAU	773	UUUAUUU A AUUUUAU
653	UUGAAGU A UUUUUUU	778	UUUAUUU U AUUUUUU
655	GAAGUAU U UUUCUUC	779	UAADGUU U AUUUUUU
656	AAGUAUU U UUUCUCA	783	UAADGUU A UGUUGUG
657	AGUAUUU U CUUCUUC	788	GUUAUUU U GUGUUUU
658	GUUUUUU C CUUCAGG	789	GUGUUUU U CUUAUAA
661	UUUUUUU C CAGGCAA	791	UUGUUUU C UAUAUAA
672	GCAAAAU U GAUAUAC	794	GUGUUUU A AUUAUAC
676	AAUUGAU A UACUUUU	805	UUCUAUU A AAACAAA
578	UUGAUUU A CUUUUUU		CAAAAAU A GACAAU
581	AUAUAUU U UUUUUUU		
682	UAUAUUU U UUUCUUA		

Table 12: Human IL-5 HH Ribozyme Sequences

nt. Position	HH Ribozyme Sequence
8	GCAAAGA CUGAUGAGGCCGAAAGGCCGAA AGGCGAU
9	GGCAAAG CUGAUGAGGCCGAAAGGCCGAA AAGGCGA
10	UGGCAAA CUGAUGAGGCCGAAAGGCCGAA AAAGGCG
12	UUUGGCA CUGAUGAGGCCGAAAGGCCGAA AGAAAGU
13	CUUUGGC CUGAUGAGGCCGAAAGGCCGAA AAGAAAG
36	GCUCUGA CUGAUGAGGCCGAAAGGCCGAA ACGUUCU
37	GGCUCUG CUGAUGAGGCCGAAAGGCCGAA AACGUUC
38	UGGUCUC CUGAUGAGGCCGAAAGGCCGAA AAACGUU
56	AADGCAG CUGAUGAGGCCGAAAGGCCGAA AGCAUCC
57	AAADGCA CUGAUGAGGCCGAAAGGCCGAA AAGCAUC
63	AAACUCA CUGAUGAGGCCGAAAGGCCGAA AUGCAGA
64	CAAACUC CUGAUGAGGCCGAAAGGCCGAA AADGCAG
69	GCUAGCA CUGAUGAGGCCGAAAGGCCGAA ACUCAAA
70	AGCUAGC CUGAUGAGGCCGAAAGGCCGAA AACUCAA
74	CAAGAGC CUGAUGAGGCCGAAAGGCCGAA AGCAAAC
78	GCUCCAA CUGAUGAGGCCGAAAGGCCGAA AGCUAGC
80	CAGCUC CUGAUGAGGCCGAAAGGCCGAA AGAGCUA
91	AUAACAG CUGAUGAGGCCGAAAGGCCGAA AGGCAGC
97	GADGGCA CUGAUGAGGCCGAAAGGCCGAA ACACGUA
104	CUGUGGG CUGAUGAGGCCGAAAGGCCGAA AUGGCAU
116	UUGUGGG CUGAUGAGGCCGAAAGGCCGAA AUUUCUG
117	CUUGUGG CUGAUGAGGCCGAAAGGCCGAA AUUUCUC
130	UUUCACC CUGAUGAGGCCGAAAGGCCGAA AUGCACT
145	CAGUGCC CUGAUGAGGCCGAAAGGCCGAA AGGUCUC
155	GAGUAGA CUGAUGAGGCCGAAAGGCCGAA AGCAGUG
156	UGAGUAG CUGAUGAGGCCGAAAGGCCGAA AAGCAGU
157	ADGAGUA CUGAUGAGGCCGAAAGGCCGAA AAAGCAG
159	CGAUGAG CUGAUGAGGCCGAAAGGCCGAA AGAAAGC
162	GUUCGAU CUGAUGAGGCCGAAAGGCCGAA AGUAGAA
165	AGAGUUC CUGAUGAGGCCGAAAGGCCGAA AUGAGUA
171	ADCAGCA CUGAUGAGGCCGAAAGGCCGAA AGUUCGA
179	CAUUGGC CUGAUGAGGCCGAAAGGCCGAA AUCAGCA
192	AUCCUCA CUGAUGAGGCCGAAAGGCCGAA AGUCUCA
200	GAACAGG CUGAUGAGGCCGAAAGGCCGAA AUCCUCA
201	GGAACAG CUGAUGAGGCCGAAAGGCCGAA AUCCUC
206	GUACAGG CUGAUGAGGCCGAAAGGCCGAA ACAGGAA
207	UGUACAG CUGAUGAGGCCGAAAGGCCGAA AACAGGA
212	UUUUUUG CUGAUGAGGCCGAAAGGCCGAA ACAGGAA
216	UGAUUUU CUGAUGAGGCCGAAAGGCCGAA AUGUACA
222	AGUUGGU CUGAUGAGGCCGAAAGGCCGAA AUUUUUA
245	CCUGAAA CUGAUGAGGCCGAAAGGCCGAA AUUUCUU

247 UCCCTGA CUGAUGAGGCCGAAAGGCCGAA AGAATUC
248 UUCCTUG CUGAUGAGGCCGAAAGGCCGAA AAGAATU
249 AUUCCCU CUGAUGAGGCCGAAAGGCCGAA AAAGAATU
257 GUGUGCC CUGAUGAGGCCGAAAGGCCGAA AUUCCCU
273 ACAGUUU CUGAUGAGGCCGAAAGGCCGAA ACUCUCC
291 UCCACAG CUGAUGAGGCCGAAAGGCCGAA ACCUCCU
305 UUUUGAA CUGAUGAGGCCGAAAGGCCGAA AGUCUUU
307 GUUUUUG CUGAUGAGGCCGAAAGGCCGAA AUAGUCU
308 AGUUUUU CUGAUGAGGCCGAAAGGCCGAA AAUAGUC
316 UAAGGAC CUGAUGAGGCCGAAAGGCCGAA AGUUUUU
319 UAUUAAG CUGAUGAGGCCGAAAGGCCGAA ACAAGUU
322 CUUUUUU CUGAUGAGGCCGAAAGGCCGAA AGGACAA
323 UCUUUUU CUGAUGAGGCCGAAAGGCCGAA AAGGACA
326 AUUUUUU CUGAUGAGGCCGAAAGGCCGAA AUUAAGG
334 GUCAADG CUGAUGAGGCCGAAAGGCCGAA AUUUUUU
338 GGCCGUC CUGAUGAGGCCGAAAGGCCGAA AUGUAUU
380 AUUGGUU CUGAUGAGGCCGAAAGGCCGAA ACUCUCC
388 GUCUAGG CUGAUGAGGCCGAAAGGCCGAA AUUGGUU
389 AGUCUAG CUGAUGAGGCCGAAAGGCCGAA AADUGGU
392 GGUAGUC CUGAUGAGGCCGAAAGGCCGAA AGGAUUU
397 UUGCAGG CUGAUGAGGCCGAAAGGCCGAA AGUCUAG
409 ACCAAGA CUGAUGAGGCCGAAAGGCCGAA ACUCUUG
410 CACCAAG CUGAUGAGGCCGAAAGGCCGAA AACUCUU
411 ACACCAA CUGAUGAGGCCGAAAGGCCGAA AAACUCU
413 UUAACCC CUGAUGAGGCCGAAAGGCCGAA AGAAACTU
419 UGUUCAU CUGAUGAGGCCGAAAGGCCGAA ACACCAA
437 UUUUUUU CUGAUGAGGCCGAAAGGCCGAA AUCCACTU
440 AACUUUC CUGAUGAGGCCGAAAGGCCGAA AUUAUCC
447 UAGUCUC CUGAUGAGGCCGAAAGGCCGAA ACUUUCU
454 ACCAGUU CUGAUGAGGCCGAAAGGCCGAA AGUCUCA
462 UGCAACA CUGAUGAGGCCGAAAGGCCGAA ACCAGUU
463 CUGCAAC CUGAUGAGGCCGAAAGGCCGAA AACCAGU
466 UGGCUGC CUGAUGAGGCCGAAAGGCCGAA ACAAAAC
479 CCUCCAA CUGAUGAGGCCGAAAGGCCGAA ADCTUUG
480 UCCUCCA CUGAUGAGGCCGAAAGGCCGAA AAUCUUU
481 CUUCUCC CUGAUGAGGCCGAAAGGCCGAA AAUCUUU
497 GCAGTAA CUGAUGAGGCCGAAAGGCCGAA AUGUCCU
498 UGCAGUA CUGAUGAGGCCGAAAGGCCGAA AAUGUCC
499 CUGCAGU CUGAUGAGGCCGAAAGGCCGAA AAADGUC
500 ACTGCAG CUGAUGAGGCCGAAAGGCCGAA AAAADGU
531 AAGGCCU CUGAUGAGGCCGAAAGGCCGAA ACUCUUU
538 GAAAAUU CUGAUGAGGCCGAAAGGCCGAA AGGCCUG
539 UGAAAAU CUGAUGAGGCCGAAAGGCCGAA AAGGCCU
542 UAUUGAA CUGAUGAGGCCGAAAGGCCGAA AUUAAGG
543 AAUAUGA CUGAUGAGGCCGAAAGGCCGAA AAUAAG
544 UAUAUUG CUGAUGAGGCCGAAAGGCCGAA AAAUUA
545 UUAUAUU CUGAUGAGGCCGAAAGGCCGAA AAAAUUA
549 UAAAUUA CUGAUGAGGCCGAAAGGCCGAA AUUGAAA
551 GUUAAAU CUGAUGAGGCCGAAAGGCCGAA AAUAUGA

554 GAAGTUA CUGAUGAGGCCGAAAGGCCGAA AUUAUAU
555 UGAAGUU CUGAUGAGGCCGAAAGGCCGAA AAUUAUA
556 COGAAGU CUGAUGAGGCCGAAAGGCCGAA AAAUUAU
560 CCCUCUG CUGAUGAGGCCGAAAGGCCGAA AGUUAUA
561 UCCUCU CUGAUGAGGCCGAAAGGCCGAA AAGUUAU
573 AAUAUAU CUGAUGAGGCCGAAAGGCCGAA ACUUUCC
577 CCUGAAA CUGAUGAGGCCGAAAGGCCGAA AUUUACT
579 UGCCUGA CUGAUGAGGCCGAAAGGCCGAA ADUAUUA
580 AUGCCUG CUGAUGAGGCCGAAAGGCCGAA AAUAUUU
581 UAUGCCU CUGAUGAGGCCGAAAGGCCGAA AAUAUAU
588 GUGOCAG CUGAUGAGGCCGAAAGGCCGAA AUGCCUG
597 UCCGGCA CUGAUGAGGCCGAAAGGCCGAA AGUGUCA
598 UUCUGGC CUGAUGAGGCCGAAAGGCCGAA AAGUGOC
611 AGAUAUU CUGAUGAGGCCGAAAGGCCGAA AUGCUUU
616 UUUUAAG CUGAUGAGGCCGAAAGGCCGAA AUUUUAU
617 AUUUUAU CUGAUGAGGCCGAAAGGCCGAA AAUUUAU
619 AUUAUUU CUGAUGAGGCCGAAAGGCCGAA AGAUAUU
620 UAUAUUU CUGAUGAGGCCGAAAGGCCGAA AAGAUAU
625 UGAAUAU CUGAUGAGGCCGAAAGGCCGAA AUUUUAU
627 UCUGAAA CUGAUGAGGCCGAAAGGCCGAA AUUAUUU
629 UAUUGA CUGAUGAGGCCGAAAGGCCGAA AUUAUAU
630 AUUAUCU CUGAUGAGGCCGAAAGGCCGAA AAUAUAU
631 GAUAUCU CUGAUGAGGCCGAAAGGCCGAA AAUAUAU
636 AUUCUGA CUGAUGAGGCCGAAAGGCCGAA AUUCUGA
638 UGAUUCU CUGAUGAGGCCGAAAGGCCGAA AUUAUCU
644 CUUCAAU CUGAUGAGGCCGAAAGGCCGAA AUUCUGA
647 AUACUUC CUGAUGAGGCCGAAAGGCCGAA AUGAUUC
653 AGGAAAA CUGAUGAGGCCGAAAGGCCGAA ACUUCAA
555 GGAGGAA CUGAUGAGGCCGAAAGGCCGAA AUACUUC
556 UGGAGGA CUGAUGAGGCCGAAAGGCCGAA AAUAUCU
657 CUGGAGG CUGAUGAGGCCGAAAGGCCGAA AAUAUCU
658 CCUGGAG CUGAUGAGGCCGAAAGGCCGAA AAAUAUC
661 UUGCCUG CUGAUGAGGCCGAAAGGCCGAA AGGAAAA
672 GUUAUUC CUGAUGAGGCCGAAAGGCCGAA AUUUUCC
676 AAAAGUA CUGAUGAGGCCGAAAGGCCGAA AUCAUAU
678 AAAAAAG CUGAUGAGGCCGAAAGGCCGAA AUUAUCA
681 AAGAAAA CUGAUGAGGCCGAAAGGCCGAA AGUAUAU
682 UAAGAAA CUGAUGAGGCCGAAAGGCCGAA AAGUAUA
683 AUUAAGAA CUGAUGAGGCCGAAAGGCCGAA AAAGUAU
684 AAUAAGA CUGAUGAGGCCGAAAGGCCGAA AAAAGUA
685 AAUAAG CUGAUGAGGCCGAAAGGCCGAA AAAAGU
686 UAAUAUA CUGAUGAGGCCGAAAGGCCGAA AAAAAAG
688 GUUAUAU CUGAUGAGGCCGAAAGGCCGAA AGAAAAA
689 AGUUAUA CUGAUGAGGCCGAAAGGCCGAA AAGAAAA
691 UAAGUA CUGAUGAGGCCGAAAGGCCGAA AUUAAGA
692 UUAAGUU CUGAUGAGGCCGAAAGGCCGAA AAUAAGA
693 GUUAAGU CUGAUGAGGCCGAAAGGCCGAA AAUAAG
697 GAADGUU CUGAUGAGGCCGAAAGGCCGAA AGUUAUA
698 AGAAGUU CUGAUGAGGCCGAAAGGCCGAA AAGUUAU

703	UUUACAG	CUGAUGAGGCCGAAAGGCCGAA	AUGUUAA
704	UUUUACA	CUGAUGAGGCCGAAAGGCCGAA	AADGUUA
708	GACAUUU	CUGAUGAGGCCGAAAGGCCGAA	ACAGAAU
715	GUUAACA	CUGAUGAGGCCGAAAGGCCGAA	ACAUUUU
719	UUUAGUU	CUGAUGAGGCCGAAAGGCCGAA	ACAGACA
720	AUUUAGU	CUGAUGAGGCCGAAAGGCCGAA	AACAGAC
724	UACUAUU	CUGAUGAGGCCGAAAGGCCGAA	AGUUUAC
725	AUAUAUU	CUGAUGAGGCCGAAAGGCCGAA	AAGUUAA
728	UAAAUAC	CUGAUGAGGCCGAAAGGCCGAA	AUUUAGU
731	UCAUAAA	CUGAUGAGGCCGAAAGGCCGAA	ACUAUUU
733	UUUCAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUU
734	AUUUCAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAU
735	CAUUUCA	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAU
745	AAUUCUU	CUGAUGAGGCCGAAAGGCCGAA	ACCAUUU
746	AAAUUCU	CUGAUGAGGCCGAAAGGCCGAA	AACCAUU
752	UUUACCA	CUGAUGAGGCCGAAAGGCCGAA	AUUUCUU
753	AUUUACC	CUGAUGAGGCCGAAAGGCCGAA	AAUUCUU
757	ACUAUUU	CUGAUGAGGCCGAAAGGCCGAA	ACCAUUU
761	AAUAUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUACC
762	UAAUAAC	CUGAUGAGGCCGAAAGGCCGAA	AAUUAAC
765	AAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	ACUAUUU
767	UUAAUAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUU
768	AUUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAU
769	CAUUAAA	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAU
771	AACAUUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUU
772	UAACAUU	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAU
773	AUAACAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAU
778	ACAACAU	CUGAUGAGGCCGAAAGGCCGAA	ACAUAUA
779	CACAACA	CUGAUGAGGCCGAAAGGCCGAA	AACAUUA
783	AGAACAC	CUGAUGAGGCCGAAAGGCCGAA	ACAUAUA
788	UUUAUAG	CUGAUGAGGCCGAAAGGCCGAA	ACACAAC
789	UUUAUUA	CUGAUGAGGCCGAAAGGCCGAA	AACACAU
791	GUUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGAACAC
794	UUUGUUU	CUGAUGAGGCCGAAAGGCCGAA	AUUUAGU
805	AGUUGUC	CUGAUGAGGCCGAAAGGCCGAA	AUUUUUG

Table 13: Mouse IL-5 HH Ribozyme Target Sequence

nt. Position	HH Target Sequence	nt. Position	HH Target Sequence
8	cGGuCUU c CUUUGCu	253	AGGGgcU A GaCAuAC
11	uCUUcCU U UGUgAA	259	UegACAU a CUGaAgA
12	CUUcCUU U GUgAAG	269	GaAGAAU C AAACUGU
36	GAAgacU U CAGAGuC	269	GaAGAAU c AAACugU
36	GaAgAcU u cAgAGUc	269	GAAGAaU c aAAcUgU
37	AAgacU C AGAGuCA	287	uGGGGGU A CUGUGGA
43	UcaGaGU c AUGAgAA	301	AAAugCU A UUCcAAA
58	GGAUUCU U CUGAcU	301	AAAugCU a uUCCaaA
59	GAUGCUU C UGCAcUU	303	AUGCUAU u CCAAAAc
59	gAUGcUU c uGcAcUU	303	AugCUAU U CcAAAAC
66	CUGCAcU U GAGUgUu	304	uGCUAUU C cAAAAcC
82	UGAcucU c aGcUGUG	315	AAcCUGU C aUUAADA
91	GcUgUGU c uggGCCA	318	cUGUcAU U AAUAAG
112	ugGAgaU U CCCAugA	319	UGUcAUU A AUAAAGA
113	gGAgaUU C CCAugAG	322	CaUUAUU A AAGAAAU
141	GAGACCU U GaCACaG	330	AAGAAAU A CAUUGAC
141	GAgACcU U GaCAcAg	334	AAUAcAU U GAcCGCC
158	gUCCgCU C AcCGAgC	334	AAUAcAU u GAcCGCC
167	cCGAgCU C UGUUGAc	384	AggCagU U CCUGGAu
196	UGAGGcU U CCUGUcC	385	ggCagUU C CUgGAuU
197	GAGGcUU C CUGUcCC	393	CUgGAuU A CUGCAA
197	gAGGCUU c CUGUcCC	405	CAAGAGU U cCUUGGU
202	UUCUGU c CCUAcuC	406	AAAGAUU c CUUGGUG
202	UUCUGU c CcUAcuc	409	AGUUcCU U GUGUGa
206	UGUCccU a cuCaUAA	481	UcaCAAU u UAAGUUA
212	UACUCAU a aAAaUCA	482	cAcAAAU U AAgUUAa
212	UacuCAU A AAAAUCA	483	AcAAUUU A AgUUaAa
218	UaaAaaU c aCcAGCU	483	AcAAUUU a aGUUAaA
218	UAAAAAU C ACCAgCU	495	AAAUUgU c AAcAgAU
218	uAAAAAU c acCAgCU	553	GCUGuuU c CaUUUAU
232	uaUGCAU U GGAaAAA	557	UUUcCAU U UauaUUU
241	gAGAAAU C UUCAGG	564	UUauAUU u aUgUCCU
241	gAgAaAU c UUcAGG	564	UUauaUU u AugUcCU
241	gagAAAU c UUCAGG	565	uaUAUUU a ugUCCuG
241	gAgAaAU c UUCAGg	565	UAUAUUU a UGUcUg
243	gaAAucU U UCAGgGg	569	UUUAUGU c cUGUaGU
243	GAAAUcU U UCAGGGg	569	uUUUAUGU c cUGUagU
244	AAAUcUU U CAGGGgc	613	AAAGUGU u uaaCCUU
245	AAUcUUU C AGGGgcU	614	AAgUGuU u aAcCUUU

620	UUAACcU u uDuGUAT	1407	cCagUUU A CUcCAGg
793	caAGgCU u UGuGcAU	1407	ccAgUUU a CUCCAGG
816	CUGagUU a UACUCcc	1410	gUUUaCU C CAGGaAA
818	GAgUUAU a cUCCcuC	1434	ADgCUUU U aUuUaAU
825	ACTcCcU c CccCUCA	1434	aUgcUUU U ADUUAAu
825	aCUccCU c CccCUCa	1434	aUgcUUU u AuUUAAU
839	AuCuCuU U cGUUGCA	1435	UgCUUUU a UuUaAUU
840	uCuCuUU c GUUGCAu	1435	ugcUUUU a uUUAAUU
863	cAAgUAU U cCAGGcu	1438	UUUUAAU U AAuUcug
864	AAgUAUU c CAGGcuG	1438	uUUUAUU U AAUucUg
864	AAGUUAU c caggCuG	1439	UUUAUUU A ADucUgU
913	gAAcUcU U GUcCaG	1443	UUUAuuU c UGuuAGa
917	UcUuggU c CAGuuGG	1447	ADUCUGU A AgADGUu
957	UUagcAU c CUUUcUc	1458	ugUUcaU a UUAUUUA
960	GCAuccU u UcUcCUA	1458	ugUUcaU A uUAUUUA
960	GcaUcCU u uCUcCUa	1460	UucADAU u ADUUAug
962	AUcCUuU c UCcUaGC	1461	UcADAUU A UUUADGA
975	gcccCUU u AgADAgA	1463	ADAUUAU U UADGAug
987	aGaUGAU A cuuAAUG	1475	AuGgAUU c aGUAAGU
990	UGAuACTU u AAugacU	1479	AUUcaGU A AgUUAaU
1000	UGACuCU c UugCuGA	1483	aGuAAGU u AAUAUUU
1027	CgggGCU U cCUgCUC	1483	aGUAAgU U AAUAUUU
1034	UCCUGcU C CUaUcuA	1484	GUAAgUU A aUAUUUA
1037	UgcUCcU A UcUAACU	1487	agUUAAU a UUuAuUA
1039	cUccuAU c UAACUUC	1487	AgUUAAU A UUUAUUa
1039	cUCcUAU c UAACUUC	1489	UUAAUaU U uAuUAca
1041	CcUAUcU A ACUUCaA	1489	UUAAuAU u UAUUaCA
1051	UUcAAuU U AAuAccC	1489	UUAAUAU U UAUUaCA
1148	uGAcUUU u cUuaUGU	1490	UAAUAUU u AuUAACAc
1213	GCUgGaU u UUGGAaa	1490	UAAUAUU U ADuAcAc
1213	gcUGGAU u uUgGAAa	1490	UAAUAUU U AUUAcAc
1214	cugGAUU U UGGAaaA	1491	AAUAUUU a uuACAcg
1215	ugGAUUU U GGAaaAG	1491	AAUAUUU a UuAcAcg
1234	ggGACAU c UccuUGC	1491	AAUAUUU A UuAcAcG
1236	GACAUcU c cuUGCAG	1491	AAUAUUU A UUAcAcG
1275	ugGGCCU U AcUUcUC	1494	ADuUAUU a CAcgUAU
1276	ggGCCUU A cUUcUCC	1502	cACGUaU A UaaUAUU
1280	CUUAcUU c UCcgUgU	1502	cAcgUAU a UAUAUUU
1298	UgAACTU a AGAaGcA	1507	AUAUAUU a UUcUaaU
1310	gcAAAGU a aAuACCa	1509	AUAUAUU U CUaAuAA
1310	GCAAAgU a aAUAcca	1509	aUaaUAU U CUAAUAA
1310	GcaAAgU a AAUAcca	1510	UAUAUUU C UaaUAAA
1350	AAAGCAU A AAADggU	1510	UAUAUUU C UaaUAAA
1358	AAADGGU U ggGAugU	1510	UAUAUUU c UaaUAAA
1370	UgUuaUU C AGgUAUC	1510	UaaUAUU C UAUAUAA
1375	UUCAGgU A UCAGggU	1512	aUaUUUU A AUAAAgC
1377	CAGgUAU C AGggUCA	1515	UUUAUUU A AAgCAGa
1383	UCAGggU C AcUGgAG		
1405	cccCAGU U UACUcCA		

Table 14: Human IL-5 Hairpin Ribozyme Sequences

nt. Position	Hairpin Ribozyme Sequence	Substrate
86	UACAGUA AGAA GUUCCA ACCAGAGAAACACACAGUUGUGUACAUUACUUGUA	UEGAGCU GGC UACGUGUA
151	GAGUGAA AGAA GUUCCA ACCAGAGAAACACACAGUUGUGUACAUUACUUGUA	UEGAGCU GCU UUCUACUC
172	UGGUAUC AGAA GAGUUC ACCAGAGAAACACACAGUUGUGUACAUUACUUGUA	GAGCUU GCU GAAAGGCA
203	UGUACGG AGAA GGAUUC ACCAGAGAAACACACAGUUGUGUACAUUACUUGUA	GAUUCCU GUU CCUGUACA

T.ble 15: Mouse IL-6 Hairpin Ribozyme Sequences

nt. Position	Hairpin Ribozyme Sequence		Substrate
75	ACUUGAGA	AGAA GACAC	ACUUGAGA
83	CCAGACAC	AGAA GAGGU	ACUUGA GUC UGUUGG
147	GAGGGAC	AGAA GUGUA	UGACACA GCU GUUGGUC
150	GGGAGGG	AGAA GUGUG	CACAGU GUC GGUUAC
154	GUUGGUG	AGAA GACGC	GUUGGUC GCU CAGGAGC
168	UGUUGUC	AGAA GAGUC	GAGGUC GCU GACAGCA
199	UGAGUAGG	AGAA GAGGC	GUUGU GUC GUUUGCA
274	GUUGGAG	AGAA GUGUA	UGAGU GUC GUUGGAG
381	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
454	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
499	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
548	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
701	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
710	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
870	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
919	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
1030	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
1170	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
1205	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
1402	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG
1421	GUUGGAG	AGAA GUGUG	GUUGGAG GCU GUUGGAG

Table 16 : Mouse IL-5 Hairpin Ribozyme Sequences

nt. Position	Hairpin Ribozyme Sequence	Substrate
75	AGCUGAGA AGAA GACAC ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	GUGUUCU GAC UUUACGU
80	CCAGACAC AGAA GAGAGU ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	ACUUCUA GUU GUGUUGG
147	GNGGGAC AGAA GUGUCA ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	UGACACA GUU GUUUGUC
150	GUUGGGG AGAA GUGUGU ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	CACAGCU GUC GGUUGAC
154	GUUGGGU AGAA GACAGC ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	GUUGUCC GUU CACGGAC
168	UGUUGUC AGAA GAGUUC ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	GAGUUCU GUU GACAGCA
199	UGGUGGG AGAA GGAAGC ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	GUUUUCU GUC CUUACUA
274	CUUCCAG AGAA GUUUGA ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	UCAAACU GUC GUUGGGG
381	AAUCCAG AGAA GUUUGU ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	CGAGCAU GUU CUUGAAU
454	CACUUGG AGAA GUUCAG ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	CUAGCAU GUU CUUGGUG
499	GUUUUCC AGAA GUUGAC ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	GUCACCA GAU GCMAAAC
548	UAAUUGA AGAA GCUAUU ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	AUAUUCU GUU UUCUUAU
701	CGGAGGG AGAA GAAAUU ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	AAUUUCU GAU CUUUUCC
710	GAGAGGA AGAA GGAGGA ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	UUUUUCU GGC UUUUUUC
870	AGUCAA AGAA GUUUG ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	CUAGCAU GAC UUGAACU
919	CUUGUCC AGAA GGUCCA ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	UGGUCCA GAU GGAACAG
1030	UUGUUGG AGAA GGAGGC ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	GUUUUCU GUU CUUUAUA
1170	AUGGACA AGAA GAUUGA ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	UGAAUCA GAC UGUUCAU
1205	CAAAUUC AGAA GUUUGA ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	UGAGACA GUU GGUUUUG
1402	CUUGAGUA AGAA GGGGGA ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	UUUUUCA GUU UAUUCCG
1421	AAACUAC AGAA GUUUUU ACCAGAGAAACACACGUGUGGURCAUUPACUUGUA	AAAAACA GAU GUUUUGU

Table 17

Mouse *re/ A* HH Target sequence

nt. Position HH Target Sequence nt. Position HH Target Sequence

19	AAUGGCU a caCaGgA	467	cCAGGCU c cuGuUCg
22	aGCCcU a cGUgGUG	469	AAGCCAU u AGcCAGC
26	CcUCaU u GcGgACa	473	UuUGAGU C AGauCAG
93	GAuUGU U uCCcUc	481	AGCGaAU C CAGACCA
94	AuUGGU u CCCCcA	501	AAcCCCU U uCAGGUU
100	UuCCCU C AUcUuUc	502	AcCCCU u CAGGUUc
103	CCUcAU C UuCCcU	508	UuCAcGU U CUUAUAG
105	CUcAUcU U uCCcUcA	509	uCAcGU C CUUAAGA
106	UCAUcU u CCcUcAG	512	cGUCCU A UAGAAGGA
129	CAGGCU C UGGgCCu	514	UCCCUA A GAgGAGC
138	GGgCCU A UGUgGAG	534	GGGAGU A uGACuUG
148	UGGAGU C AUcGAcC	556	UGGcCU C UGUUCC
151	AGAUAU c GAaCAGC	561	CUUGCU U CCAGGUG
180	AUGGcU U CCcUAu	562	UCUGCU C CAGGUGA
181	UGGcU C CGCUAA	585	aAgCCAU u AGcCAGc
186	UUCcGU A uAAaUGC	598	GGCCCU C CuCCUGa
204	GGGcGU C aGGGGC	613	CcCCGU C CUcUcAc
217	GCAGAU u CUuGGCG	616	CUGUCCU c uCAcAUc
239	CACAGU A CCACCA	617	GuCCCU C CCAGcC
262	CCACAU C AAGAUcA	620	CCUCCU C AgCCAug
268	UCAAGU C AAUGGCU	623	UCCUgcU u CCACUc
276	AAUGGCU A CACAGGA	628	AUCCgAU u UUUGAA
301	UuCGaU C UCCUGG	630	CCgADuU U UGAuAAc
303	CGaAUcU C CCUGGUC	631	CgADuUU U GAuAAcC
310	CCUGGU C ACCAAGG	638	UGgCcAU u GUuUCC
323	GGcCCU C CUcUgA	661	CCGAGU C AAGAUcU
326	uCCaCCU C ACCGGCC	667	UCAAGU C UGCCGAG
335	CCGGCU C AuCCaCA	687	CGgAACT C UGGgAGC
349	AuGAaCU U GUgGGgA	700	GCTGCCU C GGUGGGG
352	AGaUcAU c GAaCAGc	715	ADGAGU C UUCuUgC
375	GADGGCU a CUADGAG	717	GAGAUcU U CuUgCUg
376	AUGGucU C UccGgAG	718	AGAUCUU C uUgCUGU
378	GGCUaCU A UGAGGCU	721	UucUCCU c CauUGcG
391	CUGAcCU C UGCCCAG	751	AAgACAU U GAGGUGU
409	GCAGAU C CAuAGcU	759	GAGGUGU A UUUCACG
416	CCgCAGU a UCCAuAg	761	GGUGUAU U UCACGGG
417	CAuAGcU U CCAGAAC	762	GUGUAUU U CACGGGA
418	AuAGcUU C CAGAAC	763	UGUAUUU C ACGGGAC
433	UGGGgAU C CAGUGUG	792	CGAGGCU C CUUUUCu
795	GGCUCCU U UUCuCAA	1167	GAUGAGU U UuCCcCC
796	GUUCCU U UCuCAAG	1168	AUGAGUU U uCCcCCA
797	CUCCUUU U CuCAAGC	1169	UGAGUUU u CCcCCAU
798	UCCUUUU C uCAAGCU	1182	AUGcUGU U aCCaUcA
829	UGGCAU U GUGUCC	1183	UGcUGUU a CCaUcAG

834	AUUGUGU U CCGGACu	1184	GGccccU C CUcCUGa
835	UUGUGUU C CCGACuC	1187	GUccCuU c CUcaGCCe
845	GACuCCU C CgUACGC	1188	UUaCCaU C aGGGCAG
849	CUUCCgU A CGCcGAC	1198	GGgAGuU u AGuCuGa
872	cCAGGCU C CUGUuCG	1209	CAGcCCU a caCCUUC
883	UuCGaGU C UCCADGC	1215	cuGGCCU U aGCaCCG
885	CGaGUCU C CADGCAG	1229	GGuCCCU u CCucAGc
905	GCGGCCU U CuGAuCG	1237	CCCAGcU C CUGCCCC
906	CGGCCU C uGAuCGe	1250	CCAGcCU C CAGgCuC
919	GcGAGCU C AGUGAGC	1268	CCCaGCU C CuGCCcc
936	AUGGAgU U CCAGUAC	1279	CCADGGU c cCuucCu
937	UGGAgUU C CAGUACu	1281	gUGGgcU C AGCUgcG
942	UCCAGU A CuUGCCA	1286	AUgAGuU u UccCCCA
953	GCCucAU c CAcauGA	1309	CuCCUGU u CgAGUCu
962	AGAuGAU C GcCACCG	1315	cCCCAGU u CUAaCCC
965	CagUacU u gCCaGAc	1318	CAGUuCU A aCCCCgG
973	ACCGGAU U GAaGAGA	1331	gGGuCCU C CcCAGuC
986	GAgACcU u cAAGagu	1334	CuuUuCU C AaGCUGa
996	AGGACcU A UGAGACC	1389	ACCGUGU C gGAaGCC
1005	GAGACCU U CAAGAGu	1413	CUGCAGU U UGAUGcU
1006	AGACCUU C AAGAGuA	1414	UGCAGUU U GAUGcUG
1015	AGAGuAU C AUGAAGA	1437	GGGGCCU U GCUUGGC
1028	GAAGAGU C CUUUCaA	1441	CCUUGCU U GGCAACA
1031	GAGUCCU U UCAauGG	1467	GgaGUGU U CACAGAC
1032	AGUCCUU U CAauGGA	1468	gaGUGUU C ACAGACC
1033	GUCCUUU C AauGGAC	1482	CUGGCAU C uGUgGAC
1058	CGGCCU C CAaCcCG	1486	CuUCgGU a GggAACTU
1064	UaCACCU u GAuCCAa	1494	GACAACU C aGAGUUU
1072	GgCGuAU U GCUUGGC	1500	UCaGAGU U UCAGCAG
1082	UGUGCCU a CCGaAaA	1501	CaGAGUU U CAGCAGC
1083	aaGCCUU C CCGaAGu	1502	aGAGUUU C AGCAGCU
1092	CGaAaCU C AaCUUCU	1525	gGuGCAU c CCUGUGu
1097	CUCAaCU U CUGUCCC	1566	AUGGAGU A CCCUGAa
1098	UCAaCUU C UGUCCCC	1577	UGAaGCU A UAACTCG
1102	CUUCUGU C CCCAAGC	1579	AaGCUAU A ACTCGCC
1125	CAGCCCU A caCCUUC	1583	UAUAACU C GCUgGU
1127	GCCaUAU a gCcUuAC	1588	CUcUCCU A GaGAggG
1131	cAUCCCU c agCacCA	1622	CCCAGCU C CUGCCcC
1132	AcaCCUU c cCagCAU	1628	UCCUGCU u CggUaGG
1133	UCCaUcU c CagCuUC	1648	CGGGGCU u CCCAADG
1137	UUUACuU u AgCgCgc	1660	cUGaCCU C ugccCAG
1140	cCagCAU C CCUeAGC	1663	cuCUgCU U cCAGGuG
1153	GCACCAU C AACTuUG	1664	uCUgCUU c CAGGuGA
1158	AUCAACU u UGAUGAG	1665	CUCgcUU u cGGAGgU
1680	GAAGACU U CUCCUCC		
1681	AAGACUU C UCCUCCA		
1683	GACTUUCU C CUCCAUU		
1686	UUCUCCU C CADUGCG		
1690	CCUCCAU U GCGACA		

1704	AUGGACU U CUCUGCU
1705	UGGACUU C UCUGCUC
1707	GACUUCU C UGCUCTU
1721	UUUGAGU C AGAUCAG
1726	GUCAGAU C AGCUCCU
1731	AUCAGCU C CUAAGGU
1734	AGCUCCU A AGGUGCU
1754	CAUGUCU C CCAAGAG

Table 18

Human *rel A* HH Target Sequences

nt. Position HH Target Sequence nt. Position HH Target Sequence

19	AAUGGCU C GUCUGUA	467	GCAGGCU A UCAGUCA
22	GGCUCGU C UGUAGUG	469	AGGCUAU C AGUCAGC
26	CGUCUGU A GUGCAGG	473	UAUCAGU C AGCGCAU
93	GAACUGU U CCCCCUC	481	AGCGCAU C CAGACCA
94	AACUGUU C CCCCCA	501	AACCCCU U CCAAGUU
100	UCCCCCU C AUCUCCC	502	ACCCCUU C CAAGUUC
103	CCUCAU C UUCGCGG	508	UCCAAGU U CCUAUAG
105	CUCAUCU U CCGGCA	509	CCAAGUU C CUAUAGA
106	UCAUCUU C CCGGCG	512	AGUUCUU A UAGAAGA
129	CAGGCU C UGGCCCC	514	UUCCUAU A GAAGAGC
138	GGCCCCU A UGUGGAG	534	GGGGACT A CGACCTG
148	UGGAGAU C AUUGAGC	556	UGCGGCU C UGCUUCC
151	AGAUCAU U GAGCAGC	561	CCUCGUU U CCAGGUG
180	AUGGCGU U CCGCUAC	562	UCUGCUU C CAGGUGA
181	UGGCGUU C CGCUACA	585	GACCCAU C AGGCAGG
186	UUCGCGU A CAAGUGC	598	GGCCCCU C CGCCTGC
204	GGGCGCU C CGGGGCG	613	CGCCUGU C CUUCCUC
217	GCAGCAU C CCAGGCG	616	CUGUCCU U CCUCAUC
239	CACAGAU A CCAACCA	617	UGUCCUU C CUCAUCC
262	CCACCAU C AAGAUCA	620	CCUUCUU C AUCCCAU
268	UCAAGAU C AADGGCU	623	UCUCAU C CCAUUCU
276	AAUGGCU A CACAGGA	628	AUCCCAU C UUUGACA
301	UGCGCAU C UCCCUGG	630	CCCACUU U UGACAAU
303	CGCAUCU C CCUGGUC	631	CCAUCUU U GACAAUC
310	CCUUGGU C ACCAAGG	638	UGACAAU C GUGCCCC
323	GGACCCU C CUCAACG	661	CGGAGCU C AAGAUUU
326	CCCUCCU C ACCGGCC	667	UCAAGAU C UGCGGAG
335	CCGGCCU C ACCCCCA	687	CGAAACT C UGGCAGC
349	ACGAGCU U GUAGGAA	700	GUUGCCU C GUGGGGG
352	AGCUUGU A GGAAGG	715	AUGAGAU C UUCCUAC
375	GAUGGCU U CUADGAG	717	GAGAUUU U CCUACUG
376	AUGGCUU C UAUGAGG	718	AGAUUUU C CUACUGU
378	GGCUUCU A UGAGGCU	721	UCUUCUU A CUGUGUG
391	CUAGAGU C UGCCCCG	751	AGGACAU U GAGGUGU
409	GUUGCAU C CACAGUU	759	GAGGUGU A UUUCACG
416	CCACAGU U UCCAGAA	761	GGUGUAU U UCACGGG
417	CACAGUU U CCAGAAC	762	GUGUAUU U CACGGGA
418	ACAGUUU C CAGAAC	763	UGUAUUU C ACCGGAC
433	UGGGAUU C CAGUGUG	792	CGAGGCU C CUUUUCG
795	GGCUCCU U UUGCAA	1167	GAUGAGU U UCCACC
796	GUUCCUU U UCGCAAG	1168	AUGAGUU U CCCACCA
797	CUCCUUU U CGCAAGC	1169	UGAGUUU C CCACCAU
798	UCCUUUU C GCAAGCU	1182	AUGGUGU U UCCUUUU
829	UGGCCAU U GUGUCC	1183	UGGUGUU U CCUUCUG
834	AUUGUGU U CCGGACC	1184	GGUGUUU C CUUCUGG

835	UUGUGUU C CGGACCC	1187	GUUUCUU U CUGGGCA
845	GACCCUU C CCUACGC	1188	UUUUCUU C UGGGCAG
849	CCUCCUU A CGCAGAC	1198	GGCAGAU C AGCCAGG
872	GCAGGCU C CUGUGCG	1209	CAGGCCU C GGCCUUG
883	UGCGUGU C UCCAUCC	1215	UCCGCCU U GGCCCCG
885	CGUGUCU C CAUGCAG	1229	GGCCCCU C CCCAAGU
905	GCGGCCU U CCGACCG	1237	CCCAAGU C CUGCCCC
906	CGGCCUU C CGACCGG	1250	CCAGGCU C CAGCCCC
919	GGGAGCU C AGUGAGC	1268	CCUGCU C CAGCCAU
936	AUGGAUU U CCAGUAC	1279	CCAUGGU A UCAGCUC
937	UGGAUUU C CAGUACC	1281	AUGGUUU C AGCUCUG
942	UUCCAGU A CCUGCCA	1286	AUCAGCU C UGGCCCA
953	GCCAGAU A CAGACGA	1309	CCCCUGU C CCAGUCC
962	AGACGAU C GUACCCG	1315	UCCAGU C CUAGCCC
965	CGAUCCU C ACOGGAU	1318	CAGUCCU A GCCCCAG
973	ACCGGAU U GAGGAGA	1331	AGGCCUU C CUCAGGC
986	GAAACGU A AAAGGAC	1334	CCUCCU C AGGCUGU
996	AGGACAU A UGAGACC	1389	AGCUGU C AGAGGCC
1005	GAGACCU U CAAGAGC	1413	CUGCAGU U UGADGAU
1006	AGACCUU C AAGAGCA	1414	UGCAGUU U GAUGADG
1015	AGAGCAU C ADGAAGA	1437	GGGGCCU U GCUUGGC
1028	GAAGAGU C CUUUCAG	1441	CCUUGCU U GGCAACA
1031	GAGUCCU U UCAGCGG	1467	GCUUGU U CACAGAC
1032	AGUCCUU U CAGCGGA	1468	CUGUGUU C ACAGACC
1033	GUCCUUU C AGCGGAC	1482	CUGGCAU C CGUCGAC
1058	CCGGCCU C CAUCCUG	1486	CAUCCGU C GACAACT
1064	UCCACCU C GACGCAU	1494	GACAACT C CGAGUUU
1072	GACGCAU U GCUUGGC	1500	UCCAGU U UCAGCAG
1082	UGUGCCU U CCGGCAG	1501	CCGAGU U CAGCAGC
1083	GUGCCUU C CCGCAGC	1502	CGAGUUU C AGCAGCU
1092	CGCAGCU C AGCUUCU	1525	AGGGCAU A CCUGUGG
1097	CUCAGCU U CUGUCCC	1566	AUGGAGU A CCGUGAG
1098	UCAGCUU C UGUCCCC	1577	UGAGGCU A UACUCG
1102	CUUCUGU C CCCAAGC	1579	AGGCUAU A ACUCGCC
1125	CAGCCCU A UCCUUUU	1583	UAUAACU C GCUUAGU
1127	GCCCUAU C CCUUUAC	1588	CUCGCCU A GUGACAG
1131	UAUCCCU U UACGUCA	1622	CCCAGCU C CUGCUCC
1132	AUCUCCU U ACGUCAU	1628	UCCUGCU C CACUGGG
1133	UCCUUUU A CGUCAUC	1648	CGGGGCU C CCCAUG
1137	UUUACGU C AUCUCCG	1660	AUGGCCU C CUUUCAG
1140	ACGUCAU C CCUGAGC	1663	GCCUCCU U UCAGGAG
1153	GCACCAU C AACTADG	1664	CCUCCUU U CAGGAGA
1158	AUCAACT A UGADGAG	1665	CUCCUUU C AGGAGAU
1680	GAAGACU U CUCCUCC		
1681	AAGACTU C UCCUCCA		
1683	GACUUCU C CUCCAUU		
1686	UUUCCCU C CAUUGCG		
1690	CCUCCAU U GCGGACA		
1704	AUGGACU U CUCAGCC		

1705	UGGACUU C UCAGCCC
1707	GACUUCU C AGCCCTG
1721	GCTGAGU C AGAUCAG
1726	GUCAGAU C AGCUCCU
1731	AUCAGCU C CUAAGGG
1734	AGCUCCU A AGGGGGU
1754	CUGCCCU C CCCAGAG

Table 19
 Mouse *rel A* HH Ribozyme Sequences
 nt. HH Ribozyme Sequence
 Sequence

19	UCCUGUG	CUGAUGAGGCCGAAAGGCCGAA	AGCCAUU
22	CACCACG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCU
26	UGUCCGC	CUGAUGAGGCCGAAAGGCCGAA	AUGGAGG
93	GAGGGGA	CUGAUGAGGCCGAAAGGCCGAA	ACAGADC
94	UGAGGGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGAU
100	GAAAGAU	CUGAUGAGGCCGAAAGGCCGAA	AGGGGAA
103	AGGGAAA	CUGAUGAGGCCGAAAGGCCGAA	AUGAGGG
105	UGAGGGA	CUGAUGAGGCCGAAAGGCCGAA	AGAUAG
106	CUGAGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGADGA
129	AGGCCCA	CUGAUGAGGCCGAAAGGCCGAA	AAGCCUG
138	CUCCACA	CUGAUGAGGCCGAAAGGCCGAA	AAGGCCC
148	GUUCGAU	CUGAUGAGGCCGAAAGGCCGAA	AUCUCCA
151	GCUGUUC	CUGAUGAGGCCGAAAGGCCGAA	AUGADCU
180	AUAGCGG	CUGAUGAGGCCGAAAGGCCGAA	AUCGCAU
181	UAUAGCG	CUGAUGAGGCCGAAAGGCCGAA	AADCGCA
186	GCAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGCUGAA
204	GCCCGCU	CUGAUGAGGCCGAAAGGCCGAA	AGCGCCC
217	CGCCAGG	CUGAUGAGGCCGAAAGGCCGAA	AUAUCGC
239	UUGGUGG	CUGAUGAGGCCGAAAGGCCGAA	AUCUGUG
262	UGAUCUU	CUGAUGAGGCCGAAAGGCCGAA	AUGGUGG
268	AGCCAUU	CUGAUGAGGCCGAAAGGCCGAA	AUCUUGA
276	UCCUGUG	CUGAUGAGGCCGAAAGGCCGAA	AGCCAUU
301	CCAGGGA	CUGAUGAGGCCGAAAGGCCGAA	AUCUGAA
303	GACCAAG	CUGAUGAGGCCGAAAGGCCGAA	AGAUUCG
310	CCUUGGU	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGG
323	UCAGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGCC
326	GGCCGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGA
335	UGUGGAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCGG
349	UCCCCAC	CUGAUGAGGCCGAAAGGCCGAA	AGUUCAU
352	GCUGUUC	CUGAUGAGGCCGAAAGGCCGAA	AUGADCU
375	CUCAUAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCADC
376	CUCCGGA	CUGAUGAGGCCGAAAGGCCGAA	AGACCAU
378	AGCCUCA	CUGAUGAGGCCGAAAGGCCGAA	AGUAGCC
391	CUGGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAG
409	AGCUAUG	CUGAUGAGGCCGAAAGGCCGAA	AUAUCGC
416	CUAUUGA	CUGAUGAGGCCGAAAGGCCGAA	ACUGCCG
417	GUUCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGCUAUG
418	GGUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AAGCUAU
433	CACACUG	CUGAUGAGGCCGAAAGGCCGAA	AUCCCCA
467	CGAACAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCUGG
469	GCUGGCU	CUGAUGAGGCCGAAAGGCCGAA	AUGGCUU
473	CUGAUUC	CUGAUGAGGCCGAAAGGCCGAA	ACTUCAA
481	UGGUCUG	CUGAUGAGGCCGAAAGGCCGAA	AUUCGCU

501	AACGUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUTU
502	GAACGUG	CUGAUGAGGCCGAAAGGCCGAA	AAGGGGU
508	CUADTAG	CUGAUGAGGCCGAAAGGCCGAA	ACGUGAA
509	UCUADAG	CUGAUGAGGCCGAAAGGCCGAA	AACGUGA
512	UCCUCUA	CUGAUGAGGCCGAAAGGCCGAA	AGGAACG
514	GCTCCTC	CUGAUGAGGCCGAAAGGCCGAA	ADTAGGA
534	CAAGUCA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCC
556	GGAAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCA
561	CACCTUG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
562	UCACCTG	CUGAUGAGGCCGAAAGGCCGAA	AAGCAGA
585	GCUGGCU	CUGAUGAGGCCGAAAGGCCGAA	AUGGCUU
598	UCAGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGCC
613	GUGAGAG	CUGAUGAGGCCGAAAGGCCGAA	ACAGGGG
616	GADGUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGACAG
617	GGCTGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGGAC
620	CADGGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGG
623	GAGADGG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGGA
628	UADCAA	CUGAUGAGGCCGAAAGGCCGAA	ADCGGAU
630	GUADCA	CUGAUGAGGCCGAAAGGCCGAA	AAADCGG
631	GGUADC	CUGAUGAGGCCGAAAGGCCGAA	AAAADCG
638	GGAACAC	CUGAUGAGGCCGAAAGGCCGAA	AUGGCCA
661	AGAUCUU	CUGAUGAGGCCGAAAGGCCGAA	AGCTCGG
667	CUGGGCA	CUGAUGAGGCCGAAAGGCCGAA	ADCTUGA
687	GCTCCCA	CUGAUGAGGCCGAAAGGCCGAA	AGTUCGG
700	CCCCACC	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGC
715	GCAAGAA	CUGAUGAGGCCGAAAGGCCGAA	ADCTCAU
717	CAGCAAG	CUGAUGAGGCCGAAAGGCCGAA	AGADTUC
718	ACAGCAA	CUGAUGAGGCCGAAAGGCCGAA	AAGADCU
721	CGCA AUG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGAA
751	ACACTUC	CUGAUGAGGCCGAAAGGCCGAA	AUGGCUU
759	CGUGAAA	CUGAUGAGGCCGAAAGGCCGAA	ACACCTC
761	CCCGUGA	CUGAUGAGGCCGAAAGGCCGAA	ADACACC
762	UCCCGUG	CUGAUGAGGCCGAAAGGCCGAA	AAATACAC
763	GUCCCGU	CUGAUGAGGCCGAAAGGCCGAA	AAATACA
792	AGAAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCTCG
795	UUGAGAA	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCC
796	CUUGAGA	CUGAUGAGGCCGAAAGGCCGAA	AAGGAGC
797	GCUUGAG	CUGAUGAGGCCGAAAGGCCGAA	AAAGGAG
798	AGCTUGA	CUGAUGAGGCCGAAAGGCCGAA	AAAAGGA
829	GGAACAC	CUGAUGAGGCCGAAAGGCCGAA	AUGGCCA
834	AGGCCGG	CUGAUGAGGCCGAAAGGCCGAA	ACACAAD
835	GAGUCCG	CUGAUGAGGCCGAAAGGCCGAA	AACACAA
845	GCGUACG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGUC
849	GUCCGGC	CUGAUGAGGCCGAAAGGCCGAA	ACGGAGG
872	CGAACAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCTUG
883	GCAUGGA	CUGAUGAGGCCGAAAGGCCGAA	ACTUCGA
885	CUGCADG	CUGAUGAGGCCGAAAGGCCGAA	AGACTUC
905	CGADACG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCGC
906	GCGADCA	CUGAUGAGGCCGAAAGGCCGAA	AAGGCCG

919	GCUCACU	CUGADGAGGCCGAAAGGCCGAA	AGCUCGC
936	GUACUGG	CUGADGAGGCCGAAAGGCCGAA	ACTUCCAU
937	AGUACUG	CUGADGAGGCCGAAAGGCCGAA	AACUCCA
942	UGGCAAG	CUGADGAGGCCGAAAGGCCGAA	ACUGGAA
953	UCADGUG	CUGADGAGGCCGAAAGGCCGAA	ADGAGGC
962	CGGUGGC	CUGADGAGGCCGAAAGGCCGAA	ADCAUCU
965	GUCUGGC	CUGADGAGGCCGAAAGGCCGAA	AGUAUCU
973	UCUCUUC	CUGADGAGGCCGAAAGGCCGAA	ADCCGGU
986	ACUCUUG	CUGADGAGGCCGAAAGGCCGAA	AGGUCUC
996	GGUCUCA	CUGADGAGGCCGAAAGGCCGAA	AGGUCU
1005	ACUCUUG	CUGADGAGGCCGAAAGGCCGAA	AGGUCUC
1006	UACUCUU	CUGADGAGGCCGAAAGGCCGAA	AAGGUCU
1015	UCUCUAC	CUGADGAGGCCGAAAGGCCGAA	ADACUCU
1028	UUGAAAG	CUGADGAGGCCGAAAGGCCGAA	ACUCUUC
1031	CCAUUGA	CUGADGAGGCCGAAAGGCCGAA	AGGACTC
1032	UCCAUUG	CUGADGAGGCCGAAAGGCCGAA	AAGGACU
1033	GUCCAUU	CUGADGAGGCCGAAAGGCCGAA	AAAGGAC
1058	CGGUGUG	CUGADGAGGCCGAAAGGCCGAA	AGGCCGG
1064	UUGGADC	CUGADGAGGCCGAAAGGCCGAA	AGGUGUA
1072	GCACAGC	CUGADGAGGCCGAAAGGCCGAA	ADACGCC
1082	UUUCGGG	CUGADGAGGCCGAAAGGCCGAA	AGGCACA
1083	ACUUCGG	CUGADGAGGCCGAAAGGCCGAA	AAGGCUU
1092	AGAAGUU	CUGADGAGGCCGAAAGGCCGAA	AGUUCUG
1097	GGGACAG	CUGADGAGGCCGAAAGGCCGAA	AGUUGAG
1098	GGGGACA	CUGADGAGGCCGAAAGGCCGAA	AAGUUGA
1102	GCUUGGG	CUGADGAGGCCGAAAGGCCGAA	ACAGAAG
1125	GAAGGUG	CUGADGAGGCCGAAAGGCCGAA	AGGGCTG
1127	GUAAGGC	CUGADGAGGCCGAAAGGCCGAA	ADUAGGC
1131	UGGUGCU	CUGADGAGGCCGAAAGGCCGAA	AGGGADG
1132	AUGCUGG	CUGADGAGGCCGAAAGGCCGAA	AAGGUGU
1133	GAAGCUG	CUGADGAGGCCGAAAGGCCGAA	AGADGGA
1137	GCGCGCU	CUGADGAGGCCGAAAGGCCGAA	AAGUAAA
1140	GCTGAGG	CUGADGAGGCCGAAAGGCCGAA	AUGCUGG
1153	CRAAGUU	CUGADGAGGCCGAAAGGCCGAA	AUGGUGC
1158	CUCAUCA	CUGADGAGGCCGAAAGGCCGAA	AGUUGAU
1167	GGGGGAA	CUGADGAGGCCGAAAGGCCGAA	ACTUCAC
1168	UGGGGGA	CUGADGAGGCCGAAAGGCCGAA	AACUCCU
1169	ADGGGGG	CUGADGAGGCCGAAAGGCCGAA	AAACUCA
1182	UGADGGU	CUGADGAGGCCGAAAGGCCGAA	ACAGCAU
1183	CUGADGG	CUGADGAGGCCGAAAGGCCGAA	AACAGCA
1184	UCAGGAG	CUGADGAGGCCGAAAGGCCGAA	AGGGGCC
1187	GGCUGAG	CUGADGAGGCCGAAAGGCCGAA	AAGGGAC
1188	CUGCCCU	CUGADGAGGCCGAAAGGCCGAA	AUGGUAA
1198	UCAGACU	CUGADGAGGCCGAAAGGCCGAA	AACUCCC
1209	GAAGGUG	CUGADGAGGCCGAAAGGCCGAA	AGGGCTG
1215	CGGUGCU	CUGADGAGGCCGAAAGGCCGAA	AGGCCAG
1229	GCTGAGG	CUGADGAGGCCGAAAGGCCGAA	AGGGACC
1237	GGGGCAG	CUGADGAGGCCGAAAGGCCGAA	AGCUGGG
1250	GAGCCTG	CUGADGAGGCCGAAAGGCCGAA	AGGCTGG

1268	GGGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGG
1279	AGGAAGG	CUGAUGAGGCCGAAAGGCCGAA	ACCAUGG
1281	CGCAGCT	CUGAUGAGGCCGAAAGGCCGAA	AGCCAC
1286	UGGGGA	CUGAUGAGGCCGAAAGGCCGAA	AACUCAU
1309	AGACUCG	CUGAUGAGGCCGAAAGGCCGAA	ACAGGAG
1315	GGGUAG	CUGAUGAGGCCGAAAGGCCGAA	ACUGGGG
1318	CGGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGAACTG
1331	GACUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGACCC
1334	UCAGCTU	CUGAUGAGGCCGAAAGGCCGAA	AGAAAAG
1389	GGCUCC	CUGAUGAGGCCGAAAGGCCGAA	ACAGCGU
1413	AGCAUCA	CUGAUGAGGCCGAAAGGCCGAA	ACTGCAG
1414	CAGCAUC	CUGAUGAGGCCGAAAGGCCGAA	AACUGCA
1437	GCCAAGC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCC
1441	UGUUGCC	CUGAUGAGGCCGAAAGGCCGAA	AGCAAGG
1467	GUUGUG	CUGAUGAGGCCGAAAGGCCGAA	ACACTCC
1468	GGUCUGU	CUGAUGAGGCCGAAAGGCCGAA	AACACTC
1482	GUCCACA	CUGAUGAGGCCGAAAGGCCGAA	AUGCCAG
1486	AGUCCOC	CUGAUGAGGCCGAAAGGCCGAA	ACCGAAG
1494	AAACUCU	CUGAUGAGGCCGAAAGGCCGAA	AGUUGCC
1500	CUGCUGA	CUGAUGAGGCCGAAAGGCCGAA	ACTCUGA
1501	GCUCUG	CUGAUGAGGCCGAAAGGCCGAA	AACUCUG
1502	AGCUGCU	CUGAUGAGGCCGAAAGGCCGAA	AAACUCU
1525	ACACAGG	CUGAUGAGGCCGAAAGGCCGAA	AUGCACC
1566	UUCAGGG	CUGAUGAGGCCGAAAGGCCGAA	ACTCCAU
1577	CGAGUUA	CUGAUGAGGCCGAAAGGCCGAA	AGCUUCA
1579	GGCGAGU	CUGAUGAGGCCGAAAGGCCGAA	AUAGCTU
1583	ACCAGGC	CUGAUGAGGCCGAAAGGCCGAA	AGUUAUA
1588	CCUCUC	CUGAUGAGGCCGAAAGGCCGAA	AGGAGAG
1622	GGGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGG
1628	CCUACCG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGGA
1648	CADUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGCCCCG
1660	CDGGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGUCAG
1663	CACCTUG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
1664	UCACTUG	CUGAUGAGGCCGAAAGGCCGAA	AAGCAGA
1665	ACCTCCG	CUGAUGAGGCCGAAAGGCCGAA	AAGCGAG
1680	GGAGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCUUC
1681	UGGAGGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUCUU
1683	AADGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGUC
1686	CGCAUUG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGAA
1690	UGUCCGC	CUGAUGAGGCCGAAAGGCCGAA	AUGGAGG
1704	AGCAGAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCAU
1705	GAGCAGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCA
1707	AAGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGUC
1721	CUGAUCU	CUGAUGAGGCCGAAAGGCCGAA	ACTUCAA
1726	AGGAGCU	CUGAUGAGGCCGAAAGGCCGAA	AUCUGAC
1731	ACCTUAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGAU
1734	AGCACTU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCU
1754	CUCUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGCACUG

Table 20
Human *rel A* HH Ribozyme Sequences
nt. Position HH Ribozyme Sequences

19	UACAGAC	CUGAUGAGGCCGAAAGGCCGAA	AGCCAUU
22	CACUACA	CUGAUGAGGCCGAAAGGCCGAA	ACGAGCC
26	CGUGCAC	CUGAUGAGGCCGAAAGGCCGAA	ACAGACG
93	GAGGGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGUUC
94	UGAGGGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGUU
100	GGAAGAU	CUGAUGAGGCCGAAAGGCCGAA	AGGGGGA
103	CCGGGAA	CUGAUGAGGCCGAAAGGCCGAA	ADGAGGG
105	UGCCGGG	CUGAUGAGGCCGAAAGGCCGAA	AGAUGAG
106	CUGCCGG	CUGAUGAGGCCGAAAGGCCGAA	AAGADGA
129	GGGGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUG
138	CUCCACA	CUGAUGAGGCCGAAAGGCCGAA	AGGGGCC
148	GCTCAAU	CUGAUGAGGCCGAAAGGCCGAA	ADCUCCA
151	GCUGCUC	CUGAUGAGGCCGAAAGGCCGAA	ADGAUCU
180	GUAGCGG	CUGAUGAGGCCGAAAGGCCGAA	AGCGCAU
181	UGUAGCG	CUGAUGAGGCCGAAAGGCCGAA	AAGCGCA
186	GCAUUG	CUGAUGAGGCCGAAAGGCCGAA	AGCGGAA
204	GCCCGCG	CUGAUGAGGCCGAAAGGCCGAA	AGCGCCC
217	CGCCUGG	CUGAUGAGGCCGAAAGGCCGAA	ADGCTGC
239	UUGGUGG	CUGAUGAGGCCGAAAGGCCGAA	ADCUUGG
262	UGAUCUU	CUGAUGAGGCCGAAAGGCCGAA	ADGUGGG
268	AGCCAUU	CUGAUGAGGCCGAAAGGCCGAA	ADCUUGA
276	UCCUGUG	CUGAUGAGGCCGAAAGGCCGAA	AGCCAUU
301	CCAGGGA	CUGAUGAGGCCGAAAGGCCGAA	ADGCGCA
303	GACCAGG	CUGAUGAGGCCGAAAGGCCGAA	AGAUGCG
310	CCUUGGU	CUGAUGAGGCCGAAAGGCCGAA	ACCAAGG
323	CGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGGUCC
326	GGCCGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGGG
335	UGGGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCGG
349	UCCUAC	CUGAUGAGGCCGAAAGGCCGAA	AGCUUGU
352	CCUUCC	CUGAUGAGGCCGAAAGGCCGAA	ACAAAGU
375	CUCAUAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCADC
376	CCUCAUA	CUGAUGAGGCCGAAAGGCCGAA	AAGCCAU
378	AGCCUCA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCC
391	CCGGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCTCAG
409	AACUGUG	CUGAUGAGGCCGAAAGGCCGAA	ADGCAGC
416	UUCUGGA	CUGAUGAGGCCGAAAGGCCGAA	ACUGUGG
417	GUUCUGG	CUGAUGAGGCCGAAAGGCCGAA	AACUGUG
418	GGUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AAACUGU
433	CACACUG	CUGAUGAGGCCGAAAGGCCGAA	ADUCCCA
467	UGACUGA	CUGAUGAGGCCGAAAGGCCGAA	AGCCTGC
469	GCTGACT	CUGAUGAGGCCGAAAGGCCGAA	ADAGCTU
473	ADGCGCU	CUGAUGAGGCCGAAAGGCCGAA	ACUGAUA
481	UGGUCUG	CUGAUGAGGCCGAAAGGCCGAA	AUGCGCU
501	AACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUU

502	GAACUUG	CUGAUGAGGCCGAAAGGCCGAA	AAGGGGU
508	CUADAGG	CUGAUGAGGCCGAAAGGCCGAA	ACUUGGA
509	UCUADAG	CUGAUGAGGCCGAAAGGCCGAA	AACUUGG
512	UCUUCUA	CUGAUGAGGCCGAAAGGCCGAA	AGGAACU
514	GCUCUUC	CUGAUGAGGCCGAAAGGCCGAA	AUAGGAA
534	CAGGUUG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCCC
556	GGAAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCCGCA
561	CACCCGG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
562	UCACCTG	CUGAUGAGGCCGAAAGGCCGAA	AAGCAGA
585	CCUGCCU	CUGAUGAGGCCGAAAGGCCGAA	ADGGGUC
598	GCAGGCG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGCC
613	GAGGAAG	CUGAUGAGGCCGAAAGGCCGAA	ACAGGGC
616	GAUGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGACAG
617	GGADGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGACA
620	AUGGGAU	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGG
623	AAGADGG	CUGAUGAGGCCGAAAGGCCGAA	ADGAGGA
628	UGUCAAA	CUGAUGAGGCCGAAAGGCCGAA	ADGGGAU
630	AUDGUCA	CUGAUGAGGCCGAAAGGCCGAA	AGADGGG
631	GAUUGUC	CUGAUGAGGCCGAAAGGCCGAA	AAGAUGG
638	GGGGCAC	CUGAUGAGGCCGAAAGGCCGAA	AUDGUCA
661	AGAUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGCUCCG
667	CUCCGCA	CUGAUGAGGCCGAAAGGCCGAA	AUCUUGA
687	GCTGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGUUUCC
700	CCCCACC	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGC
715	GUAGGAA	CUGAUGAGGCCGAAAGGCCGAA	ADUCUAU
717	CAGUAGG	CUGAUGAGGCCGAAAGGCCGAA	AGAUCUC
718	ACAGUAG	CUGAUGAGGCCGAAAGGCCGAA	AAGADCU
721	CACACAG	CUGAUGAGGCCGAAAGGCCGAA	AGGAAGA
751	ACACCTC	CUGAUGAGGCCGAAAGGCCGAA	AUDGCUU
759	CGUGAAA	CUGAUGAGGCCGAAAGGCCGAA	ACACCTC
761	CCCGUGA	CUGAUGAGGCCGAAAGGCCGAA	AUACACC
762	UCCCGUG	CUGAUGAGGCCGAAAGGCCGAA	AAUACAC
763	GUCCCGU	CUGAUGAGGCCGAAAGGCCGAA	AAAUACA
792	CGAAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCUCC
795	UUGCGAA	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCC
796	CUUGCGA	CUGAUGAGGCCGAAAGGCCGAA	AAGGAGC
797	GCTUGCG	CUGAUGAGGCCGAAAGGCCGAA	AAAGGAG
798	AGCTUGC	CUGAUGAGGCCGAAAGGCCGAA	AAAAGGA
829	GGAACAC	CUGAUGAGGCCGAAAGGCCGAA	AUGGCCA
834	GGUCCGG	CUGAUGAGGCCGAAAGGCCGAA	ACACAAU
835	GGGUCCG	CUGAUGAGGCCGAAAGGCCGAA	AACACAA
845	GCGUAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGUC
849	GUCUGCG	CUGAUGAGGCCGAAAGGCCGAA	AGGGAGG
872	CGCACAG	CUGAUGAGGCCGAAAGGCCGAA	AGCCUCC
883	GCAUGGA	CUGAUGAGGCCGAAAGGCCGAA	ACACGCA
885	CTGCAUG	CUGAUGAGGCCGAAAGGCCGAA	AGACACG
905	CGGUCCG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCGC
906	CCGUCCG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCCG
919	GCTUACT	CUGAUGAGGCCGAAAGGCCGAA	AGCTUCC

936	GUACUGG	CUGAUGAGGCCGAAAGGCCGAA	AUUCCAU
937	GGUACUG	CUGAUGAGGCCGAAAGGCCGAA	AAUUGCA
942	UGGCAGG	CUGAUGAGGCCGAAAGGCCGAA	ACUGGAA
953	UCGUCUG	CUGAUGAGGCCGAAAGGCCGAA	AUCUGGC
962	CGGUGAC	CUGAUGAGGCCGAAAGGCCGAA	AUCGUCU
965	AUCCGGU	CUGAUGAGGCCGAAAGGCCGAA	ACGAUCG
973	UCUCUCU	CUGAUGAGGCCGAAAGGCCGAA	AUCCGGU
986	GUCCUUU	CUGAUGAGGCCGAAAGGCCGAA	ACGUUUC
996	GGUCUCA	CUGAUGAGGCCGAAAGGCCGAA	ADGUCCU
1005	GCUCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGGUCUC
1006	UGCUCUU	CUGAUGAGGCCGAAAGGCCGAA	AAGGUCU
1015	UCUUCAU	CUGAUGAGGCCGAAAGGCCGAA	ADGUCUC
1028	CUAAAG	CUGAUGAGGCCGAAAGGCCGAA	ACUCUUC
1031	CCGCUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGACUC
1032	UCCGCTG	CUGAUGAGGCCGAAAGGCCGAA	AAGGACU
1033	GUCCGCU	CUGAUGAGGCCGAAAGGCCGAA	AAAGGAC
1058	CGAGGUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCGG
1064	ADGCGUC	CUGAUGAGGCCGAAAGGCCGAA	AGGUGGA
1072	GCAAGC	CUGAUGAGGCCGAAAGGCCGAA	ADGCGUC
1082	CUGCGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCACA
1083	GUCGCGG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCAC
1092	AGAAGCU	CUGAUGAGGCCGAAAGGCCGAA	AGCUGCG
1097	GGGACAG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGAG
1098	GGGGACA	CUGAUGAGGCCGAAAGGCCGAA	AAGCUGA
1102	GCUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGAAG
1125	AAAGGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGGCUG
1127	GUAAAGG	CUGAUGAGGCCGAAAGGCCGAA	AUAGGCG
1131	UGACGUA	CUGAUGAGGCCGAAAGGCCGAA	AGGGADA
1132	ADGACGU	CUGAUGAGGCCGAAAGGCCGAA	AAGGGAU
1133	GAUGACG	CUGAUGAGGCCGAAAGGCCGAA	AAAGGGA
1137	CAGGGAU	CUGAUGAGGCCGAAAGGCCGAA	ACGUAAA
1140	GCUCAGG	CUGAUGAGGCCGAAAGGCCGAA	AUGACGU
1153	CAUAGUU	CUGAUGAGGCCGAAAGGCCGAA	AUGGUGC
1158	CUCAUCA	CUGAUGAGGCCGAAAGGCCGAA	AGUUGAU
1167	GGUGGGA	CUGAUGAGGCCGAAAGGCCGAA	ACUCAUC
1168	UGGUGGG	CUGAUGAGGCCGAAAGGCCGAA	AACUCAU
1169	ADGGUGG	CUGAUGAGGCCGAAAGGCCGAA	AAACUCA
1182	AGAAGGA	CUGAUGAGGCCGAAAGGCCGAA	ACACCAU
1183	CAGAAGG	CUGAUGAGGCCGAAAGGCCGAA	AACACCA
1184	CCAGAAG	CUGAUGAGGCCGAAAGGCCGAA	AAACACC
1187	UGCCCAAG	CUGAUGAGGCCGAAAGGCCGAA	AGGAAAC
1188	CUGCCCA	CUGAUGAGGCCGAAAGGCCGAA	AAGGAAA
1198	CCUGGCU	CUGAUGAGGCCGAAAGGCCGAA	AUCUGCC
1209	CAAGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGCTUG
1215	CGGGGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCGA
1229	ACUUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGCC
1237	GGGGCAG	CUGAUGAGGCCGAAAGGCCGAA	ACTUUGG
1250	GGGGCUG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGGG
1268	AUGGCUG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGGG

1279	GAGCTGA	CUGAUGAGGCCGAAAGGCCGAA	ACCAUGG
1281	CAGAGCT	CUGAUGAGGCCGAAAGGCCGAA	AUACCAU
1286	UGGGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGCTGAU
1309	GGACTGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGGGG
1315	GGGCTAG	CUGAUGAGGCCGAAAGGCCGAA	ACUGGGA
1318	CUGGGGC	CUGAUGAGGCCGAAAGGCCGAA	AGGACUG
1331	GCTGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGGCTU
1334	ACAGCTU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGGG
1389	GGCTCTU	CUGAUGAGGCCGAAAGGCCGAA	ACAGCTU
1413	AUCAUCA	CUGAUGAGGCCGAAAGGCCGAA	ACUGCAG
1414	CADCADC	CUGAUGAGGCCGAAAGGCCGAA	AACUGCA
1437	GCCAAAC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCC
1441	UGUUGCC	CUGAUGAGGCCGAAAGGCCGAA	AGCAAGG
1467	GUCUGUG	CUGAUGAGGCCGAAAGGCCGAA	ACACAGC
1468	GGUCUGU	CUGAUGAGGCCGAAAGGCCGAA	AACACAG
1482	GUCGACG	CUGAUGAGGCCGAAAGGCCGAA	AUGCCAG
1486	AGUUGUC	CUGAUGAGGCCGAAAGGCCGAA	ACGGAUG
1494	AAACUCG	CUGAUGAGGCCGAAAGGCCGAA	AGUUGUC
1500	CUGCTGA	CUGAUGAGGCCGAAAGGCCGAA	ACUCGGA
1501	GCTGCTG	CUGAUGAGGCCGAAAGGCCGAA	AACUCGG
1502	AGCTGCT	CUGAUGAGGCCGAAAGGCCGAA	AACTUCG
1525	CCACAGG	CUGAUGAGGCCGAAAGGCCGAA	AUGCCCT
1566	CUCAGGG	CUGAUGAGGCCGAAAGGCCGAA	ACTCCAU
1577	CGAGTUA	CUGAUGAGGCCGAAAGGCCGAA	AGCTUCA
1579	GGCGAGU	CUGAUGAGGCCGAAAGGCCGAA	AUAGCTU
1583	ACTAGGC	CUGAUGAGGCCGAAAGGCCGAA	AGUUAUA
1588	CUGGCAC	CUGAUGAGGCCGAAAGGCCGAA	AGGCGAG
1622	GGAGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGCTGGG
1628	CCAGTUG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGGA
1648	CADUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGCCCCG
1660	CUGAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCAU
1663	CTCCUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGAGGC
1664	UCUCCUG	CUGAUGAGGCCGAAAGGCCGAA	AAGGAGG
1665	ADCUCCU	CUGAUGAGGCCGAAAGGCCGAA	AAAGGAG
1680	GGAGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCUUC
1681	UGGAGGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUCUU
1683	AAUGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGUC
1686	CGCAADG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGAA
1690	UGUCCGC	CUGAUGAGGCCGAAAGGCCGAA	AUGGAGG
1704	GGCUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCAU
1705	GGGCTGA	CUGAUGAGGCCGAAAGGCCGAA	AAGUCCA
1707	CAGGGCT	CUGAUGAGGCCGAAAGGCCGAA	AGAAGUC
1721	CUGAUCT	CUGAUGAGGCCGAAAGGCCGAA	ACTCAGC
1726	AGGAGCT	CUGAUGAGGCCGAAAGGCCGAA	AUCUGAC
1731	CCCTUAG	CUGAUGAGGCCGAAAGGCCGAA	AGCTGAU
1734	ACCCCTU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCT
1754	CUCUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGGCAG

Table 21
Human rel A Hairpin Ribozyme/Target Sequences
nt. Position Hairpin Ribozyme sequence

		Substrate
90	UGAGGGGG AGAA GUUC ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	GAACU GUU CCCCCUA
156	GCUGCUUG AGAA GCUC ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	GAACA GCC CAGCAGC
362	GCCAUCCC AGAA GUCC ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	GGACU GCC GGGAUUGC
413	GUUCUGGA AGAA GUGG ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	CCACA GUU UOCAGAAC
606	GAAGGACA AGAA GCAG ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	CUGOC GCC UGUCCUUC
652	UUGAGGUC AGAA GUGU ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	ACACU GCC GAGCUCAA
695	CCCACCGA AGAA GCUG ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	CAGCU GCC UGGGUGGG
853	AGGCUGGG AGAA GCGU ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	AGCCA GAC CCGAGCCU
900	GGUCGGNA AGAA GCGG ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	GGGGG GCC UUCGGAC
955	UGACCGAUC AGAA GUUU ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	AUACA GAC GAUUGUCA
1037	GUCCGUGG AGAA GCUG ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	CAGCG GAC CCACCGAC
1045	GGCCGGGG AGAA GUGG ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	CCACG GAC CCCCAGGC
1410	CAUCAUCA AGAA GCAG ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	CUGCA GUU UGAUGAUG
1453	ACAGCUGG AGAA GUGC ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	GCACA GAC CCGAGCGU
1471	GAUGCCAG AGAA GUCA ACCAGAGAAACACACGUGUGUGGUACAUUACCUUGUA	UCACA GAC CUGGCAC

Table 22
 Mouse *rel A* Hairpin Ribozyme/Target Sequences
 nt. Position Hairpin Ribozyme sequence

		Substrate
137	GUUGCUC AGAA GUUC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GAACA GCC GAAGCAAC
273	GAGAUUG AGAA GUUC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GAACA GUU CGAUCUC
343	GCCAUCCC AGAA GUCC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GAACU GCC GGGUUGGC
366	GGGAGAG AGAA GOCU ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	AGGCU GAC CUCUGGCC
633	UUGAGCUC AGAA GUGU ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	ACACU GCC GAGCUCAA
676	CCCACCGA AGAA GCUC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GAACU GCC UCGUGGG
834	AGGCUGG AGAA GOGU ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	ACGCC GAC CCGAGCCU
881	GAUCAGAA AGAA GOCG ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	CGGGG GGC UUCUGAUC
1100	AGGUGUAG AGAA GOGG ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	CGGCA GGC CUACACCU
1205	GGGACAG AGAA GUCC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GCACC GUC CUCUGGCC
1361	GGCCUUC AGAA GOGU ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	AGGCU GUC GGAAGGCC
1385	CAGCAUCA AGAA GCAG ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	CUGCA GUU UGAUGCUG
1431	ACUCCUG AGAA GUCC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GCACA GAC CCGAGAGU
1449	GAUGCCAG AGAA GUQA ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	UCACA GAC CUGGCNUC
1802	AAGUGGG AGAA GCUG ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	CAGCU GGC CCGGACUU
2009	UGGCUCCA AGAA GUCC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GGACA GAC UGGAGCCA
2124	UGGUGUG AGAA GCAC ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	GUGCU GGC CGACACCA
2233	AUUCUGAA AGAA GOGA ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	UGGCG GGC UUCAGAAU
2354	UCAGUAA AGAA GUCU ACCAGAGAAACACACACGUGUGGUACAUUACCUUGUA	AGACA GCC UUUACUGA

Table 23: Human TNF- α HH Ribozyme Target Sequence

nt. Position	HH Target Sequence	nt. Position	HH Target Sequence
28	GGCAGGU U CUCUCC	321	GUCAGAU C AUCCUCU
29	GCAGGUU C UCUCUCU	324	AGAUCAU C UUCUGA
31	AGGUUCU C UUCUCU	326	AUCAUCU U CUCGAAC
33	GUUCUCU U CCUCUCA	327	UCAUCU C UCGAAC
34	UUCUCU C UCUCAC	329	AUCUCU C GAACCC
37	UCUUCU C UCACUA	352	AGCCUGU A GCCCAG
39	UUCUCU C ACUAUCU	361	CCCAUGU U GUAGCA
44	CCACAU A CUGACC	364	ADGUUGU A GCAACC
58	CAGGCU C CAGCUC	374	AAACCU C AAGCUG
65	CCACCU C UCUCUC	391	GGCAGU C CAGGCG
67	ACCCUCU C UCCUCG	421	AUGCCU C CUGGCA
69	CCUCUCU C CCGGGA	449	GAGAGAU A ACCAGCU
106	GCAUGAU C CGGAGG	468	GUGCAU C AGAGGG
136	AGGCGU C CCAAGA	480	GGCCUGU A CCUCAUC
165	CAGGCU C CAGGCG	484	UGUACU C AUUACU
177	CGGUGU U GUUCUC	487	ACCUCAU C UAUCCC
180	UGCUUGU U CCUCAGC	489	CUCAUCU A CCCCCAG
181	GCUGGU C CUCAGCC	492	AUCUACU C CCAGGUC
184	UGUUCU C AGCCUCU	499	CCCAGGU C CUCUCA
190	UCAGCCU C UUCUCU	502	AGGCCU C UUCAAGG
192	AGCCUCU U CUCUCU	504	GUCUCU U CAAGGGC
193	GCCUCU C UCCUCC	505	UCCUCU C AAGGGCC
195	CUCUCU C CUCCUC	525	UGCCCU C CACCAU
198	UUCUCU U CCUGAUC	538	ADGUGU C CUCACC
199	UCUCCU C CUGAUCG	541	UGCUCU C ACCACA
205	UCUGAU C GGGCAG	553	ACACCAU C AGCCGA
226	CCAGCU C UCUGCC	562	GCCCAU C GCGUCU
228	ACGCUCU U CUGCUG	568	UCGCGU C UCCUACC
229	CGCUCU C UGCUGC	570	GCGUCU C CUACCAG
243	CUGCAU U UGGAGU	573	GUCUCU A CCAGACC
244	UGCAU U GGAGGA	586	CCAAGGU C AACCUC
253	GAGUGAU C GGGCCC	592	UCAACU C CUCUCU
273	GAAGAU C CCCCAG	595	ACCUCCU C UCUGCA
286	GGGACU C UCUCUA	597	CUCCUCU C UGCCAUC
288	GACUCU C UCUAUC	604	CUGCAU C AAGAGCC
290	CCUCUCU C UAUCAG	657	CCUGGU A UGAGCC
292	UCUCUCU A AUCAGC	667	AGCCAU C UAUUGG
295	CUCUAU C AGCCUC	669	CCCAUCU A UCUGGA
302	CAGCCU C UGGCCA		

671	CAUCUAU C UGGGAGG	960	UGGGAUU C AGGAAUG
682	GAGGGGU C UCCAGC	1001	AACCACT A AGAAUUC
684	GGGGUCU U CCAGCUG	1007	UAGAAU U CAAACUG
685	GGGUUCU C CAGCUGG	1008	AAGAAUU C AAACUGG
709	ACCGACU C AGCGCUG	1021	GGGGCCU C CAGAACU
721	CUGAGAU C AAUCGGC	1029	CAGAACU C ACUGGGG
725	GADCAAU C GGCCCGA	1040	GGGGCCU A CAGCUUU
735	CCCGACU A UCUCGAC	1046	UACAGCU U UGAUCCC
737	CGACUAU C UCGACUU	1047	ACAGCUU U GAUCCCU
739	ACTUAUC C GACUUG	1051	CUUUGAU C CCUGACA
744	CUUGACU U UGCGAG	1060	CUUGACU C UGGAAUC
745	UUGACUU U GCGAGU	1067	CUUGAAU U UGGAGAC
753	GCCGAGU C UGGGCAG	1085	GGAGCCU U UGGUUCU
763	GGCAGGU C UACUUG	1086	GAGCCUU U GGUUCUG
765	CAGGUCU A CUUUGGG	1090	CUUUGGU U CUGGCCA
768	GUCUACU U UGGGAUC	1091	UUUGGUU C UGGCCAG
769	UCUACUU U GGAUCCA	1113	CAGGACU U GAGAAGA
775	UUGGGAU C AUUGCCC	1124	AAGACCU C ACCUAGA
778	GGAUCAU U GOCUUGU	1129	CUACACU A GAAAUUG
801	CGAACAU C CAACCUU	1135	UAGAAU U GACACAA
808	CCAACCU U CCCAAAC	1151	UGGACCU U AGGCCUU
809	CAACCUU C CCAAACG	1152	GGACCUU A GGCCUUC
820	AACGCCU C CCUGCC	1158	UAGGCCU U CCUCUCU
833	CCCCAAU C CCUUUAU	1159	AGGCCUU C CUCUCUC
837	AADCCCU U UAUAACC	1162	CCUCCU C UCUCACG
838	ADCCCUU U AUUAACC	1164	UUCCCUU C UCCAGAU
839	UCCCUUU A UUAACCC	1166	CCUCUCU C CAGAUUU
841	CCUUUAU U ACCCCCU	1174	CAGAUUU U UCCAGAC
842	CUUUAUU A CCCCCUC	1175	AGAUUUU U CCAGACU
849	ACCCCCU C CUUCAGA	1176	GAUGUUU C CAGACUU
852	CCCUCCU U CAGACAC	1183	CCAGACU U CCUUGAG
853	CCUCCUU C AGACACC	1184	CAGACUU C CUUGAGA
863	ACACCCU C AACCUUC	1187	ACUCCCU U GAGACAC
869	UCAACCU C UUCUGGC	1208	CAGCCCU C CCCAUGG
871	AACCUUC U CUGGCUU	1224	GCCAGCU C CCUCUAU
872	ACCUCCU C UGGCUCA	1228	GCUCCCU C UAUUUAU
878	UCUGGCU C AAAAAGA	1230	UCCCUCC A UUUAUGU
890	AGAGAAU U GGGGGCU	1232	CCUCUAU U UAUGUUU
898	GGGGGCU U AGGGUUG	1233	CUUUAUU U AUGUUUG
899	GGGGCUU A GGGUUGG	1234	UCUAUUU A UGUUUGC
904	UUAGGGU C GGAACCC	1238	UUUAUGU U UGCACUU
917	CCAAGCU U AGAACTU	1239	UUUAUGU U GCACUUG
918	CAAGCUU A GAACUUU	1245	UUGCACU U GUGAUUA
924	UAGAACU U UAAGCAA	1251	UUGGAAU U AUUUUAU
925	AGAACUU U AAGCAAC	1252	UGGAAU A UUUAUA
926	GAACUUU A AGCAACA	1254	UGAAUUA U UAUAUUU
945	CACCAU U CGAAACC	1255	GAUAUUU U AUUAUUU
946	ACCACUU C GAAACCU	1256	AUUAUUU A UUAUUUA
959	CUGGGAU U CAGGAUU	1258	UAUUUAU U AUUUUAU

1259	AUUUAUU A UUUUAUU	1440	UGUUUUU U AAAAUUU
1261	UUUAUUU U UUUUAUU	1441	GUUUUUU A AAAUAUU
1262	UAUUUAU U AUUUUAU	1446	UUAAAAU A UUAUCCU
1263	AUUUAUU A UUUUAUA	1448	AAAAUAU U AUUUUAU
1265	UAUUUAU U UUUUAUU	1449	AAAAUAU A UUUUAUU
1266	AUUUAUU U AUUUUAU	1451	AUAUUUA C UGAUUUA
1267	UUUAUUU A UUAUUUA	1456	AUUUAUU U AAGUUUU
1269	UAUUUAU U AUUUUAU	1457	UUUAUUU A AGUUUUU
1270	AUUUAUU A UUUUAUU	1461	AUUUAUU U GUUUUUU
1272	UUUAUUU U UUUUAUU	1464	AAGUUUU C UAAACAA
1273	UAUUUAU U AUUUUAU	1466	GUUUUUU A AACAAUU
1274	AUUUAUU A UUUUAUU	1479	UGUUUUU U UGUUUUU
1276	UAUUUAU U UUUUAUU	1480	GUUUUUU U GUUUUUU
1277	AUUUAUU U AUUUUAU	1494	CAUUUUU C AUUUUUU
1278	UUUAUUU A UUUUAUU	1498	UUUUUUU C AUUUUUU
1280	UAUUUAU U UUUUAUU	1501	CAUUUUU U GUUUUUU
1281	AUUUAUU U AUUUUAU	1512	GAGUUUU C UGUUUUU
1282	UUUAUUU A CAGUUUA	1517	CUUUUUU C CCUUUUU
1294	UGAUUUU A UUUUAUU	1528	AGGUUUU U GUUUUUU
1296	AAGUUUU U UUUUAUU	1533	GUUUUUU C UGUUUUU
1297	AAGUUUU U AUUUUAU	1537	UGUUUUU A AUUUUUU
1298	UGAUUUU A UUUUAUU	1540	CUUUUUU C GUUUUUU
1300	UAUUUAU U UGUUUUU	1546	UGUUUUU A CUUUUUU
1301	AUUUAUU U GUUUUUU	1549	GUUUUUU A UUUUAUU
1315	CGUUUUU A UUUUAUU	1551	CUUUUUU U CAGUUUU
1317	GUUUUUU C UGUUUUU	1552	UAUUUUU C AGUUUUU
1334	CGAUUUU A GUUUUUU	1566	GAGAAUU A AAGUUUU
1345	GUUUUUU U GUUUUUU	1572	UAAAGGU U GUUUUUU
1350	CUUUUUU C AGAUUUU	1576	GUUUUUU U AGGAAAG
1359	GAGUUUU U UUUUAUU	1577	GUUUUUU A GGAAGA
1360	ACAUUUU U UUUUAUU		
1361	CAUUUUU U CUUUUUU		
1362	AUUUUUU C CUUUUUU		
1386	GAACAAU A GUUUUUU		
1393	AGGUUUU U CUUUUUU		
1394	GUUUUUU C CUUUUUU		
1401	CUUUUUU A GUUUUUU		
1414	CUUUUUU C GUUUUUU		
1422	GUUUUUU U CUUUUUU		
1423	GUUUUUU C CUUUUUU		
1425	GUUUUUU U CUUUUUU		
1426	CUUUUUU U CUUUUUU		
1427	CUUUUUU U CUUUUUU		
1431	UUUUUUU U AUUUUUU		
1432	UUUUUUU A UUUUUUU		
1436	AUUUAUU U UUUUUUU		
1437	UAUUUAU U UUUUUUU		
1438	UAUUUAU U UUUUUUU		

Table 24: Human TNF- α Hammerhead Ribozyme Sequences

nt. Position	HH Ribozyme Sequence
28	GGAGAG CUGAUGAGGCCGAAAGGCCGAA ACCUGCC
29	AGGAAGA CUGAUGAGGCCGAAAGGCCGAA AACCUCC
31	AGAGGAA CUGAUGAGGCCGAAAGGCCGAA AGAACCU
33	UGAGAGG CUGAUGAGGCCGAAAGGCCGAA AGAGAAC
34	GUGAGAG CUGAUGAGGCCGAAAGGCCGAA AAGAGAA
37	UADGUGA CUGAUGAGGCCGAAAGGCCGAA AGGAAGA
39	AGUADGU CUGAUGAGGCCGAAAGGCCGAA AGAGGAA
44	GGGUCAG CUGAUGAGGCCGAAAGGCCGAA AUGGUGAG
58	GAGGGUG CUGAUGAGGCCGAAAGGCCGAA AGCGGUG
65	GGGGAGA CUGAUGAGGCCGAAAGGCCGAA AGGGGUG
67	CAGGGGA CUGAUGAGGCCGAAAGGCCGAA AGAGGGU
69	UCCAGGG CUGAUGAGGCCGAAAGGCCGAA AGAGAGG
106	CGUCCCG CUGAUGAGGCCGAAAGGCCGAA AUCAUCC
136	UCUUGGG CUGAUGAGGCCGAAAGGCCGAA AGCGCCU
165	CCGCCUG CUGAUGAGGCCGAAAGGCCGAA AGCCCUU
177	GAGGAAC CUGAUGAGGCCGAAAGGCCGAA AGCACCG
180	GCUGAGG CUGAUGAGGCCGAAAGGCCGAA ACAAGCA
181	GGCUGAG CUGAUGAGGCCGAAAGGCCGAA AACAAGC
184	AGAGGCU CUGAUGAGGCCGAAAGGCCGAA AGGAACA
190	AGGAGAA CUGAUGAGGCCGAAAGGCCGAA AGGCUGA
192	GAAGGAG CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
193	GGAGGA CUGAUGAGGCCGAAAGGCCGAA AAGAGGC
195	CAGGAAG CUGAUGAGGCCGAAAGGCCGAA AGAAGAG
198	GADCAGG CUGAUGAGGCCGAAAGGCCGAA AGGAGAA
199	CGAUCAG CUGAUGAGGCCGAAAGGCCGAA AAGGAGA
205	CUGCCAC CUGAUGAGGCCGAAAGGCCGAA AUCAGGA
226	GGCAGAA CUGAUGAGGCCGAAAGGCCGAA AGCGUGG
228	CAGGCAG CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
229	GCAGGCA CUGAUGAGGCCGAAAGGCCGAA AAGAGCG
243	CACUCCA CUGAUGAGGCCGAAAGGCCGAA AGUGCAG
244	UCACTCC CUGAUGAGGCCGAAAGGCCGAA AAGUGCA
253	GGGGGCC CUGAUGAGGCCGAAAGGCCGAA AUCACTC
273	CCUGGGG CUGAUGAGGCCGAAAGGCCGAA ACTCUUC
286	UUAGAGA CUGAUGAGGCCGAAAGGCCGAA AGGUCCC
288	GADUAGA CUGAUGAGGCCGAAAGGCCGAA AGAGGUC
290	CUGAUUA CUGAUGAGGCCGAAAGGCCGAA AGAGAGG
292	GGCUGAU CUGAUGAGGCCGAAAGGCCGAA AGAGAGA
295	GAGGGCU CUGAUGAGGCCGAAAGGCCGAA AUUAGAG
302	UGGGCCA CUGAUGAGGCCGAAAGGCCGAA AGGGCUG

321	AGAAGAU	CUGAUGAGGCCGAAAGGCCGAA	AUCUGAC
324	UCGAGAA	CUGAUGAGGCCGAAAGGCCGAA	ADGAUCU
326	GUUCGAG	CUGAUGAGGCCGAAAGGCCGAA	AGAUGAU
327	GGUUCGA	CUGAUGAGGCCGAAAGGCCGAA	AAGAUCA
329	GGGGUUC	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
352	CADGGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCU
361	UUGCUAC	CUGAUGAGGCCGAAAGGCCGAA	ACADGGG
364	GGUUUGC	CUGAUGAGGCCGAAAGGCCGAA	ACACAUU
374	UCAGCUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUU
391	GCCACTG	CUGAUGAGGCCGAAAGGCCGAA	AGCUGCC
421	UGGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCAU
449	AGCUGGU	CUGAUGAGGCCGAAAGGCCGAA	AUCUCUC
468	GCCUUCU	CUGAUGAGGCCGAAAGGCCGAA	AUGGCAC
480	GADGAGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCC
484	AGUAGAU	CUGAUGAGGCCGAAAGGCCGAA	AGGUACA
487	GGGAGUA	CUGAUGAGGCCGAAAGGCCGAA	ADGAGGU
489	CUGGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGADGAG
492	GACCCGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAU
499	UGAAGAG	CUGAUGAGGCCGAAAGGCCGAA	ACCCGGG
502	CCUUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGGACCU
504	GCCCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGAGGAC
505	GGCCUUC	CUGAUGAGGCCGAAAGGCCGAA	AAGAGGA
525	AUGGGUG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGCA
538	GGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCACAU
541	UGUGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCA
553	UGC GGCU	CUGAUGAGGCCGAAAGGCCGAA	ADGGUGU
562	AGACGGC	CUGAUGAGGCCGAAAGGCCGAA	ADGCGGC
568	GGUAGGA	CUGAUGAGGCCGAAAGGCCGAA	ACGGCGA
570	CUGGUAG	CUGAUGAGGCCGAAAGGCCGAA	AGACGGC
573	GGUCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGAC
586	GGAGGUU	CUGAUGAGGCCGAAAGGCCGAA	ACCUUGG
592	CAGAGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGUUGA
595	UGGCAGA	CUGAUGAGGCCGAAAGGCCGAA	AGGAGGU
597	GADGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGAGGAG
604	GGCUUCU	CUGAUGAGGCCGAAAGGCCGAA	AUGGCCAG
657	GGGCUCA	CUGAUGAGGCCGAAAGGCCGAA	ACCAGGG
667	CCAGAUU	CUGAUGAGGCCGAAAGGCCGAA	AUGGGCU
669	UCCAGA	CUGAUGAGGCCGAAAGGCCGAA	AGAUGGG
671	CCUCCCA	CUGAUGAGGCCGAAAGGCCGAA	AUAGAUU
682	GCUUGAA	CUGAUGAGGCCGAAAGGCCGAA	ACCCUUC
684	CAGCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGACCCC
685	CCAGCUG	CUGAUGAGGCCGAAAGGCCGAA	AAGACCC
709	CAGCGCU	CUGAUGAGGCCGAAAGGCCGAA	AGUCGGU
721	GCCGAUU	CUGAUGAGGCCGAAAGGCCGAA	AUCUCAG
725	UCGGGCC	CUGAUGAGGCCGAAAGGCCGAA	AUUGAUC
735	GUCGAGA	CUGAUGAGGCCGAAAGGCCGAA	AGUCGGG
737	AAGUCCA	CUGAUGAGGCCGAAAGGCCGAA	AUAGUCC
739	CAAAGUC	CUGAUGAGGCCGAAAGGCCGAA	AGAUAGU
744	CUCCGCA	CUGAUGAGGCCGAAAGGCCGAA	AGUCGAG

745	ACUCGGC	CUGAUGAGGCCGAAAGGCCGAA	AAGUCGA
753	CUGCCCA	CUGAUGAGGCCGAAAGGCCGAA	ACUCGGC
763	CAAAGUA	CUGAUGAGGCCGAAAGGCCGAA	ACUCGGC
765	CCCAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGACCCUG
768	GAUCCCA	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
769	UGAUCCC	CUGAUGAGGCCGAAAGGCCGAA	AAGUAGA
775	GGGCAAU	CUGAUGAGGCCGAAAGGCCGAA	ADCCCAA
778	ACAGGGC	CUGAUGAGGCCGAAAGGCCGAA	ADGAUCC
801	AAGGUUG	CUGAUGAGGCCGAAAGGCCGAA	AUGUUCG
808	GUUUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUUGG
809	CGUUGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGGUUG
820	GGCAGGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCGUU
833	AUAAAGG	CUGAUGAGGCCGAAAGGCCGAA	AUUGGGG
837	GGUAAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGGAUU
838	GGGTAUU	CUGAUGAGGCCGAAAGGCCGAA	AAGGGAU
839	GGGGUAA	CUGAUGAGGCCGAAAGGCCGAA	AAAGGCA
841	AGGGGGU	CUGAUGAGGCCGAAAGGCCGAA	AUAAAGG
842	GAGGGGG	CUGAUGAGGCCGAAAGGCCGAA	AADAAAG
849	UCUGAAG	CUGAUGAGGCCGAAAGGCCGAA	AGGGGGU
852	GUUGUCU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGGG
853	GGUGUCU	CUGAUGAGGCCGAAAGGCCGAA	AAGGAGG
863	AGAGGUU	CUGAUGAGGCCGAAAGGCCGAA	AGGGUGU
869	GCCAGAA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUGA
871	GAGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGAGGUU
872	UGAGCCA	CUGAUGAGGCCGAAAGGCCGAA	AAGAGGU
878	UCUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGCCAGA
890	AGCCCCC	CUGAUGAGGCCGAAAGGCCGAA	AUUCUCU
898	CGACCCU	CUGAUGAGGCCGAAAGGCCGAA	AGCCCCC
899	CCGACCC	CUGAUGAGGCCGAAAGGCCGAA	AAGCCCC
904	GGGUUCC	CUGAUGAGGCCGAAAGGCCGAA	ACCCUAA
917	AAGUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGCUUGG
918	AAAGUUC	CUGAUGAGGCCGAAAGGCCGAA	AAGCUUG
924	UUGCUUA	CUGAUGAGGCCGAAAGGCCGAA	AGUUCUA
925	GUUGCUU	CUGAUGAGGCCGAAAGGCCGAA	AAGUUCU
926	UGUUGCU	CUGAUGAGGCCGAAAGGCCGAA	AAAGUUC
945	GGUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AGUGGUG
946	AGGUUUC	CUGAUGAGGCCGAAAGGCCGAA	AAGUGGU
959	AUUCUUG	CUGAUGAGGCCGAAAGGCCGAA	ADCCCAAG
960	CAUUCUU	CUGAUGAGGCCGAAAGGCCGAA	AADCCCA
1001	GAAUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGUGGUU
1007	CAGUUUG	CUGAUGAGGCCGAAAGGCCGAA	AUUCUUA
1008	CCAGUUU	CUGAUGAGGCCGAAAGGCCGAA	AADUCUU
1021	AGUUCUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCC
1029	CCCCAGU	CUGAUGAGGCCGAAAGGCCGAA	AGUUCUG
1040	AAAGCUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCC
1046	GGGAUCA	CUGAUGAGGCCGAAAGGCCGAA	AGCUGUA
1047	AGGGADC	CUGAUGAGGCCGAAAGGCCGAA	AAGCUUG
1051	UGUCAGG	CUGAUGAGGCCGAAAGGCCGAA	AUCAAAG
1060	GAUUGCA	CUGAUGAGGCCGAAAGGCCGAA	ADGUCAG

1067	GUCUCCA	CUGADGAGGCCGAAAGGCCGAA	AUUC CAG
1085	AGAACCA	CUGADGAGGCCGAAAGGCCGAA	AGGCUCC
1086	CAGAAC	CUGADGAGGCCGAAAGGCCGAA	AAGGCUU
1090	UGGCCAG	CUGADGAGGCCGAAAGGCCGAA	ACCAAAG
1091	CUGGCCA	CUGADGAGGCCGAAAGGCCGAA	AACCAA
1113	UCUUCUC	CUGADGAGGCCGAAAGGCCGAA	AGUCCUG
1124	UCUAGGU	CUGADGAGGCCGAAAGGCCGAA	AGGUCUU
1129	CAAUUUC	CUGADGAGGCCGAAAGGCCGAA	AGGUGAG
1135	UUGUGUC	CUGADGAGGCCGAAAGGCCGAA	AUUUCUA
1151	AAGGCCU	CUGADGAGGCCGAAAGGCCGAA	AGGUCCA
1152	GAAGGCC	CUGADGAGGCCGAAAGGCCGAA	AAGGUCC
1158	AGAGAGG	CUGADGAGGCCGAAAGGCCGAA	AGGUUA
1159	GAGAGAG	CUGADGAGGCCGAAAGGCCGAA	AAGGCCU
1162	CUGGAGA	CUGADGAGGCCGAAAGGCCGAA	AGGAAGG
1164	AUCUGGA	CUGADGAGGCCGAAAGGCCGAA	AGAGGAA
1166	ACAUUCG	CUGADGAGGCCGAAAGGCCGAA	AGAGAGG
1174	GUCUGGA	CUGADGAGGCCGAAAGGCCGAA	ACAUUCG
1175	AGUCUGG	CUGADGAGGCCGAAAGGCCGAA	AACAUUC
1176	AAGUCUG	CUGADGAGGCCGAAAGGCCGAA	AAACAUC
1183	CUCAAGG	CUGADGAGGCCGAAAGGCCGAA	AGUCUGG
1184	UCUCAAG	CUGADGAGGCCGAAAGGCCGAA	AAGUCUG
1187	GUGUCUC	CUGADGAGGCCGAAAGGCCGAA	AGGAAGU
1208	CCAUUGG	CUGADGAGGCCGAAAGGCCGAA	AGGGCUG
1224	AUAGAGG	CUGADGAGGCCGAAAGGCCGAA	AGCUGGC
1228	AUAUAUA	CUGADGAGGCCGAAAGGCCGAA	AGGGAGC
1230	ACAUAAA	CUGADGAGGCCGAAAGGCCGAA	AGAGGGA
1232	AAACAUA	CUGADGAGGCCGAAAGGCCGAA	AUAGAGG
1233	CAACAUA	CUGADGAGGCCGAAAGGCCGAA	AAUAGAG
1234	GCAACA	CUGADGAGGCCGAAAGGCCGAA	AAAUAGA
1238	AAGUGCA	CUGADGAGGCCGAAAGGCCGAA	ACAUAAA
1239	CAAGUGC	CUGADGAGGCCGAAAGGCCGAA	AACAUAA
1245	UAUUCAC	CUGADGAGGCCGAAAGGCCGAA	AGUGCAA
1251	AUAUAUA	CUGADGAGGCCGAAAGGCCGAA	AUCACAA
1252	UAUAUA	CUGADGAGGCCGAAAGGCCGAA	AUUCACA
1254	AUAUAUA	CUGADGAGGCCGAAAGGCCGAA	AUAUAUA
1255	AAUAUAU	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1256	UAUAUA	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1258	AAUAUAU	CUGADGAGGCCGAAAGGCCGAA	AUAUAUA
1259	AAUAUA	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1261	AUAUAUA	CUGADGAGGCCGAAAGGCCGAA	AUAUAUA
1262	AAUAUAU	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1263	UAUAUA	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1265	AAUAUA	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1266	AAUAUAU	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1267	UAUAUA	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1269	AAUAUAU	CUGADGAGGCCGAAAGGCCGAA	AUAUAUA
1270	AAUAUA	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU
1272	AUAUAUA	CUGADGAGGCCGAAAGGCCGAA	AUAUAUA
1273	AAUAUAU	CUGADGAGGCCGAAAGGCCGAA	AAUAUAU

1274	AAADTAA	CUGAUGAGGCCGAAAGGCCGAA	AAADTAU
1276	GTAAATA	CUGAUGAGGCCGAAAGGCCGAA	ATAAATA
1277	UGTAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAATAAU
1278	CUGTAAA	CUGAUGAGGCCGAAAGGCCGAA	AAADTAA
1280	AUCCGUA	CUGAUGAGGCCGAAAGGCCGAA	ATAAATA
1281	CAUCUGU	CUGAUGAGGCCGAAAGGCCGAA	AAATAAU
1282	UCADUCG	CUGAUGAGGCCGAAAGGCCGAA	AAATAAA
1294	AAADTAA	CUGAUGAGGCCGAAAGGCCGAA	ACAUTCA
1296	CCAAATA	CUGAUGAGGCCGAAAGGCCGAA	ATACAUU
1297	CCCAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAATCAU
1298	UCCCAA	CUGAUGAGGCCGAAAGGCCGAA	AAATACA
1300	UCCCCA	CUGAUGAGGCCGAAAGGCCGAA	ATAAATA
1301	GUCUCC	CUGAUGAGGCCGAAAGGCCGAA	AAATAAU
1315	CCCAGGA	CUGAUGAGGCCGAAAGGCCGAA	ACCCCCG
1317	CCCCCAG	CUGAUGAGGCCGAAAGGCCGAA	ATACCCC
1334	CAGCUC	CUGAUGAGGCCGAAAGGCCGAA	ACAUTGG
1345	CUGAGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGCAGC
1350	CADGCTU	CUGAUGAGGCCGAAAGGCCGAA	AGCCAAG
1359	CACGGAA	CUGAUGAGGCCGAAAGGCCGAA	ACAUGUC
1360	UCACGGA	CUGAUGAGGCCGAAAGGCCGAA	AACAUUU
1361	UUCACGG	CUGAUGAGGCCGAAAGGCCGAA	AAACADG
1362	UUUCACG	CUGAUGAGGCCGAAAGGCCGAA	AAAACAU
1386	AACAGCC	CUGAUGAGGCCGAAAGGCCGAA	AUTGUTU
1393	ACADGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGCCT
1394	UACADGG	CUGAUGAGGCCGAAAGGCCGAA	AACAGCC
1401	AGGGGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAUGGG
1414	AGGCACA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCAG
1422	UCRAAAG	CUGAUGAGGCCGAAAGGCCGAA	AGGCACA
1423	AUCRAAA	CUGAUGAGGCCGAAAGGCCGAA	AAGGCAC
1425	UAADCAA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGGC
1426	ATAADCA	CUGAUGAGGCCGAAAGGCCGAA	AAGAAGG
1427	CAUADCC	CUGAUGAGGCCGAAAGGCCGAA	AAAGAAG
1431	AAAACAU	CUGAUGAGGCCGAAAGGCCGAA	ADCAAAA
1432	AAAAACA	CUGAUGAGGCCGAAAGGCCGAA	AADCAAA
1436	UUUAAA	CUGAUGAGGCCGAAAGGCCGAA	ACAATAU
1437	UUUUAAA	CUGAUGAGGCCGAAAGGCCGAA	AACATAA
1438	AUUUUAA	CUGAUGAGGCCGAAAGGCCGAA	AAACATA
1439	UAUUUUA	CUGAUGAGGCCGAAAGGCCGAA	AAAACAU
1440	AUAUUUU	CUGAUGAGGCCGAAAGGCCGAA	AAAAACA
1441	AAUAUUU	CUGAUGAGGCCGAAAGGCCGAA	AAAAAAC
1446	CAGADAA	CUGAUGAGGCCGAAAGGCCGAA	AUUUUAA
1448	AUCAGAU	CUGAUGAGGCCGAAAGGCCGAA	ATAUUUU
1449	AAUCAGA	CUGAUGAGGCCGAAAGGCCGAA	AAUAUUU
1451	UUADCA	CUGAUGAGGCCGAAAGGCCGAA	ATAAUAU
1456	ACAACTU	CUGAUGAGGCCGAAAGGCCGAA	AUCAGAU
1457	GACAACTU	CUGAUGAGGCCGAAAGGCCGAA	AUCAGA
1461	UUUAGAC	CUGAUGAGGCCGAAAGGCCGAA	ACTUUUU
1464	UUGUUUA	CUGAUGAGGCCGAAAGGCCGAA	ACAACTU
1466	CAUUGUU	CUGAUGAGGCCGAAAGGCCGAA	AGACAAC

1479	GUCACCA	CUGAUGAGGCCGAAAGGCCGAA	AUCAGCA
1480	GGUCACC	CUGAUGAGGCCGAAAGGCCGAA	AUCAGC
1494	AADGAGU	CUGAUGAGGCCGAAAGGCCGAA	ACAGUUG
1498	CAGCRAU	CUGAUGAGGCCGAAAGGCCGAA	AGUGACA
1501	CCUCAGC	CUGAUGAGGCCGAAAGGCCGAA	ADGAGUG
1512	GGGAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUC
1517	COCUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGCAGAG
1528	CAGACAC	CUGAUGAGGCCGAAAGGCCGAA	ACUCCCU
1533	GAUUACA	CUGAUGAGGCCGAAAGGCCGAA	ACACAAC
1537	GGCCGAU	CUGAUGAGGCCGAAAGGCCGAA	ACAGACA
1540	GUAGGCC	CUGAUGAGGCCGAAAGGCCGAA	AUUACAG
1546	UGAAUAG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCGA
1549	CACUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGUAGGC
1551	GCCACTG	CUGAUGAGGCCGAAAGGCCGAA	AUAGUAG
1552	CGCCACT	CUGAUGAGGCCGAAAGGCCGAA	AUUAGUA
1566	CAACCTU	CUGAUGAGGCCGAAAGGCCGAA	AUUUCUC
1572	CCUAAGC	CUGAUGAGGCCGAAAGGCCGAA	ACCUUUA
1576	CUUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGCAACC
1577	UCUUUCC	CUGAUGAGGCCGAAAGGCCGAA	AAGCAAC

Table 25: Mouse TNF-a HH Target Sequences

nt. Position	HH Target Sequence	nt. Position	HH Target Sequence
66	UgGAAAU a GcuCCeA	324	GgGUGAU c GGuCCCC
101	GGCAGGU U CUgUeCC	347	GAGAAgU u cCCAAaU
101	GGCAGgU u CuGUeCC	364	CCUCeCU C UeADGAG
102	GCAGGUU C UgUeCCU	366	UCeCUU C ADGAGuu
102	gCAGgUU c ugUCCCU	366	UeCCCUU C auCAGuU
106	GUUCUgU c CCUUCa	369	CUUeAU C AGuuCUa
110	UgUeCCU u UCAUeA	376	CAGuuCU a UGGCCCA
111	gUCCCUU u CaUCAC	390	AgACCUU C AcaCUeA
111	guCCCUU u CAUeAc	396	ucaCAeU C AGADCAU
112	UeCCCUU C AUeACU	401	eUCAGAU C ADUUCU
116	UuUCACU C AeUGgec	404	AGADCAU C UUCUeA
137	GCCaCAU C uCCeUCC	406	ADADCUU U CUeAAA
139	caCAuCU C CCUCeAg	406	AUeADCUU U eUeAAA
177	GCAUGAU C CGeGACG	407	UCAUCUU C UeAAau
207	AGGCaCU C CCCeAaA	409	ADUUCUU C aAAauuC
228	GGGGCUU C CAGAAU	409	AuCUuCU c AaAAUUC
228	GGGGCUU c CAGaCU	409	aUeUeU c AAAauUc
236	CAGaACU C CAGGCG	432	AGCCUGU A GCCCACG
236	CAGaACU c eAGgeGg		
249	GGUGCUU a UgUCUeA		
249	GGUGCUU a UGUeUCA	444	AcGUeGU A GCAAACC
		501	AcGCCCU C CUGGCCA
261	UCAGCCU C UUCUCaU	560	gGgUUGU a CCUuguC
261	UCAgCCU C UUCUeau	560	GGguUGU A CCUugUC
263	AGCCCUU U CUeAUUC	564	UGUACCU u gUUCUACU
263	AgCCCUU U CUeAUUC	567	ACCUgU C UACUCCC
264	GCCUUCU C UeAUUCC	569	CUugUUCU A CUCCACG
264	gCCUUCU C UeAUUCC	572	gUCUACU C CCAGGUu
266	CCUUCU C aUUCUUG	572	GUUeACU C CCAGGUu
269	UUCUCaU U CCUGeUu	572	GUUeACU C CCAGGUu
270	UCUCaU C CUGeUuG	579	CCCAGGU u CUUCUCA
276	UCCUGeU u GUUGCAG	580	CCAGGUU c uCUUeAa
297	CCACGCU C UUCUGuC	580	CCAGGUU c UCUUeAa
299	ACGCUCU U CUGuCUa	582	AGGUUCU C UUCaagg
300	CGCUCU C UGUUeAC	582	AGGUUCU C UUCaagg
304	CUUCUgU c uAcUGaa	584	GUUCUUCU U CAAGGGA
306	UeUGUeU a eUgAAeU	585	UuUCUUCU C AAGGGA
314	CUGaACU U eGgGUG	608	CcCGaCU a CgugCUC
315	UGaACU c GGgUGA	615	aCgUGeU C CUCAeCC
315	UGaACU c GGGguGa	615	AcGUGCU C CUCAeCC
324	gGGUGaU c GgUCCeC	618	UGCUUCU C ACCACA

630	ACACCgU C AGCCGau	940	GuCUACU c cUCAgAg
630	ACACCgU C AgCCgaU	943	UACUccU C AGAgcCc
638	agcCgAU u uGCUAUc	972	UCUaaCU u AgAAAGg
643	aUUUGcU a uCUcAuA	972	ucUaaCU u AGAaAgG
645	UuGCuaU C UCauACC	973	CUaACuU A GAAAggG
647	GCuaUCU C aUAACCAG	984	AGgGgAU U auGGcuc
663	agAAaGU C AACCUCC	984	AGGGgaU U aUGgCUc
669	UCAACCU C CUCUCUG	985	GGGGauU a uGGcUCA
669	UcAAccU c cUcUCUG	997	UcAGAgU c CAACucU
672	ACCUCCU C UCUGCCg	1010	CuguGCU c AGAgCUU
674	CUCUCU C UGCCgUC	1017	cAGAgCU U UCaaCAA
681	cUCCgU C AagaGcC	1018	AGAgCUU U cAaCAAC
681	CUGCCgU C AAGAGCC	1019	GAgCUUU c AaCAACu
681	CUGcCgU C aaGAgcC	1073	UGGGCCU c ucAUgCA
734	CCCUGGU A UGAGCCC	1096	AAgGAcU C AAaugGG
734	CccUGGU a ugaGCCc	1106	aUGGGcU U uccGAAU
744	AGCCCAU a UAcCUUG	1107	UGGGcUU u ccGAAUu
746	CCCAUaU A cCUGGGA	1108	GGgCUUU c cGaaUUC
759	GAgGAGU C uuCCAGc	1115	CcGAAuU C ACUGGaG
759	GAGGaGU C UUCcAGC	1133	CGAAugU C CAuuCcU
761	GGaGUU U CCAGCUG	1164	gagUGgU c AgGUUGc
762	GaGUUU C CAGCUGG	1180	UcUgUcU c agaAUgA
786	ACCaACU C AGCGCUG	1203	aaGAuCU c AGGCCUU
798	CUGAGgU C AAUCuGC	1210	cAGGCCU U CCUaccU
802	GgUCAAU C uGCCCaA	1211	AGGCCUU C CUaccUU
812	CCCaAgU A cuUaGAC	1214	CCUCCCU a cCUuCAG
816	AgUAcuU a GACUUUG	1218	CcuAACcU u CaGACCU
821	uUaGACU U UGCgGAG	1218	CCuaCCU U CAGACcu
822	UaGACUU U GCgGAGU	1218	cCuAACcU u cAgACCU
830	GCgGAGU C cGGGCAG	1218	CCUaccU u CAGAccU
840	GGCAGGU C UACUUUG	1219	CuaCCUU C AGACcuu
842	CAGGUUU A CUUUUGa	1219	CuAACCUU c agACcUU
842	CAGguUc a CUUugGA	1226	CaGACCU U uCCAgAC
842	cagGuCU a CUUUGGA	1226	CAGAccU U UCCAGAC
845	GUUACU U UGGagUC	1227	agACCUU u CCAGACu
846	UCUACUU U GGagUCA	1227	AGAccUU U CCAGACU
852	UUGGagU C AUUGCuC	1228	GAccUUU C CAGACUc
855	GagUCAU U GCuCUGU	1238	gACUcuU c cCUGAGG
887	AUCCAUU c ucUAACC	1262	CAGCCuU C CUcAcaG
891	AuuCuCU a CCCaGCC	1283	CCCCcU C uaUUUAU
905	CCcCaCU C UgaCCCC	1283	cCCcCCU C UAUUAU
905	cCCCaCU c UgaCCCC	1285	CCCCCUU A UUAUAU
905	CcCCACU c uGAccCC	1287	CcuCUAU u UauAUUU
914	GAcCCcU U uacUCUG	1287	CCUCUAU U UAUaUUU
915	ACCCCUU u acUCuGA	1288	CUUAUU U AUaUUUG
919	CUUUAcU c ugaCCcC	1289	UCUAUUU A UaUUUUG
928	GACCCcU u UaDugUC	1293	UUUAUAU U UGCACUU
928	gAcCCCU U UAUUguC	1293	uUUaUAU u UGcAcUU
932	CCUUUAU U guCuACU	1294	UUUAUAU U GCACUUA

1300	UUGCAU U aDuADUu	1462	aCCuUGU u GCCuCCU
1303	CAcuDaU u AuDuADU	1470	GccuCeU C UUUUGcU
1304	acDuADU A UUGADUA	1472	cuCcUcU U UUGcUUA
1306	UuADUAD U UADUADU	1473	uCcUcU U UGcUUAU
1307	uADUADU U ADUADUU	1474	CcUcUUU U GcUUAUG
1307	UaDUaDU U AuuADuU	1478	UUUUGcU U AUGUUUA
1308	ADUADUU A UGADUUA	1479	UUUGcUU a UGuuuAa
1310	UauDuAD U ADUADU	1479	UUUGcUU A UGUUUaa
1310	UADUADU U ADUADU	1484	UUAUGUU U aaaAcAA
1310	UADUADU U ADUADU	1498	AAAUauU U ADUUAAc
1311	ADUADU A UUGADUU	1511	AcccAaU U GUUUAA
1311	ADUADU A UUGADUU	1514	cAaUUGU C UuAAuAA
1311	AuuADU A DuAuU	1516	aUUGUcU u AAuAAcG
1313	UUAUADU U UAUUAU	1529	CgcugAU u UGUUGAC
1313	UUAUADU U UAUUAU	1529	cGUGAU U UGUUGAC
1313	uUAUADU u UauUUAu	1530	gCUGAU u gGUGacC
1314	UUAUADU U ADUADU	1530	GCUGAU U GGUGACC
1314	UUAUADU U ADUADU	1563	UgaAcCU c UGcUCCC
1315	ADUADU A UUGADUA	1563	ugaaCCU C UGcUCCC
1317	UADUADU U UAUUAU	1568	CUCUGU C CCCAcGG
1318	ADUADU U ADUADU	1589	UGaCUGU A ADuGcCC
1319	UUGADUU A UGADUA	1592	CUGUAU u GcCCUAC
1326	ADUADU A UUGADUU	1617	GAGAAU A AAGAUcG
1328	UADUADU U UAUUgC	1623	UAAAGaU c GCUUAAA
1329	ADUADU U ADUgCu	1633	UUAaaaU a aaAAaCC
1330	UUGADUU A UUGCu	25	AgGgaCU a gCCagGA
1332	UADUADU U UgCuAU		
1333	ADUADU U gCuADG		
1337	auUUGCU U AuGAAuG		
1338	uUUGCU A uGAuGu		
1346	UGAADU A UUGADU		
1348	AAUGAU U UAUUGG		
1349	ADUADU U AUUGGa		
1350	UGADUU A UUGGaA		
1352	uADUADU u UGGAAGG		
1352	UADUADU U UGGAAGg		
1353	AUUAADU U GGAAGgC		
1369	GGGUGU C CUGGaGG		
1398	gCUguCU U cAGACAg		
1398	GCUguCU U cagaCAG		
1412	GACADU U UCUUGG		
1413	ACADGU U UCUUGA		
1414	CADGUU U CUUGAA		
1415	ADGUUU C uGUGAA		
1415	ADGUUU c UgugAaA		
1438	gaGUGU c CCCAccU		
1451	CUGGCU C UCUaCCU		
1453	ggCCUCU C UaCCuUG		

Table 26: Mouse TNF- α Hammerhead Ribozyme Sequences

nt. Position	Mouse HH Ribozyme Sequence
25	UCCUGGC CUGAUGAGGCCGAAAGGCCGAA AGUCCCU
66	UGGGAGC CUGAUGAGGCCGAAAGGCCGAA AUUUCCA
101	GGGACAG CUGAUGAGGCCGAAAGGCCGAA ACCUGCC
101	GGGACAG CUGAUGAGGCCGAAAGGCCGAA ACCUGCC
102	AGGGACA CUGAUGAGGCCGAAAGGCCGAA AACUGCC
102	AGGGACA CUGAUGAGGCCGAAAGGCCGAA AACUGCC
106	UGAAAGG CUGAUGAGGCCGAAAGGCCGAA ACAGAAC
110	UGAGUGA CUGAUGAGGCCGAAAGGCCGAA AGGGACA
111	GUGAGUG CUGAUGAGGCCGAAAGGCCGAA AAGGGAC
111	GUGAGUG CUGAUGAGGCCGAAAGGCCGAA AAGGGAC
112	AGUGAGU CUGAUGAGGCCGAAAGGCCGAA AAAGGGA
115	GGCCAGU CUGAUGAGGCCGAAAGGCCGAA AGUGAAA
137	GGAGGGA CUGAUGAGGCCGAAAGGCCGAA AUGUGGC
139	CUGGAGG CUGAUGAGGCCGAAAGGCCGAA AGAUGUG
177	CGUCGGG CUGAUGAGGCCGAAAGGCCGAA AUCADGC
207	UUUGGGG CUGAUGAGGCCGAAAGGCCGAA AGUGCCU
228	AGUUCUG CUGAUGAGGCCGAAAGGCCGAA AAGCCCC
228	AGUUCUG CUGAUGAGGCCGAAAGGCCGAA AAGCCCC
236	CCGCCUG CUGAUGAGGCCGAAAGGCCGAA AGUUCUG
236	CCGCCUG CUGAUGAGGCCGAAAGGCCGAA AGUUCUG
249	UGAGACA CUGAUGAGGCCGAAAGGCCGAA AGGCACC
249	UGAGACA CUGAUGAGGCCGAAAGGCCGAA AGGCACC
261	AUGAGAA CUGAUGAGGCCGAAAGGCCGAA AGGCUGA
261	AUGAGAA CUGAUGAGGCCGAAAGGCCGAA AGGCUGA
263	GAADGAG CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
263	GAADGAG CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
264	GGAADGA CUGAUGAGGCCGAAAGGCCGAA AAGAGGC
264	GGAADGA CUGAUGAGGCCGAAAGGCCGAA AAGAGGC
266	CAGGAAT CUGAUGAGGCCGAAAGGCCGAA AGAAGAG
269	AAGCAGG CUGAUGAGGCCGAAAGGCCGAA AUGAGAA
270	CAAGCAG CUGAUGAGGCCGAAAGGCCGAA AADGAGA
276	CUGCCAC CUGAUGAGGCCGAAAGGCCGAA AGCAGGA
297	GACAGAA CUGAUGAGGCCGAAAGGCCGAA AGCGUGG
299	UAGACAG CUGAUGAGGCCGAAAGGCCGAA AGAGCGU
300	GUGAGCA CUGAUGAGGCCGAAAGGCCGAA AAGAGCG
304	UUCAGUA CUGAUGAGGCCGAAAGGCCGAA ACAGAAG
306	AGUUCAG CUGAUGAGGCCGAAAGGCCGAA AGACAGA
314	CACCCCG CUGAUGAGGCCGAAAGGCCGAA AGUUCAG
315	UCACCCC CUGAUGAGGCCGAAAGGCCGAA AAGUCCA

315	UCAAACC	CUGAUGAGGCCGAAAGGCCGAA	AAGTUCA
324	GGGGACC	CUGAUGAGGCCGAAAGGCCGAA	AUCAACC
324	GGGGACC	CUGAUGAGGCCGAAAGGCCGAA	AUCAACC
347	AUUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACTUUCU
364	CUGAUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGGAGG
366	AACUGAU	CUGAUGAGGCCGAAAGGCCGAA	AGAGGGA
366	AACUGAU	CUGAUGAGGCCGAAAGGCCGAA	AGAGGGA
369	UAGAACU	CUGAUGAGGCCGAAAGGCCGAA	AUGAGAG
376	UGGGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCG
390	UGAGGCU	CUGAUGAGGCCGAAAGGCCGAA	AGGCGCU
396	AUGAUCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUGUA
401	AGAAGAU	CUGAUGAGGCCGAAAGGCCGAA	AUCGAGG
404	UUGAGAA	CUGAUGAGGCCGAAAGGCCGAA	AUGAUCU
406	UUUGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGAGGAU
406	UUUGAGG	CUGAUGAGGCCGAAAGGCCGAA	AGAGGAU
407	AUUUGUA	CUGAUGAGGCCGAAAGGCCGAA	AAGAUGA
409	GAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
409	GAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
409	GAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
432	CGUGGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCU
444	GGUUUGC	CUGAUGAGGCCGAAAGGCCGAA	ACGACGU
501	UGGCCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGGCGU
560	GACAAGG	CUGAUGAGGCCGAAAGGCCGAA	ACAAACC
560	GACAAGG	CUGAUGAGGCCGAAAGGCCGAA	ACAAACC
564	AGUAGAC	CUGAUGAGGCCGAAAGGCCGAA	AGGUACA
567	GGGAGUA	CUGAUGAGGCCGAAAGGCCGAA	ACAAAGU
569	CUGGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGACAAG
572	AACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
572	AACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
572	AACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
579	UGAAGAG	CUGAUGAGGCCGAAAGGCCGAA	ACCUGGG
580	UUGAAGA	CUGAUGAGGCCGAAAGGCCGAA	AACUUGG
580	UUGAAGA	CUGAUGAGGCCGAAAGGCCGAA	AACUUGG
582	CCUUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGAAACU
582	CCUUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGAAACU
584	UCCCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGAGAAC
585	GUCCCUU	CUGAUGAGGCCGAAAGGCCGAA	AAGAGAA
608	GAGCAAG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCGG
615	GGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAAGU
615	GGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAAGU
618	UGUGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCA
630	AUCGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACGGUGU
630	AUCGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACGGUGU
638	GAUAGCA	CUGAUGAGGCCGAAAGGCCGAA	AUCGGCU
643	UAUGAGA	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAU
645	GGUADGA	CUGAUGAGGCCGAAAGGCCGAA	AUAGCAA
647	CGGUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGAUAGC

Table 26: Mouse TNF- α Hammerhead Ribozyme Sequences

nt. Position	Mouse HH Ribozyme Sequence
25	UCCUGGC CUGAUGAGGCCGAAAGGCCGAA AGUCCCU
66	UGGGAGC CUGAUGAGGCCGAAAGGCCGAA AUUUCCA
101	GGGACAG CUGAUGAGGCCGAAAGGCCGAA ACCUGCC
101	GGGACAG CUGAUGAGGCCGAAAGGCCGAA ACCUGCC
102	AGGGACA CUGAUGAGGCCGAAAGGCCGAA AACUUGC
102	AGGGACA CUGAUGAGGCCGAAAGGCCGAA AACUUGC
106	UGAAAGG CUGAUGAGGCCGAAAGGCCGAA ACAGAAC
110	UGAGUGA CUGAUGAGGCCGAAAGGCCGAA AGGGACA
111	GUGAGUG CUGAUGAGGCCGAAAGGCCGAA AAGGGAC
111	GUGAGUG CUGAUGAGGCCGAAAGGCCGAA AAGGGAC
112	AGUGAGU CUGAUGAGGCCGAAAGGCCGAA AAAGGGA
115	GGCCAGU CUGAUGAGGCCGAAAGGCCGAA AGUGAAA
137	GGAGGGA CUGAUGAGGCCGAAAGGCCGAA AUGUGGC
139	CUGGAGG CUGAUGAGGCCGAAAGGCCGAA AGAUGUG
177	CGUCGCG CUGAUGAGGCCGAAAGGCCGAA ADCAUCC
207	UUUGGGG CUGAUGAGGCCGAAAGGCCGAA AGUGCCU
228	AGUUCUG CUGAUGAGGCCGAAAGGCCGAA AAGCCCC
228	AGUUCUG CUGAUGAGGCCGAAAGGCCGAA AAGCCCC
236	CGGCTUG CUGAUGAGGCCGAAAGGCCGAA AGUUCUG
236	CGGCTUG CUGAUGAGGCCGAAAGGCCGAA AGUUCUG
249	UGAGACA CUGAUGAGGCCGAAAGGCCGAA AGGCACC
249	UGAGACA CUGAUGAGGCCGAAAGGCCGAA AGGCACC
261	AUGAGAA CUGAUGAGGCCGAAAGGCCGAA AGGCTGA
261	AUGAGAA CUGAUGAGGCCGAAAGGCCGAA AGGCTGA
263	GAUUGAG CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
263	GAUUGAG CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
264	GGAAUGA CUGAUGAGGCCGAAAGGCCGAA AAGAGGC
264	GGAAUGA CUGAUGAGGCCGAAAGGCCGAA AAGAGGC
266	CAGGAAT CUGAUGAGGCCGAAAGGCCGAA AGAAGAG
269	AAGCAGG CUGAUGAGGCCGAAAGGCCGAA AUGAGAA
270	CAAGCAG CUGAUGAGGCCGAAAGGCCGAA AAUGAGA
276	CUGCCAC CUGAUGAGGCCGAAAGGCCGAA AGCAGGA
297	GACAGAA CUGAUGAGGCCGAAAGGCCGAA AGCGUGG
299	UAGACAG CUGAUGAGGCCGAAAGGCCGAA AGAGCGU
300	GUAGACA CUGAUGAGGCCGAAAGGCCGAA AAGAGCG
304	UUCAGUA CUGAUGAGGCCGAAAGGCCGAA ACAGGAG
306	AGUUCAG CUGAUGAGGCCGAAAGGCCGAA AGACAGA
314	CAGCCCG CUGAUGAGGCCGAAAGGCCGAA AGUUCAG
315	UACCCC CUGAUGAGGCCGAAAGGCCGAA AAGUACA

315	UCAAACCC	CUGAUGAGGCCGAAAGGCCGAA	AAGTUCA
324	GGGGACC	CUGAUGAGGCCGAAAGGCCGAA	AUCAACC
324	GGGGACC	CUGAUGAGGCCGAAAGGCCGAA	AUCAACC
347	AUUUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACTUCUC
364	CUGAUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGGAGG
366	AACUGAU	CUGAUGAGGCCGAAAGGCCGAA	AGAGGGA
366	AACUGAU	CUGAUGAGGCCGAAAGGCCGAA	AGAGGGA
369	UAGAACU	CUGAUGAGGCCGAAAGGCCGAA	ADGAGAG
376	UGGGCCA	CUGAUGAGGCCGAAAGGCCGAA	AGAACCG
390	UGAGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGGCCU
396	AUGADCU	CUGAUGAGGCCGAAAGGCCGAA	AGGUGCA
401	AGAAGAU	CUGAUGAGGCCGAAAGGCCGAA	AUCCGAG
404	UUAGAGU	CUGAUGAGGCCGAAAGGCCGAA	AUGADCU
406	UUUUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGADGAG
406	UUUUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGADGAG
407	AUUUUGA	CUGAUGAGGCCGAAAGGCCGAA	AGAUGA
409	GAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
409	GAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
409	GAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
432	CGUGGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAGGCU
444	GGUUUGC	CUGAUGAGGCCGAAAGGCCGAA	ACGACCU
501	UGGGCAG	CUGAUGAGGCCGAAAGGCCGAA	AGGGCGU
560	GACAAGG	CUGAUGAGGCCGAAAGGCCGAA	ACAACCC
560	GACAAGG	CUGAUGAGGCCGAAAGGCCGAA	ACAACCC
564	AGUAGAC	CUGAUGAGGCCGAAAGGCCGAA	AGGUACA
567	GGGAGUA	CUGAUGAGGCCGAAAGGCCGAA	ACAAGGU
569	CUGGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGACAAG
572	AACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
572	AACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
572	AACUUGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
579	UGAAGAG	CUGAUGAGGCCGAAAGGCCGAA	AACUUGG
580	UUGAAGA	CUGAUGAGGCCGAAAGGCCGAA	AACUUGG
580	UUGAAGA	CUGAUGAGGCCGAAAGGCCGAA	AACUUGG
582	CCUUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGAACCU
582	CCUUGAA	CUGAUGAGGCCGAAAGGCCGAA	AGAACCU
584	UCCCUUG	CUGAUGAGGCCGAAAGGCCGAA	AGAGAAC
585	GUCCCUU	CUGAUGAGGCCGAAAGGCCGAA	AAGAGAA
608	GAGCACG	CUGAUGAGGCCGAAAGGCCGAA	AGUCCGG
615	GGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAAGU
615	GGGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AGCAAGU
618	UGUGGGU	CUGAUGAGGCCGAAAGGCCGAA	AGGAGCA
630	AUCGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACGGGCU
630	AUCGGCU	CUGAUGAGGCCGAAAGGCCGAA	ACGGGCU
638	GADAGCA	CUGAUGAGGCCGAAAGGCCGAA	AUCGGCU
643	UADGAGA	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAU
645	GUADUGA	CUGAUGAGGCCGAAAGGCCGAA	AUAGCAA
647	CUGGUAU	CUGAUGAGGCCGAAAGGCCGAA	AGAUAGC

663	GGAGGTU	CUGADGAGGCCGAAAGGCCGAA	ACUUTCU
669	CAGAGAG	CUGADGAGGCCGAAAGGCCGAA	AGGUTGA
669	CAGAGAG	CUGADGAGGCCGAAAGGCCGAA	AGGUTGA
672	CGGCAGA	CUGADGAGGCCGAAAGGCCGAA	AGGAGGU
674	GACGGCA	CUGADGAGGCCGAAAGGCCGAA	AGAGGAG
681	GGCUCU	CUGADGAGGCCGAAAGGCCGAA	ACGGCAG
681	GGCUCU	CUGADGAGGCCGAAAGGCCGAA	ACGGCAG
681	GGCUCU	CUGADGAGGCCGAAAGGCCGAA	ACGGCAG
734	GGGCUCA	CUGADGAGGCCGAAAGGCCGAA	ACCAAGG
734	GGGCUCA	CUGADGAGGCCGAAAGGCCGAA	ACCAAGG
744	CCAGGUA	CUGADGAGGCCGAAAGGCCGAA	ADGGGCU
746	UCCCAAG	CUGADGAGGCCGAAAGGCCGAA	ATAAGGG
759	GCUGGAA	CUGADGAGGCCGAAAGGCCGAA	ACUCCTC
759	GCUGGAA	CUGADGAGGCCGAAAGGCCGAA	ACUCCTC
761	CAGCUGG	CUGADGAGGCCGAAAGGCCGAA	AGACTCC
762	CCAGCTG	CUGADGAGGCCGAAAGGCCGAA	AAGACTC
786	CAGCGTU	CUGADGAGGCCGAAAGGCCGAA	AGUUGGU
798	GCAGAUU	CUGADGAGGCCGAAAGGCCGAA	ACCTCAG
802	UUGGGCA	CUGADGAGGCCGAAAGGCCGAA	ADUGACC
812	GUCUAAG	CUGADGAGGCCGAAAGGCCGAA	ACUUGGG
816	CAAAGUC	CUGADGAGGCCGAAAGGCCGAA	AAGUACT
821	CUCCGCA	CUGADGAGGCCGAAAGGCCGAA	AGUCCAA
822	ACUCCGC	CUGADGAGGCCGAAAGGCCGAA	AAGUCCA
830	CUGCCCG	CUGADGAGGCCGAAAGGCCGAA	ACUCCGC
840	CAAAGUA	CUGADGAGGCCGAAAGGCCGAA	ACCUCCG
842	UCCAAAG	CUGADGAGGCCGAAAGGCCGAA	AGACCTG
842	UCCAAAG	CUGADGAGGCCGAAAGGCCGAA	AGACCTG
842	UCCAAAG	CUGADGAGGCCGAAAGGCCGAA	AGACCTG
845	GACTUCC	CUGADGAGGCCGAAAGGCCGAA	AGUAGAC
846	UGACTCC	CUGADGAGGCCGAAAGGCCGAA	AAGUAGA
852	GAGCAAU	CUGADGAGGCCGAAAGGCCGAA	ACUCCAA
855	ACAGAGC	CUGADGAGGCCGAAAGGCCGAA	ADGACTC
887	GGGUAGA	CUGADGAGGCCGAAAGGCCGAA	AADGGAU
891	GGCTGGG	CUGADGAGGCCGAAAGGCCGAA	AGAGAAU
905	GGGGUCA	CUGADGAGGCCGAAAGGCCGAA	AGUGGGG
905	GGGGUCA	CUGADGAGGCCGAAAGGCCGAA	AGUGGGG
905	GGGGUCA	CUGADGAGGCCGAAAGGCCGAA	AGUGGGG
914	CAGAGUA	CUGADGAGGCCGAAAGGCCGAA	AGGGGTC
915	UCAGAGU	CUGADGAGGCCGAAAGGCCGAA	AAGGGGU
919	GGGGUCA	CUGADGAGGCCGAAAGGCCGAA	AGUAAAG
928	GACAAUA	CUGADGAGGCCGAAAGGCCGAA	AGGGGTC
928	GACAAUA	CUGADGAGGCCGAAAGGCCGAA	AGGGGTC
932	AGUAGAC	CUGADGAGGCCGAAAGGCCGAA	AUAAGGG
940	CUCUGAG	CUGADGAGGCCGAAAGGCCGAA	AGUAGAC
943	GGGCTCU	CUGADGAGGCCGAAAGGCCGAA	AGGAGUA
972	CCUUUCU	CUGADGAGGCCGAAAGGCCGAA	AGUUAGA
972	CCUUUCU	CUGADGAGGCCGAAAGGCCGAA	AGUUAGA
973	CCCUUUC	CUGADGAGGCCGAAAGGCCGAA	AAGUUAG
984	GAGCCAU	CUGADGAGGCCGAAAGGCCGAA	AUCCCTU

984	GAGCCAT	CUGAUGAGGCCGAAAGGCCGAA	AUCCCCU
985	UGAGCCA	CUGAUGAGGCCGAAAGGCCGAA	AAUCCCC
997	AGAGUUG	CUGAUGAGGCCGAAAGGCCGAA	ACUCCGA
1010	AAGCUCU	CUGAUGAGGCCGAAAGGCCGAA	AGCACAG
1017	UUGUUGA	CUGAUGAGGCCGAAAGGCCGAA	AGCUCUG
1018	GUUGUUG	CUGAUGAGGCCGAAAGGCCGAA	AAGCUCU
1019	AGUUGUU	CUGAUGAGGCCGAAAGGCCGAA	AAAGCUC
1073	UGCAUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCCA
1096	CCCAUUT	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUU
1106	AUUCGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCAU
1107	AAUUCGG	CUGAUGAGGCCGAAAGGCCGAA	AAGCCCA
1108	GAADUCG	CUGAUGAGGCCGAAAGGCCGAA	AAAGCCC
1115	CUCCAGU	CUGAUGAGGCCGAAAGGCCGAA	AAUUCGG
1133	AGGAADG	CUGAUGAGGCCGAAAGGCCGAA	ACAUUCG
1164	GCAACCU	CUGAUGAGGCCGAAAGGCCGAA	ACCAUCU
1180	UCAUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGAACA
1203	AAGGCTU	CUGAUGAGGCCGAAAGGCCGAA	AGAUUCU
1210	AGGUAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCUG
1211	AAGGUAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCTU
1214	CGAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGG
1218	AGGUUCG	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGG
1218	AGGUUCG	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGG
1218	AGGUUCG	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGG
1218	AGGUUCG	CUGAUGAGGCCGAAAGGCCGAA	AGGUAGG
1219	AAGGUCT	CUGAUGAGGCCGAAAGGCCGAA	AAGGUAG
1219	AAGGUCT	CUGAUGAGGCCGAAAGGCCGAA	AAGGUAG
1226	GUCUGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCG
1226	GUCUGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGUUCG
1227	AGUCUGG	CUGAUGAGGCCGAAAGGCCGAA	AAGGUCT
1227	AGUCUGG	CUGAUGAGGCCGAAAGGCCGAA	AAGGUCT
1228	GAGUCUG	CUGAUGAGGCCGAAAGGCCGAA	AAAGGUC
1238	CCUCAGG	CUGAUGAGGCCGAAAGGCCGAA	AAGAGUC
1262	CUUGAG	CUGAUGAGGCCGAAAGGCCGAA	AAGGCTG
1283	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGGGGG
1283	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGGGGG
1285	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGGGGG
1287	AAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAAGAG
1287	AAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAAGAG
1288	CAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAAGAG
1289	GCAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AAUAAGA
1293	AAGUGCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1293	AAGUGCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1294	UAAGUGC	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1300	AAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGUGCAA
1303	AAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAAGUG
1304	UAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AAUAAGU
1306	AAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1307	AAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAUA
1307	AAUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AAUAUAUA

1308	UAAUUA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAAU
1310	AAUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAAAUU
1310	AAUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAAAUU
1310	AAUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AUAAAUU
1311	AAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1311	AAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1311	AAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1313	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1313	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1313	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1314	AAUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1314	AAUAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1315	UAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAAU
1317	AAUUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1318	AAAUAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1319	UAAUUA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAAA
1326	AAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAAU
1328	GCAAUUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1329	AGCAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1330	AAGCAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUAAA
1332	AUAAGCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1333	CAUAAGC	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1337	CAUUCAU	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAU
1338	ACAUUCA	CUGAUGAGGCCGAAAGGCCGAA	AAGCAAA
1346	AAAUAAA	CUGAUGAGGCCGAAAGGCCGAA	ACAUUCA
1348	CCAAUAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1349	UCCAAAU	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
1350	UUCCAAA	CUGAUGAGGCCGAAAGGCCGAA	AAAUACA
1352	CCUCCCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1352	CCUCCCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
1353	GCCUCCC	CUGAUGAGGCCGAAAGGCCGAA	AAUAAAU
1369	CCUCCAG	CUGAUGAGGCCGAAAGGCCGAA	ACACCCC
1398	CUGUCUG	CUGAUGAGGCCGAAAGGCCGAA	AGACAGC
1398	CUGUCUG	CUGAUGAGGCCGAAAGGCCGAA	AGACAGC
1412	CACAGAA	CUGAUGAGGCCGAAAGGCCGAA	ACAUUCU
1413	UCACAGA	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
1414	UUCACAG	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
1415	UUUCACA	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
1415	UUUCACA	CUGAUGAGGCCGAAAGGCCGAA	AAUACAU
1438	AGGUGGG	CUGAUGAGGCCGAAAGGCCGAA	ACAGGUC
1451	AGGUGGA	CUGAUGAGGCCGAAAGGCCGAA	AGGUGAG
1453	CAAGGUA	CUGAUGAGGCCGAAAGGCCGAA	AGAGGCC
1455	AACAAGG	CUGAUGAGGCCGAAAGGCCGAA	AGAGAGG
1462	AGGAGGC	CUGAUGAGGCCGAAAGGCCGAA	ACAAGGU
1470	AGCAAAA	CUGAUGAGGCCGAAAGGCCGAA	AGGAGGC
1472	UAAGCAA	CUGAUGAGGCCGAAAGGCCGAA	AGAGGAG
1473	AUAAGCA	CUGAUGAGGCCGAAAGGCCGAA	AAGAGGA
1474	CAUAAGC	CUGAUGAGGCCGAAAGGCCGAA	AAAGAGG
1478	UAAACAU	CUGAUGAGGCCGAAAGGCCGAA	AGCAAAA

1479	UTAAACA	COGAUGAGGCCGAAAGGCCGAA	AAGCAAA
1479	UTAAACA	COGAUGAGGCCGAAAGGCCGAA	AAGCAAA
1484	UUGUUUU	COGAUGAGGCCGAAAGGCCGAA	AACAATA
1498	GUUAGA	COGAUGAGGCCGAAAGGCCGAA	AAUAUUU
1511	UUAAGAC	COGAUGAGGCCGAAAGGCCGAA	AUUGGGU
1514	UUAUUAA	COGAUGAGGCCGAAAGGCCGAA	ACAADUG
1516	CGUUUUU	COGAUGAGGCCGAAAGGCCGAA	AGACAAU
1529	GUCAACA	COGAUGAGGCCGAAAGGCCGAA	AUCAGCG
1529	GUCAACA	COGAUGAGGCCGAAAGGCCGAA	AUCAGCG
1530	GGUACAC	COGAUGAGGCCGAAAGGCCGAA	AUUCAGC
1530	GGUACAC	COGAUGAGGCCGAAAGGCCGAA	AUUCAGC
1563	GGGAGCA	COGAUGAGGCCGAAAGGCCGAA	AGGUUCA
1563	GGGAGCA	COGAUGAGGCCGAAAGGCCGAA	AGGUUCA
1568	CGUGGGG	COGAUGAGGCCGAAAGGCCGAA	AGCAGAG
1589	GGCAAUU	COGAUGAGGCCGAAAGGCCGAA	ACAGUCA
1592	GUAGGGC	COGAUGAGGCCGAAAGGCCGAA	AUUAACG
1617	CGAUUUU	COGAUGAGGCCGAAAGGCCGAA	AUUUCUC
1623	UUUAAGC	COGAUGAGGCCGAAAGGCCGAA	AUCUUUA
1633	GGUUUUU	COGAUGAGGCCGAAAGGCCGAA	AUUUUAA

Table 27: Human TNF- α Hairpin Ribozyme Sequences

nt. Position	Hairpin Ribozyme Sequence		Substrate
46	AGCCGUGG	AGAA GUUGU	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
54	GAGGUGG	AGAA GUUGU	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
185	GAGGAGA	AGAA GAGGA	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
201	CUGCCAG	AGAA GGAAG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
230	GUGCAGCA	AGAA GAAGG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
234	CNAAGUC	AGAA GCGAG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
254	CCUCUGG	AGAA GAUCAC	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
296	GCCAGAG	AGAA GAUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
317	AGAGAGU	AGAA GACUC	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
387	GCCACUG	AGAA GCGGU	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
404	AUUGGCC	AGAA GUGUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
453	GCACACC	AGAA GGUUU	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
518	GUGGAGB	AGAA GCUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
554	GGCAUCC	AGAA GUUGU	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
565	UGGUAGB	AGAA GCGAG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
576	UGACUUG	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
607	CCUUCUC	AGAA GUAAC	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
704	AGGCUCA	AGAA GUAUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
726	GUAGUUG	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
730	UGAGGUA	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
824	GGGUAUG	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1042	GGGUAUA	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1168	CUGGAAAC	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1178	UCAGGAA	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1202	AUGGGAG	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1220	AUAGGGG	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1284	AUACAUU	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1340	UGAGCAA	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA
1390	UACUUGG	AGAA GGUUG	ACCAGAGAAACACACGUGUGGUAACAUAUACCUUGUA

1452	ACAACUUA	AGAA	GAUUAU	ACCAGAGNAAACACACACGUGUGUGUACAUUACCUUGUA	AUUUAUU	GAU	UUAAGUUGU
1475	GUACACCA	AGAA	GCAUUG	ACCAGAGNAAACACACACGUGUGUGUACAUUACCUUGUA	CANUGCU	GAU	UUGGUGUAC
1513	CCUUGGG	AGAA	GAGGCC	ACCAGAGNAAACACACACGUGUGUGUACAUUACCUUGUA	GCCCCU	CCU	CCCCAGGG
1541	GAUUGUA	AGAA	GAUUAU	ACCAGAGNAAACACACACGUGUGUGUACAUUACCUUGUA	GUUAUUG	GCC	UUAUUAUC

Table 28: Mouse TNF- α Hairpin Ribozyme Sequences

nt. Position	Hairpin Ribozyme Sequence		Substrate
103	GUCAAGG AGAA GAAU	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	AGGUU GUC CCUUUCAC
256	UGAGACA AGAA GAGCA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	UGUUA GUC UCUUUCUA
272	CUCCACA AGAA GGAUG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CAUUU GCU UGUUGGAG
301	GUUAGUA AGAA GAGAG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CUUUU GUC UACUGAAC
325	CCUUUGG AGAA GAUAC	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	GUUUG GUC CCUAAAGG
370	GGCCUAG AGAA GUAUG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CUUUA GUU CUUUGGCC
383	GUUGAGG AGAA GGUCA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	UGGUU GAC CCUUCACAC
397	AGAGAGG AGAA GAGGU	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	ACUUA GAU CAUUCUUC
467	GCACUUC AGAA GUUUU	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	ACGACA GCU GAGUGGCC
546	APCCUUC AGAA GGUAC	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	GGUUA GUC GAGUGGUU
549	UACAUCC AGAA GUUCC	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	GUUUG GCU GGUUGGUU
598	GUAGUUG AGAA GUUCC	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	GUUUG GCU GGUUGGUU
603	AGCAGUA AGAA GUUCC	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CAAGG GUC CCUUCUAC
631	ACCAUUC AGAA GUUCC	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CUUUC GAC UAGUGUUC
634	GUUAGCA AGAA GUUCC	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	ACGUU GUC GGUUGGUU
675	CUUUGAC AGAA GAGAG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	GUUUG GCU UGUUGUAC
691	GUUUGAC AGAA GAGAG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CUUUC GUC GUUAGGAG
764	CCUUUCC AGAA GGUUU	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	AGUUU GUC CCUUCUAC
803	AGUACUUG AGAA GGUUA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	UCUUA GCU GAGAGAGG
895	AGGUGGG AGAA GGUUG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	UCUUA GCU GAGAGAGG
906	GUUAGGG AGAA GGUUG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CUUUA GCU CCUUCUUC
920	UUAAGGG AGAA GGUUA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CUUUA GCU CCUUCUUC
953	AGGACACA AGAA GGUUG	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	UUAUU GAC CCUUCUUC
1175	CAUUCUA AGAA GGUUA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	GUUUU GUC UGUUGGUU
1220	CUUAGAG AGAA GGUUA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	UGUUU GUC UGUUGGUU
1230	AGGAGAG AGAA GGUUA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	ACUUA GAC CUUUCUUC
1256	GUUAGGA AGAA GGUUA	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	CUUUA GAC UGUUGGUU
1274	UUAAGGG AGAA GGUUU	ACGAGGAAACACAGGUGUGGACAUUACUUGUA	AGUUA GUC UGUUGGUU

1393	UGUUGAA AGA GGUCC ACCAGGAGACACGUGUGGUCACUAUACUUGGA	GGAGCU GUC UUCAGCA
1435	CAGGUGG AGA GGUCC ACCAGGAGACACGUGUGGUCACUAUACUUGGA	CUAGCU GUC CUCACUUG
1525	GUACCAA AGA GGUUA ACCAGGAGACACGUGUGGUCACUAUACUUGGA	UAGGCU GAU UUGGUCAC
1542	GUUGAGC AGA GGUUG ACCAGGAGACACGUGUGGUCACUAUACUUGGA	CCAGGCU GUC GUUACUAC
1564	CGUGGGG AGA GAGGU ACCAGGAGACACGUGUGGUCACUAUACUUGGA	AACUUCU GUU CUCACUUG

Table 29: Human *bcr/abl* HH Target Sequence

Sequence ID No.	HH Target Sequence
<u>b2-a2</u> <u>junction</u>	
20	UGGCCAACA AUA AGGAGAGAGCC
21	GAAGAGCC CUU CAGGGGCGAGU
22	AAGAGGCC UUC AGGGGCGAGUA

b3-a2
junction

23	UAAGCGAG UUC AAAAGCCCUUC
24	UCAAAGCC CUU CAGGGGCGAGU
25	CAAAAGGCC UUC AGGGGCGAGUA

Table 30: Human *bcr-abl* HH Ribozyme Sequences

Sequence ID No.	HH Ribozyme Sequence
26	GGCUUCUCCU CUGAUGAGGCCGAAAGGCCGAA AUUGAUGGUA
27	ACUGGCCGCTG CUGAUGAGGCCGAAAGGCCGAA AAGGCCUUCUC
28	UACUGGCCGCT CUGAUGAGGCCGAAAGGCCGAA AAGGCCUUCU
29	GAAGGGCUUUU CUGAUGAGGCCGAAAGGCCGAA AACUCUGCUUA
30	ACUGGCCGCTG CUGAUGAGGCCGAAAGGCCGAA AAGGCCUUUGA
31	UACUGGCCGCT CUGAUGAGGCCGAAAGGCCGAA AAGGCCUUUG

Table 31: RSV (1B) HH Target Sequence

nt. Position	HH Target Sequence	nt. Position	HH Target Sequence
10	GGCAAAU A AADCAAU	276	AAAAUAU A CUGAAUA
14	AAUAAAU C AAUUCAG	283	ACUGAAU A CAACACA
18	AADCAAU U CAGCCAA	295	ACAAAUA A UGGCACU
19	AUCAAU C AGCCAAC	303	UGGCACU U UCCTUAU
54	CAADGAU A AUAACCC	304	GGCACU U CCCCUAAG
57	UGAUAAU A CACCACA	305	GCACU U C CCAUAGC
77	UGAUGAU C ACAGACA	309	UUUCCCU A UGCCAAU
94	AGACCGU U GUCACUU	317	UGCCAAU A UUCACCA
97	CCGUUGU C ACUUGAG	319	CCAUAU U CAUCAAU
101	UGUCACU U GAGACCA	320	CAUAU C AUCAADG
110	AGACCAU A AUAACAU	323	UAUUAU C AAUCAAAG
113	CCAUAAU A ACAUCAC	327	CAUCAAU C AUGAUGG
118	AUAACAU C ACUACCC	337	GAUGGGU U CUUAGAA
122	CAUACU A ACCAGAG	338	AUGGGUU C UUAAGAU
134	GAGACAU C AUAACAC	340	GGGUUUU U AGAAUAGC
137	ACAUCAU A ACACACA	341	GGUUCUU A GAADGCA
148	CACAAAU U UAUAUAC	350	AAUGCAU U GGCADUA
149	ACAAAUU U AUAUAU	356	UUGGCAU U AAGCCUA
150	CAAAUUU A UAUAUU	357	UGGCAU A AGCCUAC
152	AAUUUAU A UACUUGA	363	UAAGCCU A CAAAGCA
154	UUUAUAU A CUUGAUA	372	AAAGCAU A CUCCCAU
157	AUAUAU U GAUAAAU	375	GCAUAU C CCAUAU
161	ACUUGAU A AADCAUG	380	CUCCCAU A AUAUACA
165	GAUAAAU C AUGAUG	383	CCAUAAU A UACAAGU
176	AAUGCAU A GUGAGAA	385	AUAUAU A CAAGUAU
188	GAAAAU U GAUGAAA	391	UACAAGU A UGAUUC
208	GCCACAU U UACAUUC	396	GUADGAU C UCAAUCC
209	CCACAUU U ACAUUC	398	AUGAUU C AAUCCAU
210	CACAUU A CAUUCU	402	UCUCAU C CAUAAAU
214	UUUAUAU U CUGGUC	406	AAUCCAU A AAUUUCA
215	UUACAU C CUGGUA	410	CACAAU U UCAACAC
221	UCCUGGU C AACUAUG	411	AUAUUU U CAACACA
226	GUCAAU A UGAAADG	412	UAAUUU C AACACAA
239	UGAAAU A UUAACA	421	ACACAU A UUCACAC
241	AAACUAU U ACACAAA	423	ACAAUAU U CACACAA
242	AACUAU A CACAAAG	424	CAUAU C ACACAAU
251	ACAAAGU A GGAAGCA	432	ACACAU C UAAAACA
261	AAGCAU A AAUAUA	434	ACAAUCU A AAACAAC
265	ACUAAU A UAAAAA	446	AACAACU C UAUGCAU
267	UAAUAU A AAAAAUA	448	CAUUCU A UGCAUA
274	AAAAAAU A UACUGAA	454	UAUGCAU A ACTUAUC

458	CADTACT	A	UACUCCA
460	UACTCAT	A	CUCCATA
463	CTADACT	C	CADAGOC
467	ACUCCAT	A	GUCCAGA
470	CCADTAG	C	CAGADGG
489	UGAAAAU	U	ADAGUAA
490	GAAAAUU	A	UAGUAAU
492	AAAUUAA	A	GUAAUUU
495	UUADTAG	A	AUUUAAA

Table 32: RSV (1B) HH Ribozyme Sequence

nt. Position	HH Ribozyme Sequence
10	AUUGAUU CUGAUGAGGCCGAAAGGCCGAA AUUUGCC
14	CUGAUUU CUGAUGAGGCCGAAAGGCCGAA AUUUUUU
18	UUGGCUU CUGAUGAGGCCGAAAGGCCGAA AUUGAUU
19	GUUGGUU CUGAUGAGGCCGAAAGGCCGAA AAUUGAU
54	GGUGUUA CUGAUGAGGCCGAAAGGCCGAA AUCAUUG
57	UGUGGUG CUGAUGAGGCCGAAAGGCCGAA AUUAUCA
77	UGUCUGU CUGAUGAGGCCGAAAGGCCGAA AUCAUCA
94	AAGUGAC CUGAUGAGGCCGAAAGGCCGAA ACGGUCU
97	CUCAAGU CUGAUGAGGCCGAAAGGCCGAA ACAACGG
101	UGGUCUC CUGAUGAGGCCGAAAGGCCGAA AGUGACA
110	AUGUUUU CUGAUGAGGCCGAAAGGCCGAA AUGGUCU
113	GUGAUGU CUGAUGAGGCCGAAAGGCCGAA AUUADGG
118	GGUUAGU CUGAUGAGGCCGAAAGGCCGAA AUGUUUU
122	CUUGUGU CUGAUGAGGCCGAAAGGCCGAA AGUGAUG
134	GUGUUUU CUGAUGAGGCCGAAAGGCCGAA AUGUCUC
137	UGUGUGU CUGAUGAGGCCGAAAGGCCGAA AUGAUGU
148	GUUAUAU CUGAUGAGGCCGAAAGGCCGAA AUUUGUG
149	AGUAUAU CUGAUGAGGCCGAAAGGCCGAA AAUUGUU
150	AAUAUAU CUGAUGAGGCCGAAAGGCCGAA AAUUGUG
152	UCAAGUA CUGAUGAGGCCGAAAGGCCGAA AUUAUUU
154	UAUCAAG CUGAUGAGGCCGAAAGGCCGAA AUUAUAU
157	AUUUAUC CUGAUGAGGCCGAAAGGCCGAA AGUAUAU
161	CAUGAUU CUGAUGAGGCCGAAAGGCCGAA AUCAAGU
165	CAUUCAU CUGAUGAGGCCGAAAGGCCGAA AUUUUUC
176	UUCUCAC CUGAUGAGGCCGAAAGGCCGAA AUGCAUU
188	UUUCAUC CUGAUGAGGCCGAAAGGCCGAA AGUUUUC
208	GAADGUA CUGAUGAGGCCGAAAGGCCGAA AUGGGGC
209	GGAADGU CUGAUGAGGCCGAAAGGCCGAA AAUGGGG
210	AGGAADG CUGAUGAGGCCGAAAGGCCGAA AAADGUG
214	GACCAAG CUGAUGAGGCCGAAAGGCCGAA AUGUAAA
215	UGACCAG CUGAUGAGGCCGAAAGGCCGAA AAUGUAA
221	CADAGUU CUGAUGAGGCCGAAAGGCCGAA ACCAGGA
226	CAUUUCA CUGAUGAGGCCGAAAGGCCGAA AGUUGAC
239	UGUGUAA CUGAUGAGGCCGAAAGGCCGAA AGUUUCA
241	UUUGUGU CUGAUGAGGCCGAAAGGCCGAA AUAGUUU
242	CUUUGUG CUGAUGAGGCCGAAAGGCCGAA AAADAGU
251	UGCUUCC CUGAUGAGGCCGAAAGGCCGAA ACUUUGU
261	UUUAUAU CUGAUGAGGCCGAAAGGCCGAA AGUGCUU
265	UUUUUUA CUGAUGAGGCCGAAAGGCCGAA AUUUAGU
267	UAUUUUU CUGAUGAGGCCGAAAGGCCGAA AUUAUUU
274	UUCAGUA CUGAUGAGGCCGAAAGGCCGAA AUUUUUU
276	UAUUCAG CUGAUGAGGCCGAAAGGCCGAA AUUAUUU

283	UGGUGUG	CUGAUGAGGCCGAAAGGCCGAA	AUUCAGU
295	AGUGCCA	CUGAUGAGGCCGAAAGGCCGAA	AUUUUGU
303	AUAGGGA	CUGAUGAGGCCGAAAGGCCGAA	AGUGCCA
304	CADAGGG	CUGAUGAGGCCGAAAGGCCGAA	AAGUGCC
305	GCAUAGG	CUGAUGAGGCCGAAAGGCCGAA	AAAGUGC
309	AUUGGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGGAUA
317	UGAUGAA	CUGAUGAGGCCGAAAGGCCGAA	AUUGGCA
319	AUUGAUG	CUGAUGAGGCCGAAAGGCCGAA	AUAUUGG
320	GAUUGAU	CUGAUGAGGCCGAAAGGCCGAA	AAUAUUG
323	CADGAUU	CUGAUGAGGCCGAAAGGCCGAA	ADGAUAU
327	CCAUCAU	CUGAUGAGGCCGAAAGGCCGAA	AUUGAUG
337	UUCUAAG	CUGAUGAGGCCGAAAGGCCGAA	ACCCAUU
338	AUUCUAA	CUGAUGAGGCCGAAAGGCCGAA	AAUCCAU
340	GCAUUCU	CUGAUGAGGCCGAAAGGCCGAA	AGAAUCC
341	UGCAUUC	CUGAUGAGGCCGAAAGGCCGAA	AAGAAUCC
350	UAADGCC	CUGAUGAGGCCGAAAGGCCGAA	AUGCAUU
356	UAGGCUU	CUGAUGAGGCCGAAAGGCCGAA	AUGCCAA
357	GUAGGCU	CUGAUGAGGCCGAAAGGCCGAA	AADGCCA
363	UGCUUUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCUUA
372	AUGGGAG	CUGAUGAGGCCGAAAGGCCGAA	ADGCUUU
375	AUUAUUG	CUGAUGAGGCCGAAAGGCCGAA	AGUAUUG
380	UGUAUAU	CUGAUGAGGCCGAAAGGCCGAA	ADGGGAG
383	ACUUGUA	CUGAUGAGGCCGAAAGGCCGAA	AUUAUUG
385	AUAUUGG	CUGAUGAGGCCGAAAGGCCGAA	AUAUUAU
391	GAGAUCA	CUGAUGAGGCCGAAAGGCCGAA	ACUUGUA
396	GGAUUGA	CUGAUGAGGCCGAAAGGCCGAA	ADCAUAU
398	ADGGAUU	CUGAUGAGGCCGAAAGGCCGAA	AGAUCAU
402	AUUUAUG	CUGAUGAGGCCGAAAGGCCGAA	AUUGAGA
406	UGAAAUU	CUGAUGAGGCCGAAAGGCCGAA	ADGGAUU
410	GUGUUGA	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUG
411	UGUGUUG	CUGAUGAGGCCGAAAGGCCGAA	AAUUAUA
412	UUGUGUU	CUGAUGAGGCCGAAAGGCCGAA	AAAUUAU
421	GUGUGAA	CUGAUGAGGCCGAAAGGCCGAA	AUUGUGU
423	UUGUGUG	CUGAUGAGGCCGAAAGGCCGAA	AUAUUGU
424	AUUGUGU	CUGAUGAGGCCGAAAGGCCGAA	AAUAUUG
432	UGUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUGUGU
434	GUUGUUU	CUGAUGAGGCCGAAAGGCCGAA	AGAUUGU
446	AUGCAUA	CUGAUGAGGCCGAAAGGCCGAA	AGUUGUU
448	UAUUGCA	CUGAUGAGGCCGAAAGGCCGAA	AGAGUUG
454	GUAUAGU	CUGAUGAGGCCGAAAGGCCGAA	AUGCAUA
458	UGGAGUA	CUGAUGAGGCCGAAAGGCCGAA	AGUAUUG
460	UAUGGAG	CUGAUGAGGCCGAAAGGCCGAA	AUAUUAU
463	GACUAUG	CUGAUGAGGCCGAAAGGCCGAA	AGUAUAG
467	UCUGGAC	CUGAUGAGGCCGAAAGGCCGAA	AUGGAGU
470	CCAUUCU	CUGAUGAGGCCGAAAGGCCGAA	ACUAUUG
489	UAUAUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUUAU
490	AUAUAUA	CUGAUGAGGCCGAAAGGCCGAA	AUUUUAU
492	AAAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
495	UUUAUAU	CUGAUGAGGCCGAAAGGCCGAA	ACTUAUA

Table 33 : RSV (1C) HH target Sequence

nt. Position	Target Sequence	nt. Position	Target Sequence
10	GGCAAAU A AGAADUU	165	UACAUUU A ACUAACG
16	UAGAAGU U UGADAAG	169	UUUAACU A ACGCUUU
17	AAGAAGU U GADAAGU	175	UAAAGCU U UGGCUAA
21	AUUUGAU A AGUACCA	176	AACGCUU U GGCUAAG
25	GADAAGU A CCACUUA	181	UUUGGCU A AGGCAGU
31	UACCACTU U AAADUUA	192	CAGUGAU A CAUACAA
32	ACCACTU A AADUUA	196	GADACAU A CAADCAA
36	CUUAAAU U UAACUCC	201	AUACAAU C AAADUGA
37	UUAAAUU U AACUCCC	206	AUCAAU U GAADGGC
38	UAAAUUU A ACUCCCU	216	AUGGCAU U GUGUUUG
42	UUUAACU C CCUUGGU	221	AUUGUGU U UGUGCAU
46	ACUCCCU U GGUUAGA	222	UUGUGUU U GUGCAUG
50	CCUUGGU U AGAGADG	231	UGCAUGU U AUUACAA
51	CUUGGUU A GAGADGG	232	GCADGUU A UUAACAAG
67	CAGCAAU U CAUUGAG	234	AUGUUUAU U ACAAGUA
68	AGCAAUU C ADUGAGU	235	UGUUUAU A CAAGUAG
71	AADUCAU U GAGUADG	241	UACAAGU A GUGAUUU
76	AUUGAGU A UGADAAA	247	UAGUGAU A UUUGCCC
81	GUADGAU A AAAGUUA	249	GUGAUUU U UGCCCUA
87	UAAAAGU U AGAUUAC	250	UGAUUUU U GCCCUAA
88	AAAAGUU A GAUUAUA	256	UUGCCCU A AUUAUUA
92	GUUAGAU U ACAAAAU	259	CCCUAAU A AUUAUAU
93	UUAGAUU A CAAAADU	262	UAAUAUU A AUADUGU
100	ACAAAAU U UGUUGGA	265	UAAUAUU A UUGUAUG
101	CAAAAUU U GUUUGAC	267	AUAUAUU U GUAGUAA
104	AADUUGU U UGACAAU	270	AUAUUGU A GUAAAAU
105	AUUUGUU U GACUADG	273	UUGUAGU A AAADCCA
120	AUGAAGU A GCAUUGU	278	GUAAAAU C CAADUUC
125	GUAGCAU U GUUAAAA	283	AUCCAAU U UCACAAC
128	GCAUUGU U AAAAUA	284	UCCAAUU U CACAACA
129	CAUUGUU A AAAAUUA	285	CCAAUUU C ACAACAA
135	UAAAAAU A ACAUGCU	300	UGCCAGU A CUACAAA
143	ACAUGCU A UACUGAU	303	CAGUACU A CAAAADG
145	AUGCUAU A CUGAUUA	316	UGGAGGU U AUUAUUG
151	UACUGAU A AADUAAU	317	GGAGGUU A UAUAUGG
155	GADAAAU U AADACAU	319	AGGUUAU A UAUGGGA
156	AUAAAUU A AUACAUU	321	GUUAUAU A UGGGAAA
159	AADUAUU A CAUUUUA	338	AUGGAUU U AACACAU
163	AADACAU U UAACUUA	339	UGGAUUU A ACACAUU
164	AUACAUU U AACUAAC	346	AACACAU U GCUUCA

350	CATGGCT C TCAACCT
352	TGGGCTT C AACCTAA
358	TCAACCT A ADGGGCT
364	TAADGGT C TACTAGA
366	ADGGGCT A CTAGAGG
369	GCTTACT A GADGACA
379	TGACAAU T GCGAAAU
387	GCGAAAU T AAADGCT
388	TGAAAUU A AAAGCTC
392	ATTAUUU T CCCCAAA
393	TCTAAAU C CCCAAA
395	AAADGCT C CAAAAA
405	AAAAACT A AGGAGU
412	AAGGATU T CACAAU
413	AGGAGU C AACAGG
427	GACCAAU T ATAGAA
428	ACCAAU A TAGAAU
430	CAATUAU A UGAATCA
436	TATGAU C AATUAC
440	AAACAAU T AATCGAA
441	ATCAAUU A TCGAAU
443	CAATUAU C UGAATCA
449	TCGAAU T ACUUGGA
450	CTGAUU A CUGGATU
453	AATUACTU T GGAUUG
458	CUUGGATU T UGATCU
459	TUGGATU T GATCUA
463	ATUUGAU C UTAATCC
465	TUGATCU T AATCCAU
466	UGATCUU A ATCCATA
469	TCTUAU C CATAAAU
473	AATCCAU A AATATA
477	CATAAAU T AATATA
478	ATAAAU A TAAATA
480	AAATUAU A AATATA
483	TATUAU T AATATCA
484	TATUAU A AATATCA
487	AATUAU A TCAACTA
489	TATAUAU C AACTAGC
494	ATCAACTU A GCAATTC
501	AGCAAU C AAGGCA
507	TCAAGU C ACTATCA
511	TGUCATU A ACACCAU
519	ACACCAU T AGTUAU
520	CACCAU A GTUATA
523	CATUAGU T AATATA
524	ATUAGUU A AATATA

Table 34: RSV (1C) HH Ribozyme Sequence

nt. Position	HH Ribozyme Sequence
10	AAAUUCU CUGADGAGGCCGAAAGGCCGAA AUUUGCC
16	CUUAUCA CUGADGAGGCCGAAAGGCCGAA AUUCUCA
17	ACUUAAC CUGADGAGGCCGAAAGGCCGAA AAUUCUU
21	UGGUACU CUGADGAGGCCGAAAGGCCGAA AUCAAAU
25	UAAGUGG CUGADGAGGCCGAAAGGCCGAA ACUUAAC
31	UAAAUUU CUGADGAGGCCGAAAGGCCGAA AGUGGUA
32	UUAUUU CUGADGAGGCCGAAAGGCCGAA AAGUGGU
36	GGAGUUA CUGADGAGGCCGAAAGGCCGAA AUUUUAG
37	GGAGUUU CUGADGAGGCCGAAAGGCCGAA AAUUUAA
38	AGGGAGU CUGADGAGGCCGAAAGGCCGAA AAUUUUA
42	ACCAAGG CUGADGAGGCCGAAAGGCCGAA AGUUAAA
46	UCUAACC CUGADGAGGCCGAAAGGCCGAA AGGGAGU
50	CADUCUU CUGADGAGGCCGAAAGGCCGAA ACCAAGG
51	CCAUUCU CUGADGAGGCCGAAAGGCCGAA AACCAAG
67	CUCAADG CUGADGAGGCCGAAAGGCCGAA AUUGCUG
68	ACUCAAU CUGADGAGGCCGAAAGGCCGAA AAUUGCU
71	CAUACUC CUGADGAGGCCGAAAGGCCGAA AUGAAUU
76	UUUAUCA CUGADGAGGCCGAAAGGCCGAA ACUCAAU
81	UAAUUUU CUGADGAGGCCGAAAGGCCGAA AUCAUAC
87	GUAAUCU CUGADGAGGCCGAAAGGCCGAA ACUUUUA
88	UGUAUUC CUGADGAGGCCGAAAGGCCGAA AACUUUU
92	AUUUUUG CUGADGAGGCCGAAAGGCCGAA AUCUAAU
93	AAUUUUG CUGADGAGGCCGAAAGGCCGAA AAUUCUA
100	UCAAAAC CUGADGAGGCCGAAAGGCCGAA AUUUUUG
101	GUCAAAC CUGADGAGGCCGAAAGGCCGAA AAUUUUG
104	AUUUGUA CUGADGAGGCCGAAAGGCCGAA ACAAAAU
105	CAUUGUC CUGADGAGGCCGAAAGGCCGAA AACAAAU
120	ACAADGC CUGADGAGGCCGAAAGGCCGAA ACUUCAU
125	UUUUUAC CUGADGAGGCCGAAAGGCCGAA AUGCUAC
128	UAUUUUU CUGADGAGGCCGAAAGGCCGAA ACAADGC
129	UUUUUUU CUGADGAGGCCGAAAGGCCGAA AACAAUG
135	AGCAUGU CUGADGAGGCCGAAAGGCCGAA AUUUUUA
143	AUCAGUA CUGADGAGGCCGAAAGGCCGAA AGCAUGU
145	UUUUCAG CUGADGAGGCCGAAAGGCCGAA AUAGCAU
151	AUUAAUU CUGADGAGGCCGAAAGGCCGAA AUCAGUA
155	AUGUAUU CUGADGAGGCCGAAAGGCCGAA AUUUUAC
156	AAUGUAU CUGADGAGGCCGAAAGGCCGAA AAUUUAU
159	UUAAADG CUGADGAGGCCGAAAGGCCGAA AUUAUUU
163	UUAGUUA CUGADGAGGCCGAAAGGCCGAA AUGUAUU
164	GUUAGUU CUGADGAGGCCGAAAGGCCGAA AAUGUAU
165	CGUUAUU CUGADGAGGCCGAAAGGCCGAA AAUUGUA

169	AAAGCGU	CUGAUGAGGCCGAAAGGCCGAA	AGUUAAA
175	UUAAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGCGTUA
176	CUUAGCC	CUGAUGAGGCCGAAAGGCCGAA	AAGCGUU
181	ACCGCCU	CUGAUGAGGCCGAAAGGCCGAA	AGCCAAA
192	UUGUADG	CUGAUGAGGCCGAAAGGCCGAA	AUCACUG
196	UUGAUDG	CUGAUGAGGCCGAAAGGCCGAA	AUGUACC
201	UCAAUUU	CUGAUGAGGCCGAAAGGCCGAA	AUUGUUA
206	GCCAUUC	CUGAUGAGGCCGAAAGGCCGAA	AUUGAUU
216	CAAACAC	CUGAUGAGGCCGAAAGGCCGAA	AUGCCAU
221	ADGCACA	CUGAUGAGGCCGAAAGGCCGAA	ACACAAU
222	CADGCAC	CUGAUGAGGCCGAAAGGCCGAA	AACACAA
231	UUGUAAU	CUGAUGAGGCCGAAAGGCCGAA	ACADGCA
232	CUUGUAA	CUGAUGAGGCCGAAAGGCCGAA	AACADGC
234	UAUUUGU	CUGAUGAGGCCGAAAGGCCGAA	AUAACAU
235	CUAUUUG	CUGAUGAGGCCGAAAGGCCGAA	AUAUACA
241	AUAUCAC	CUGAUGAGGCCGAAAGGCCGAA	ACUUGUA
247	GGGCAAA	CUGAUGAGGCCGAAAGGCCGAA	ACCACUA
249	UAGGGCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUCAC
250	UUAAGGC	CUGAUGAGGCCGAAAGGCCGAA	AUAUACA
256	UUUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGGGCAA
259	AUAUUUA	CUGAUGAGGCCGAAAGGCCGAA	AUUAGGG
262	ACAAUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUA
265	ACTUCAA	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUA
267	UUACTAC	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUA
270	AUUUUAC	CUGAUGAGGCCGAAAGGCCGAA	ACAAUAU
273	UGGAUUU	CUGAUGAGGCCGAAAGGCCGAA	ACTUCAA
278	GAAAUUG	CUGAUGAGGCCGAAAGGCCGAA	AUUUUAC
283	GUUGUGA	CUGAUGAGGCCGAAAGGCCGAA	AUUGGAU
284	UGUUGUG	CUGAUGAGGCCGAAAGGCCGAA	AAUUGGA
285	UUGUUGU	CUGAUGAGGCCGAAAGGCCGAA	AAAUUGG
300	UUUGUAG	CUGAUGAGGCCGAAAGGCCGAA	ACUGGCA
303	CADUUUG	CUGAUGAGGCCGAAAGGCCGAA	AGUACUG
316	CATAUAU	CUGAUGAGGCCGAAAGGCCGAA	ACCUCCA
317	CCATAUA	CUGAUGAGGCCGAAAGGCCGAA	AACCUCC
319	UCCCAUA	CUGAUGAGGCCGAAAGGCCGAA	AUAACCU
321	UUUCCCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAAC
338	ADGUGUU	CUGAUGAGGCCGAAAGGCCGAA	AUUCCAU
339	AADGUGU	CUGAUGAGGCCGAAAGGCCGAA	AUUCCA
346	UGAGAGC	CUGAUGAGGCCGAAAGGCCGAA	AUGUGUU
350	AGGUUGA	CUGAUGAGGCCGAAAGGCCGAA	AGCAADG
352	UUAGGUU	CUGAUGAGGCCGAAAGGCCGAA	AGAGCAA
358	AGACCAU	CUGAUGAGGCCGAAAGGCCGAA	AGGUUGA
364	UCUAGUA	CUGAUGAGGCCGAAAGGCCGAA	ACCAUUA
366	CADCUAG	CUGAUGAGGCCGAAAGGCCGAA	AGACCAU
369	UGUCAUC	CUGAUGAGGCCGAAAGGCCGAA	AGUAGAC
379	AUUUCAC	CUGAUGAGGCCGAAAGGCCGAA	AUUGUCA
387	AGAAUUU	CUGAUGAGGCCGAAAGGCCGAA	AUUUCAC
388	GAGAAUU	CUGAUGAGGCCGAAAGGCCGAA	AAUUUCA
392	UUUGGAG	CUGAUGAGGCCGAAAGGCCGAA	AUUUAAU

393	UUUUGGA	CUGAUGAGGCCGAAAGGCCGAA	AADUUAA
395	UUUUUUG	CUGAUGAGGCCGAAAGGCCGAA	AGAAUUU
405	AADCACT	CUGAUGAGGCCGAAAGGCCGAA	AGUUUUU
412	AUUGUUG	CUGAUGAGGCCGAAAGGCCGAA	AADCACTU
413	CAUUGUU	CUGAUGAGGCCGAAAGGCCGAA	AADCACTU
427	UUCAUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUGGUC
428	AUUCATA	CUGAUGAGGCCGAAAGGCCGAA	AADUGGU
430	UGAUUCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUG
436	GAUAUUU	CUGAUGAGGCCGAAAGGCCGAA	AUUCATA
440	UUCAGAU	CUGAUGAGGCCGAAAGGCCGAA	AUUGAUU
441	AUUCAGA	CUGAUGAGGCCGAAAGGCCGAA	AUUGAUU
443	UAUUUCA	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUG
449	UCCAAGU	CUGAUGAGGCCGAAAGGCCGAA	AUUCAGA
450	AUCCAAG	CUGAUGAGGCCGAAAGGCCGAA	AUUCAG
453	CAAUCC	CUGAUGAGGCCGAAAGGCCGAA	AGUAUUU
458	AAGAUCA	CUGAUGAGGCCGAAAGGCCGAA	AUCCAAG
459	UAAGAUU	CUGAUGAGGCCGAAAGGCCGAA	AUCCAAG
463	GGAUUAA	CUGAUGAGGCCGAAAGGCCGAA	AUCCAAG
465	AUGGAUU	CUGAUGAGGCCGAAAGGCCGAA	AGAUCAA
466	UAUGGAU	CUGAUGAGGCCGAAAGGCCGAA	AAGAUCA
469	AUUUADG	CUGAUGAGGCCGAAAGGCCGAA	AUUAAGA
473	UAUAUUU	CUGAUGAGGCCGAAAGGCCGAA	AUGGAUU
477	UAUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUG
478	UUUAUUU	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUG
480	UAUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUG
483	UGAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUU
484	UUGAUUA	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUA
487	UAGUUUA	CUGAUGAGGCCGAAAGGCCGAA	AUUUAUA
489	GCUAGUU	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUA
494	GAUUUGC	CUGAUGAGGCCGAAAGGCCGAA	AGUUUAU
501	UGACUUU	CUGAUGAGGCCGAAAGGCCGAA	AUUUGCU
507	UGUUAGU	CUGAUGAGGCCGAAAGGCCGAA	ACAUUGA
511	AUGGUGU	CUGAUGAGGCCGAAAGGCCGAA	AGUGACA
519	AUUUAUU	CUGAUGAGGCCGAAAGGCCGAA	AUGGUGU
520	UAUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUUUGUG
523	UUUAUUU	CUGAUGAGGCCGAAAGGCCGAA	ACTUAUG
524	UUUAUUU	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUA

Table 35: RSV (N) HH Target Sequence

nt. Position	HH Target Sequence	nt. Position	HH Target Sequence
9	GGCAAAU A CAAAGAU	217	GGUADGU U AUADGGG
21	GAUGGCU C UUAGCAA	218	GUADGUU A UADGGCA
23	UGGCUU U AGCAAAG	220	AUGGUUU A UGGGADG
24	GGCUCU A GCAAAGU	229	GCGADGU C UAGGUUA
32	GCAAAGU C AAGUUGA	231	GAUGUUU A GGUUAGG
37	GUCAAGU U GAUUGAU	235	UCUAGGU U AGGAAGA
45	GAUGAU A CACUCAA	236	CUAGGUU A GGAAGAG
50	AUACAU C AACAAAG	254	ACACCAU A AAAAUAC
60	CAAAGAU C AACUUCU	260	UAAAUU A CCAGAG
65	AUCAAU U CUGUCAU	263	AAUAU C AGAGADG
66	UCAAUU C UGUCAUC	277	GCGGGAU A UCAUGUA
70	CUUCUGU C AUCCAGC	279	GCGGAU C AUGUAAA
73	CUGUCAU C CAGCAA	284	AUCAUGU A AAAGCAA
82	AGCAAAU A CACCAUC	299	AUGGAGU A GAUGUAA
89	ACACCAU C CAAAGGA	305	UAGAGUU A ACAACAC
108	AGGAGAU A GUUUGA	315	AACACAU C GUCAAGA
111	AGAUAGU A UUGAUAC	318	ACAUUGU C AAGACAU
113	AUAGUAU U GAUACUC	326	AAGACAU U AAGGAA
117	UAUUGAU A CUCUUA	327	AGACAUU A AUGGAA
120	UGAUACU C CUAAUUA	346	AUGAAAU U UGAAGUG
123	UACUUCU A AUUADGA	347	UGAAAUU U GAAGGUU
126	UCCUAAU U AUGAUUU	355	GAAGUGU U AACAUUG
127	CCUAAU A UGADGUG	356	AAGUGUU A ACAUUGG
146	AACACAU C AAUAAGU	361	UUAACAU U GCGAAGC
150	CAUCAAU A AGUUAUG	370	GCAAGCU U AACAAU
154	AAUAAGU U ADGUGGC	371	CAAGCUU A ACAACUG
155	AUAAGUU A UGUGGCA	383	CUGAAAU U CAAAUCA
166	GGCAUGU U AUUAADC	384	UGAAAUU C AAADCAA
167	GCAUGUU A UUAUACA	389	UCCAAAU C AACAUUG
169	AUGUUUU U AAUCACA	395	UCAACAU U GAGAUAG
170	UGUUUUU A AUACACG	401	UUGAGAU A GAUUCUA
173	UAUUUUU C ACAGAAG	406	AUAGAAU C UAGAAAA
186	AGAUGCU A AUCAUAA	408	AGAAU C GAAAUUC
189	UGCUAAU C AUAAAUU	415	AGAAAAU C CUACAAA
192	UAUACAU A AAUCCAC	418	AAAUCCU A CAAAAA
196	CAUAAAU U CACUGGG	431	AAAUCCU A AAAGAAA
197	AUAUAAU C ACUGGGU	449	GAGAGGU A GCUCCAG
205	ACUGGGU U AAUAGGU	453	GGUAGCU C CAGAAUA
206	CUGGGUU A AUAGGUA	460	CCAGAAU A CAGGCAU
209	GGUUAUU A GGUADGU	472	CAUGACU C UCCUGAU
213	AAUAGGU A UGUUAUA	474	UGACUCU C CUGADUG

480	UCCUGAU U GUGGGAU	696	UUUUGGU A UAGCACA
491	GGAUAGU A AUAUUAU	698	UUGGUAU A GCACAAU
494	UGAUAAU A UUAUGUA	706	GCACAAU C UUCUACC
496	AUAUAU U AUGGUAU	708	ACAAUCU U CUACCAG
497	UAUAUAU A UGUADAG	709	CAADCUU C UACCAGA
501	AUUAAGU A UAGCAGC	711	AUCUUCU A CCAGAGG
503	UADGUAU A GCAGCAU	726	UGGCAGU A GAGUGA
511	GCAGCAU U AGUAADA	731	GUAGAUU U GAAGGGA
512	CAGCAU A GUAAUA	740	AAGGGAU U UUGCAG
515	CAUUAU A AUAACUA	741	AGGGAUU U UUGCAGG
518	UAGUAU A AUAUAU	742	GGGAUUU U UGCAGGA
522	AAUAACU A AAUUAAC	743	GGAUUUU U GCAGGAU
526	ACUAUAU U AGCAGCA	751	GCAGGAU U GUUAUAG
527	CUAAAUU A GCAGCAG	754	GGAUUGU U UAUGAAU
544	GACAGAU C UGGUCUU	755	GAUUGUU U AUGAAGU
549	AUCUGGU C UACAGC	756	AUUGUUU A UGAADGC
551	COGGUCU U ACAGCCG	766	AAUGCCU A UGGUGCA
552	UGGUCUU A CAGCCGU	787	GUGAUUU U ACGGUGG
563	COGUGAU U AGGAGAG	788	UGAUUUU A CGGUGGG
564	COGUAU A GGAGAGC	800	GGGGAGU C UUAGCAA
573	GAGAGCU A AUAADGU	802	GGAGUCU U AGCAAAA
576	AGCUAAU A AUGUCCU	803	GAGUCUU A GCAAAAU
581	AUAADGU C CUAAAA	811	GCAAAAU C AGUAAA
584	AUGUCCU A AAAAAG	815	AAUCAGU U AAAAUA
603	GAAACGU U ACAAGG	816	AUCAGUU A AAAUAU
604	AAACGUU A CAAAGGC	822	UAAAAAU A UUAAGUU
613	AAAGGUU U ACUACCC	824	AAAAUAU U AUGUUAAG
614	AAGGCUU A CUACCCA	825	AAUAUAU A UGUUAAGG
617	GCUUAU A CCAAGG	829	AUUAAGU U AGGACAU
629	AGGACAU A GCCAACA	830	UUAAGUU A GGACADG
640	AACAGCU U CUADGAA	840	ACADGCU A GUGUGCA
641	ACAGCUU C UADGAAG	866	AACRAU U GUUGAGG
643	AGCUUCU A UGAAGUG	869	AAGUUGU U GAGGUUU
652	GAGUGU U UGAAAA	875	UUGAGGU U UAUGAAU
653	AAGUGUU U GAAAAAC	876	UGAGGUU U AUGAADA
663	AAAACAU C CCCACUU	877	GAGGUUU A UGAADAU
670	CCCCACU U UAADAGU	883	UAADGAU A UGCCCCA
671	CCCACUU U AUAAGUG	895	CAAAAAU U GGGUGGU
672	CCACUUU A UAADGU	913	GCAGGAU U CUACCAU
674	ACUUAU A GAUGUUU	914	CAGGAU C UACCAUA
680	UAGADGU U UUGUUC	916	GGAUUCU A CCAUAUA
681	AGADGUU U UGUUCA	921	CUACCAU A UAUGAA
682	GAUGUUU U UGUUCAU	923	ACCAUAU A UUGAACA
683	AUGUUUU U GUUCAU	925	CAUAUAU U GAACAAC
686	UUUUUGU U CAUUUG	943	AAAGCAU C AUUAUA
687	UUUUUGU C AUUUUGG	946	GCAUCAU U AUUAUCU
690	UGUUCAU U UUGGUAU	947	CADCAU A UUAUCUU
691	GUUCAU U UGGUAUA	949	UCAUAU U AUCUUUG
692	UUCAUUU U GGUADAG	950	CAUAUAU A UCUUGA

952	UUUUUUU C UUUUUUU
954	UUUUUUU U UUUUUUU
955	UUUUUUU U UUUUUUU
960	UUUUUUU C UUUUUUU
964	UUUUUUU U UUUUUUU
965	UUUUUUU U UUUUUUU
966	UUUUUUU C UUUUUUU
969	UUUUUUU C UUUUUUU
973	UUUUUUU U UUUUUUU
974	UUUUUUU C UUUUUUU
976	UUUUUUU C UUUUUUU
983	UUUUUUU A UUUUUUU
986	UUUUUUU A UUUUUUU
988	UUUUUUU U UUUUUUU
989	UUUUUUU A UUUUUUU
1007	UUUUUUU A UUUUUUU
1013	UUUUUUU A UUUUUUU
1024	UUUUUUU A UUUUUUU
1032	UUUUUUU A UUUUUUU
1044	UUUUUUU C UUUUUUU
1050	UUUUUUU C UUUUUUU
1052	UUUUUUU A UUUUUUU
1054	UUUUUUU A UUUUUUU
1072	UUUUUUU A UUUUUUU
1085	UUUUUUU C UUUUUUU
1103	UUUUUUU U UUUUUUU
1104	UUUUUUU A UUUUUUU
1108	UUUUUUU A UUUUUUU
1115	UUUUUUU A UUUUUUU
1118	UUUUUUU A UUUUUUU
1123	UUUUUUU U UUUUUUU
1139	UUUUUUU A UUUUUUU
1146	UUUUUUU A UUUUUUU
1148	UUUUUUU C UUUUUUU
1155	UUUUUUU C UUUUUUU
1160	UUUUUUU U UUUUUUU
1161	UUUUUUU A UUUUUUU
1164	UUUUUUU C UUUUUUU
1173	UUUUUUU A UUUUUUU
1181	UUUUUUU A UUUUUUU
1187	UUUUUUU U UUUUUUU
1188	UUUUUUU U UUUUUUU
1193	UUUUUUU U UUUUUUU
1194	UUUUUUU A UUUUUUU

Table 36: RSV (N) HH Ribozyme Sequence

nt. Position	HH Ribozyme Sequence
9	ADCUUG CUGADGAGGCCGAAAGGCCGAA AUUUGCC
21	UUGCUAA CUGADGAGGCCGAAAGGCCGAA AGCCAUU
23	CUUUGCU CUGADGAGGCCGAAAGGCCGAA AGAGCCA
24	ACUUUGC CUGADGAGGCCGAAAGGCCGAA AAGAGCC
32	UCACTU CUGADGAGGCCGAAAGGCCGAA ACUUUGC
37	AUCAUUC CUGADGAGGCCGAAAGGCCGAA ACUUGAC
45	UUGAGUG CUGADGAGGCCGAAAGGCCGAA AUCAUUC
50	CUUUGUU CUGADGAGGCCGAAAGGCCGAA AGUGUAU
60	AGAAGUU CUGADGAGGCCGAAAGGCCGAA ADCUUUG
65	ADGACAG CUGADGAGGCCGAAAGGCCGAA AGUUGAU
66	GADGACA CUGADGAGGCCGAAAGGCCGAA AAGUUGA
70	GCUGGAU CUGADGAGGCCGAAAGGCCGAA ACAGAAG
73	UUUGCUG CUGADGAGGCCGAAAGGCCGAA ADGACAG
82	GADGGUG CUGADGAGGCCGAAAGGCCGAA AUUUGCU
89	UCCGUUG CUGADGAGGCCGAAAGGCCGAA AUGGUGU
108	UCAADAC CUGADGAGGCCGAAAGGCCGAA ADCUCCU
111	GUADCAA CUGADGAGGCCGAAAGGCCGAA ACTUACU
113	GAGUAUC CUGADGAGGCCGAAAGGCCGAA AUACUAU
117	UUAGGAG CUGADGAGGCCGAAAGGCCGAA AUCAADA
120	UAADUAG CUGADGAGGCCGAAAGGCCGAA AGUADCA
123	UCADAAU CUGADGAGGCCGAAAGGCCGAA AGGAGUA
126	ACAUCAU CUGADGAGGCCGAAAGGCCGAA AUUAGGA
127	CACADCA CUGADGAGGCCGAAAGGCCGAA AAUUAAG
146	ACUUAUU CUGADGAGGCCGAAAGGCCGAA AUGUGUU
150	CAUAACU CUGADGAGGCCGAAAGGCCGAA AUUGAUG
154	GCCACAU CUGADGAGGCCGAAAGGCCGAA ACUUAUU
155	UGCCACA CUGADGAGGCCGAAAGGCCGAA AACUUAU
166	GAUUAUU CUGADGAGGCCGAAAGGCCGAA ACAUGCC
167	UGAUUAA CUGADGAGGCCGAAAGGCCGAA AACAUUC
169	UGUGAUU CUGADGAGGCCGAAAGGCCGAA AUUAACU
170	CUUGAUU CUGADGAGGCCGAAAGGCCGAA AAUAACA
173	CUUCUGU CUGADGAGGCCGAAAGGCCGAA AUUAADA
186	UUADGAU CUGADGAGGCCGAAAGGCCGAA AGCAUCU
189	AAUUAUU CUGADGAGGCCGAAAGGCCGAA AUUAGCA
192	GUGAAUU CUGADGAGGCCGAAAGGCCGAA ADGAUUA
196	CCCAGUG CUGADGAGGCCGAAAGGCCGAA AUUUUUG
197	ACCCAGU CUGADGAGGCCGAAAGGCCGAA AAUUAUU
205	ACCUUAU CUGADGAGGCCGAAAGGCCGAA ACCCAGU
206	UACCUAU CUGADGAGGCCGAAAGGCCGAA AACCCAG
209	ACAUACC CUGADGAGGCCGAAAGGCCGAA AUUAACC
213	UAUAACA CUGADGAGGCCGAAAGGCCGAA ACCUAUU

217	CGCAUAT	CUGADGAGGCGGAAAGGCCGAA	ACAUAAC
218	UCCCAUA	CUGADGAGGCGGAAAGGCCGAA	AACAUAAC
220	CADCGCA	CUGADGAGGCGGAAAGGCCGAA	AUAACAUA
229	UAACCUA	CUGADGAGGCGGAAAGGCCGAA	ACAUCGC
231	CCUAACC	CUGADGAGGCGGAAAGGCCGAA	AGACAUAC
235	UCUCCU	CUGADGAGGCGGAAAGGCCGAA	ACCUAGA
236	CCUCCU	CUGADGAGGCGGAAAGGCCGAA	AACCUAG
254	GUUUTU	CUGADGAGGCGGAAAGGCCGAA	ADGGUGU
260	CUCUGAG	CUGADGAGGCGGAAAGGCCGAA	AUUUUUA
263	CAUCUCU	CUGADGAGGCGGAAAGGCCGAA	AGUAUUU
277	UACAUCA	CUGADGAGGCGGAAAGGCCGAA	ADCCCGC
279	UUUACAU	CUGADGAGGCGGAAAGGCCGAA	ADUACCC
284	UUGCUUU	CUGADGAGGCGGAAAGGCCGAA	ACAUGAU
299	UUACAU	CUGADGAGGCGGAAAGGCCGAA	ACUCCAU
305	GUUGUGU	CUGADGAGGCGGAAAGGCCGAA	ACAUCUA
315	UCUUGAC	CUGADGAGGCGGAAAGGCCGAA	ADGUGUU
318	ADGUCUU	CUGADGAGGCGGAAAGGCCGAA	ACGADGU
326	UUCCAUU	CUGADGAGGCGGAAAGGCCGAA	ADGUCUU
327	UUUCCAU	CUGADGAGGCGGAAAGGCCGAA	ADGUCUU
346	CACUCCA	CUGADGAGGCGGAAAGGCCGAA	AUUUCCAU
347	ACAUCUC	CUGADGAGGCGGAAAGGCCGAA	AUUUCCA
355	CAADGUU	CUGADGAGGCGGAAAGGCCGAA	ACAUCUC
356	CCAADGU	CUGADGAGGCGGAAAGGCCGAA	AACAUUU
361	GUUGGCC	CUGADGAGGCGGAAAGGCCGAA	ADGUUUA
370	AGUUGUU	CUGADGAGGCGGAAAGGCCGAA	AGCUUGC
371	CAGUUGU	CUGADGAGGCGGAAAGGCCGAA	AAGCUUG
383	UGAUUUG	CUGADGAGGCGGAAAGGCCGAA	AUUUCAG
384	UUGAUUU	CUGADGAGGCGGAAAGGCCGAA	AUUUCCA
389	CAADGUU	CUGADGAGGCGGAAAGGCCGAA	AUUUGAA
395	CUAUCUC	CUGADGAGGCGGAAAGGCCGAA	ADGUUGA
401	UAGAUUC	CUGADGAGGCGGAAAGGCCGAA	ADUCUAA
406	UUUUCUA	CUGADGAGGCGGAAAGGCCGAA	AUUUCUA
408	GADUUUC	CUGADGAGGCGGAAAGGCCGAA	AGAUCUU
415	UUUGUAG	CUGADGAGGCGGAAAGGCCGAA	AUUUUUU
418	UUUUUUG	CUGADGAGGCGGAAAGGCCGAA	AGGADUU
431	UUUCUUU	CUGADGAGGCGGAAAGGCCGAA	AGCAUUU
449	CCUGAGC	CUGADGAGGCGGAAAGGCCGAA	ACCUUUC
453	UAUUCUG	CUGADGAGGCGGAAAGGCCGAA	AGCUAAC
460	ADGUCUG	CUGADGAGGCGGAAAGGCCGAA	AUUUCUG
472	ADUAGGA	CUGADGAGGCGGAAAGGCCGAA	AGUCADG
474	CAUDCAG	CUGADGAGGCGGAAAGGCCGAA	AGAGUCA
480	ADCCAC	CUGADGAGGCGGAAAGGCCGAA	ADUAGGA
491	AUAUAUA	CUGADGAGGCGGAAAGGCCGAA	ADUADCC
494	UACAUAA	CUGADGAGGCGGAAAGGCCGAA	AUUADCA
496	UAUAUAU	CUGADGAGGCGGAAAGGCCGAA	AUAUAUA
497	CUAUAUA	CUGADGAGGCGGAAAGGCCGAA	AUAUAUA
501	GUUGCUA	CUGADGAGGCGGAAAGGCCGAA	ACAUAUA
503	AUGCUGC	CUGADGAGGCGGAAAGGCCGAA	AUAUAUA
511	UAUUAUA	CUGADGAGGCGGAAAGGCCGAA	ADGUCUG

512	UUAUAC	CUGAUGAGGCCGAAAGGCCGAA	AADGCTG
515	UAGUUAU	CUGAUGAGGCCGAAAGGCCGAA	ACUAADG
518	AUUUAGU	CUGAUGAGGCCGAAAGGCCGAA	ADUACTA
522	GCUAAUU	CUGAUGAGGCCGAAAGGCCGAA	AGUUUUU
526	UGGUGCU	CUGAUGAGGCCGAAAGGCCGAA	AUUUAGU
527	CUGCUGC	CUGAUGAGGCCGAAAGGCCGAA	AAUUUAG
544	AAGACCA	CUGAUGAGGCCGAAAGGCCGAA	ADGUGGC
549	GCGUAA	CUGAUGAGGCCGAAAGGCCGAA	ACCAGAU
551	CGGCGU	CUGAUGAGGCCGAAAGGCCGAA	AGACCAG
552	ACGGCUG	CUGAUGAGGCCGAAAGGCCGAA	AAGACCA
563	CUCUCU	CUGAUGAGGCCGAAAGGCCGAA	ADCAAGG
564	GUCUCC	CUGAUGAGGCCGAAAGGCCGAA	AADCAAG
573	ACAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGCUCUC
576	AGGACAU	CUGAUGAGGCCGAAAGGCCGAA	ADUAGCU
581	UUUUUAG	CUGAUGAGGCCGAAAGGCCGAA	ACAUUAU
584	CAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGGACAU
603	CCUUUGU	CUGAUGAGGCCGAAAGGCCGAA	ACGUUUC
604	GCCUUUG	CUGAUGAGGCCGAAAGGCCGAA	AACGUUU
613	GGGUAGU	CUGAUGAGGCCGAAAGGCCGAA	AGCCUUU
614	UGGUUAG	CUGAUGAGGCCGAAAGGCCGAA	AAGCCUU
617	CCUUGGG	CUGAUGAGGCCGAAAGGCCGAA	AGUAAAG
629	UGUUGGC	CUGAUGAGGCCGAAAGGCCGAA	ADGUCCU
640	UUCAUAG	CUGAUGAGGCCGAAAGGCCGAA	AGCGGUU
641	CUUCAUA	CUGAUGAGGCCGAAAGGCCGAA	AAGCUGU
643	CACUUCA	CUGAUGAGGCCGAAAGGCCGAA	AGAAGCU
652	UUUUUCA	CUGAUGAGGCCGAAAGGCCGAA	ACACUUC
653	GUUUUUC	CUGAUGAGGCCGAAAGGCCGAA	AACACUU
663	AAGUGGG	CUGAUGAGGCCGAAAGGCCGAA	ADGUUUU
670	ADCUADA	CUGAUGAGGCCGAAAGGCCGAA	AGUGGGG
671	CADCUAU	CUGAUGAGGCCGAAAGGCCGAA	AAGUGGG
672	ACADCUA	CUGAUGAGGCCGAAAGGCCGAA	AAAGUGG
674	AAACADC	CUGAUGAGGCCGAAAGGCCGAA	ADAAAGU
680	GAACAAA	CUGAUGAGGCCGAAAGGCCGAA	ACADCUA
681	UGAACAA	CUGAUGAGGCCGAAAGGCCGAA	AACADCU
682	AUGAACAA	CUGAUGAGGCCGAAAGGCCGAA	AAACADC
683	AADGAAC	CUGAUGAGGCCGAAAGGCCGAA	AAAACAU
686	CAAAADG	CUGAUGAGGCCGAAAGGCCGAA	ACAAAAA
687	CCAAAAD	CUGAUGAGGCCGAAAGGCCGAA	AACAAAA
690	AUAACCA	CUGAUGAGGCCGAAAGGCCGAA	ADGAACA
691	UAUAACA	CUGAUGAGGCCGAAAGGCCGAA	AAUGAAC
692	CUUAACC	CUGAUGAGGCCGAAAGGCCGAA	AAADGAA
696	UGUGCUA	CUGAUGAGGCCGAAAGGCCGAA	ACCAAAA
698	AUUGUGC	CUGAUGAGGCCGAAAGGCCGAA	AUAACCA
706	GGUAGAA	CUGAUGAGGCCGAAAGGCCGAA	AUUGUGC
708	CUGGUAG	CUGAUGAGGCCGAAAGGCCGAA	AGAUUGU
709	UCUGGUA	CUGAUGAGGCCGAAAGGCCGAA	AAGADUG
711	CCUCUGG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGAU
726	UCAACUC	CUGAUGAGGCCGAAAGGCCGAA	ACTGCCA
731	UCCCUUC	CUGAUGAGGCCGAAAGGCCGAA	ACTCUAC

740	CUGCAA	CUGAUGAGGCCGAAAGGCCGAA	ADCCCTU
741	CCUGCA	CUGAUGAGGCCGAAAGGCCGAA	AAADCCU
742	UCCUGCA	CUGAUGAGGCCGAAAGGCCGAA	AAADCCC
743	ADCCUGC	CUGAUGAGGCCGAAAGGCCGAA	AAADCC
751	CADAAAC	CUGAUGAGGCCGAAAGGCCGAA	ADCCUGC
754	ADUCAUA	CUGAUGAGGCCGAAAGGCCGAA	ACAAUCC
755	CADUCAU	CUGAUGAGGCCGAAAGGCCGAA	AACAAUC
756	GCAUCA	CUGAUGAGGCCGAAAGGCCGAA	AAACAAU
766	UGACCA	CUGAUGAGGCCGAAAGGCCGAA	AGGCADU
787	CCACCGU	CUGAUGAGGCCGAAAGGCCGAA	ACADCAC
788	CCACCG	CUGAUGAGGCCGAAAGGCCGAA	AACADCA
800	UUGCUAA	CUGAUGAGGCCGAAAGGCCGAA	ACUCCCC
802	UUUGCU	CUGAUGAGGCCGAAAGGCCGAA	AGACTCC
803	AUUUUGC	CUGAUGAGGCCGAAAGGCCGAA	AAGACTC
811	UUUAACU	CUGAUGAGGCCGAAAGGCCGAA	AUUUUGC
815	UAUUUUU	CUGAUGAGGCCGAAAGGCCGAA	ACUGAUU
816	AUAUUUU	CUGAUGAGGCCGAAAGGCCGAA	AACUGAU
822	AACAUA	CUGAUGAGGCCGAAAGGCCGAA	AUUUUUA
824	CUAACAU	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUU
825	CCUAACA	CUGAUGAGGCCGAAAGGCCGAA	AUAUUUU
829	ADGUCCU	CUGAUGAGGCCGAAAGGCCGAA	ACAUAAU
830	CADGUCC	CUGAUGAGGCCGAAAGGCCGAA	AACAUA
840	UGCACAC	CUGAUGAGGCCGAAAGGCCGAA	AGCADGU
866	CCUCAAC	CUGAUGAGGCCGAAAGGCCGAA	ACUUGUU
869	AAACUUC	CUGAUGAGGCCGAAAGGCCGAA	ACAACTU
875	AUUCAU	CUGAUGAGGCCGAAAGGCCGAA	ACCUCAA
876	UAUUCAU	CUGAUGAGGCCGAAAGGCCGAA	AACUCA
877	AUAUCA	CUGAUGAGGCCGAAAGGCCGAA	AAACUUC
883	UUGGCA	CUGAUGAGGCCGAAAGGCCGAA	ADUCAUA
895	ACCACCC	CUGAUGAGGCCGAAAGGCCGAA	AUUUUUG
913	ADGGUAG	CUGAUGAGGCCGAAAGGCCGAA	ADCCUGC
914	UADGGUA	CUGAUGAGGCCGAAAGGCCGAA	AAUCCUG
916	UAUAUUG	CUGAUGAGGCCGAAAGGCCGAA	AGAADCC
921	UUCAAUA	CUGAUGAGGCCGAAAGGCCGAA	ADGGUAG
923	UGUUCAA	CUGAUGAGGCCGAAAGGCCGAA	AUAUGGU
925	GUUGUUC	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUG
943	UAUAUAU	CUGAUGAGGCCGAAAGGCCGAA	ADGCUUU
946	AGAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AUGAUUC
947	AAGAUUA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAG
949	CAAGAU	CUGAUGAGGCCGAAAGGCCGAA	AUAADGA
950	UCAAGA	CUGAUGAGGCCGAAAGGCCGAA	AUAADG
952	AGUCAAA	CUGAUGAGGCCGAAAGGCCGAA	AUAUAUA
954	UGAGUCA	CUGAUGAGGCCGAAAGGCCGAA	AGAUUAU
955	UUGAGUC	CUGAUGAGGCCGAAAGGCCGAA	AAGAUUA
960	GGAAAUU	CUGAUGAGGCCGAAAGGCCGAA	AGUCAAA
964	GUGAGGA	CUGAUGAGGCCGAAAGGCCGAA	AUUGAGU
965	AGUGAGG	CUGAUGAGGCCGAAAGGCCGAA	AAUUGAG
966	AAGUGAG	CUGAUGAGGCCGAAAGGCCGAA	AAAUUGA
969	GAGAAAU	CUGAUGAGGCCGAAAGGCCGAA	AGGAAAU

973	ACUGGAG	CUGAUGAGGCCGAAAGGCCGAA	AGGAGG
974	CACUGGA	CUGADGAGGCCGAAAGGCCGAA	AAGGAG
976	UACACUG	CUGAUGAGGCCGAAAGGCCGAA	AGAAGG
983	CUAAUAC	CUGADGAGGCCGAAAGGCCGAA	ACACUG
986	UGCCUAA	CUGAUGAGGCCGAAAGGCCGAA	ACTACAC
988	AUUGCCU	CUGAUGAGGCCGAAAGGCCGAA	AUAUAC
989	CAUUGCC	CUGAUGAGGCCGAAAGGCCGAA	AUAUAC
1007	UUAUGCC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCG
1013	CUCCCAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1024	ACCUCUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1032	CUCCGUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1044	AGAUUUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1050	UUAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1052	CAUUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1054	UGCAUUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1072	UUCAGCA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1085	UUUCUUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1103	UGUAGUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1104	CUUAGUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1108	UACACUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1115	AGUUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1118	UUAAGUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1123	UGUUAUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1139	UAGCCUC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1146	UGUUUGA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1148	GAUUGUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1155	UUUAGUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1160	UUGGAUU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1161	UUUGGAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1164	UCUUUUG	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1173	ACAUCAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1181	AAAGCUC	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1187	UUAUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1188	UUUAUUA	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1193	UUUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU
1194	UUUUUAU	CUGAUGAGGCCGAAAGGCCGAA	AGGCCU

Table 37: RSV (1B) HP Ribozyme/Substrate Sequence

nt. Position	HP Ribozyme Sequence	Substrate
70	CUGGAGUC AGA GUCUUU ACCAGAGAGAACACACACGUGUGUGGUAUUAUACCUUGUA	AAAGACU GAU GAUCACAG
91	CAGUGBAC AGA GUCUCA ACCAGAGAGAACACACACGUGUGUGGUAUUAUACCUUGUA	UAGAGAC GAU GUCACUUG
472	CAGGCUCC AGA GAGCUA ACCAGAGAGAACACACACGUGUGUGGUAUUAUACCUUGUA	UAGUCCA GAU GAGGCUUG

Table 38: RSV (N) IIP Ribozyme/Substrate Sequence

nt. Position	Hairpin Ribozyme Sequence	Substrate
476	AUCCACCA AGAA GGAGAG ACCAGAGAAACACACGUGUGGUAUUAUACCUUGUA	CUCUCU GAU UGUGGUAU
540	AGACCCAG AGAA GUCCCC ACCAGAGAAACACACGUGUGGUAUUAUACCUUGUA	GGGACA GAU CUGGUCUU
554	CUAUUCAC AGAA GUAAAG ACCAGAGAAACACACGUGUGGUAUUAUACCUUGUA	UCUUAU GGC GUGAUUAG
636	UUCAUAGA AGAA GUUAGC ACCAGAGAAACACACGUGUGGUAUUAUACCUUGUA	GCCACA GCU UCUAUGAA
998	CCUAGGCC AGAA GCAUUG ACCAGAGAAACACACGUGUGGUAUUAUACCUUGUA	CAUUGU GCU GCCUAGG
1156	UUGGAUUA AGAA GAUGUU ACCAGAGAAACACACGUGUGGUAUUAUACCUUGUA	AACAUA GCU UAUUCCAA

Table 39: Large-Scale Synthesis

Sequence	Activator [Added/Final] (min)	Amidite [Added/Final] (min)	Time*	% Full Length Product
A ₉ T	T [0.50/0.33]	[0.1/0.02]	15 m	85
A ₉ T	S [0.25/0.17]	[0.1/0.02]	15 m	89
(GGU) ₃ GGT	T [0.50/0.33]	[0.1/0.02]	15 m	78
(GGU) ₃ GGT	S [0.25/0.17]	[0.1/0.02]	15 m	81
C ₉ T	T [0.50/0.33]	[0.1/0.02]	15 m	90
C ₉ T	S [0.25/0.17]	[0.1/0.02]	15 m	97
U ₉ T	T [0.50/0.33]	[0.1/0.02]	15 m	80
U ₉ T	S [0.25/0.17]	[0.1/0.02]	15 m	85
A (36-mer)	T [0.50/0.33]	[0.1/0.02]	15/15m	21
A (36-mer)	S [0.25/0.17]	[0.1/0.02]	15/15 m	25
A (36-mer)	S [0.50/0.24]	[0.1/0.03]	15/15 m	25
A (36-mer)	S [0.50/0.18]	[0.1/0.05]	15/15 m	38
A (36-mer)	S [0.50/0.18]	[0.1/0.05]	10/5 m	42

*Where two coupling times are indicated the first refers to RNA coupling and the second to 2'-O-methyl coupling. S = 5-S-Ethyltetrazole, T = tetrazole activator. A is 5' -uc_u ccA UCU GAU GAG GCC GAA AGG CCG AAA AUC ccu -3' where lowercase represents 2'-O-methylnucleotides.

Table 40: Base Deprotection

Sequence	Deprotection Reagent	Time (min)	T °C	% Full Length Product
iBu(GGU) ₄	NH ₄ OH/EtOH	16 h	55	62.5
	MA	10 m	65	62.7
	AMA	10 m	65	74.8
	MA	10 m	55	75.0
	AMA	10 m	55	77.2
iPrP(GGU) ₄	NH ₄ OH/EtOH	4 h	65	44.8
	MA	10 m	65	65.9
	AMA	10 m	65	59.8
	MA	10 m	55	61.3
	AMA	10 m	55	60.1
C ₉ U	NH ₄ OH/EtOH	4 h	65	75.2
	MA	10 m	65	79.1
	AMA	10 m	65	77.1
	MA	10 m	55	79.8
	AMA	10 m	55	75.5
A (36-mer)	NH ₄ OH/EtOH	4 h	65	22.7
	MA	10 m	65	28.9

Table 41: 2'-O-Alkylsilyl Deprotection

Sequence	Deprotection Reagent	Time (min)	T °C	% Full Length Product
A ₉ T	TBAF	24 h	20	84.5
	1.4 M HF	0.5 h	65	81.0
(GGU) ₄	TBAF	24 h	20	60.9
	1.4 M HF	0.5 h	65	67.8
C ₁₀	TBAF	24 h	20	86.2
	1.4 M HF	0.5 h	65	86.1
U ₁₀	TBAF	24 h	20	84.8
	1.4 M HF	0.5 h	65	84.5
B (36-mer)	TBAF	24 h	20	25.2
	1.4 M HF	1.5 h	65	30.6
A (36-mer)	TBAF	24 h	20	29.7
	1.4 M HF	1.5 h	65	30.4

B is 5'- UCU CCA UCU GAU GAG GCC GAA AGG CCG AAA AUC CCU -3'.

*Table 42: NMR Data for UC Dimers containing
Phosphorothioate Linkage*

Synthesis #	Type	Delivery	Eq.	Wait	ASE (%)
3524	ribo	2 x 3 s	10.4	2 x 100 s	95.9
3525	ribo	2 x 3 s	10.4	2 x 75 s	92.6
3530	ribo	2 x 3 s	10.4	2 x 75 s	92.1
3526	ribo	1 x 5 s	08.6	1 x 300 s	100.0
3578	ribo	1 x 5 s	08.6	1 x 250 s	100.0
3529	ribo	1 x 5 s	08.6	1 x 150 s	73.7

**Table 43: NMR Data for 15-mer RNA containing
Phosphorothioate Linkages**

Synthesis #	Type	Delivery	Eq.	Wait	ASE (%)
3581	ribo	1 x 5 s	08.6	1 x 250 s	99.6
3663	ribo	2 x 4 s	13.8	2 x 300 s	100.0
3582	2'-O-Me	1 x 5 s	08.6	1 x 250 s	99.7
3668	2'-O-Me	2 x 4 s	13.8	2 x 300 s	99.8
3682	2'-O-Me	1 x 5 s	08.6	1 x 300 s	99.8

Table 44. Kinetics of Self-Processing *In Vitro*

Self-Processing Constructs	k (min ⁻¹)*
HH	1.16 ± 0.08
HDV	0.56 ± 0.15
HP(GC)	0.36 ± 0.06
HP(GU)	0.054 ± 0.003

* k represents the unimolecular rate constant for ribozyme self-cleavage determined from a non-linear, least-squares fit (KaleidaGraph, Synergy Software, Reeding, PA) to the equation:

$$(\text{Fraction Uncleaved Transcript}) = \frac{1}{kt} (1 - e^{-kt})$$

The equation describes the extent of ribozyme processing in the presense of ongoing transcription (Long & Uhlenbeck, 1994 Proc. Natl. Acad. Sci. USA 91, 6977) as a function of time (t) and the unimolecular rate constant for cleavage (k). Each value of k represents the average (± range) of values determined from two experiments.

Table 45

Entry	Modification	$t_{1/2}$ (m) Activity (t_A)	$t_{1/2}$ (m) Stability (t_S)	$\beta = t_S/t_A$ $\times 10$
1	U4 & U7 = U	1	0.1	1
2	U4 & U7 = 2'-O-Me-U	4	260	650
3	U4 = 2'=CH ₂ -U	6.5	120	180
4	U7 = 2'=CH ₂ -U	8	280	350
5	U4 & U7 = 2'=CH ₂ -U	9.5	120	130
6	U4 = 2'=CF ₂ -U	5	320	640
7	U7 = 2'=CF ₂ -U	4	220	550
8	U4 & U7 = 2'=CF ₂ -U	20	320	160
9	U4 = 2'-F-U	4	320	800
10	U7 = 2'-F-U	8	400	500
11	U4 & U7 = 2'-F-U	4	300	750
12	U4 = 2'-C-Allyl-U	3	>500	>1700
13	U7 = 2'-C-Allyl-U	3	220	730
14	U4 & U7 = 2'-C-Allyl-U	3	120	400
15	U4 = 2'-araF-U	5	>500	>1000
16	U7 = 2'-araF-U	4	350	875
17	U4 & U7 = 2'-araF-U	15	500	330
18	U4 = 2'-NH ₂ -U	10	500	500
19	U7 = 2'-NH ₂ -U	5	500	1000
20	U4 & U7 = 2'-NH ₂ -U	2	300	1500
21	U4 = dU	6	100	170
22	U4 & U7 = dU	4	240	600

CLAIMS**What is claimed is:**

- 5 1. An enzymatic nucleic acid molecule which cleaves ICAM-1 mRNA, IL-5 mRNA, *rel A* mRNA, TNF- α mRNA sites shown in Table 23, 25, 27, or 28, CML associated mRNA selected from those identified as SEQ. ID NOS 1-25, or RSV mRNA or RSV genomic RNA in a region selected from the group consisting of 1C, 1B and N.
- 10 2. The enzymatic nucleic acid molecule of claim 1, the binding arms of which contain sequences complementary to any one of the sequences defined in any of those in Tables 2, 3, 6-9, 11, 13, 15-23, 27, 28, 31, 33, 34, 36, and 37..
3. The enzymatic nucleic acid molecule of claim 1 or 2, wherein said nucleic acid molecule is in a hammerhead motif.
- 15 4. The enzymatic nucleic acid molecule of claim 1 or 2, wherein said RNA molecule is in a hairpin, hepatitis delta virus, group 1 intron, *Neurospora* VS RNA or RNaseP RNA motif.
5. The enzymatic nucleic acid molecule of claim 1 or 2, comprising between 12 and 100 bases complementary to said mRNA or genomic RNA.
- 20 6. The enzymatic nucleic acid molecule of claim 5 comprising between 14 and 24 bases complementary to said mRNA or genomic RNA.
7. The enzymatic nucleic acid molecule of claim 1 or 2, comprising between 5 and 23 bases complementary to said mRNA or genomic RNA.
- 25 8. The enzymatic nucleic acid molecule of claim 7 comprising between 10 and 18 bases complementary to said mRNA or genomic RNA.
9. An enzymatic nucleic acid molecule consisting essentially of a sequence selected from the group of those shown in Tables 4-8, 10, 12, 14-16, 19-22, 24, 26-28, 30, 32, 34 and 36-38.
- 30 10. A mammalian cell including an enzymatic nucleic acid molecule of claims 1 or 2.

11. The cell of claim 10, wherein said cell is a human cell.
12. An expression vector including nucleic acid encoding an enzymatic nucleic acid molecule or multiple enzymatic molecules of claims 1 or 2 in a manner which allows expression of that enzymatic RNA molecule(s) within a mammalian cell.
13. A mammalian cell including an expression vector of claim 12.
14. The cell of claim 13, wherein said cell is a human cell.
15. A method for treatment of a pathological condition related to the mRNA level of ICAM-1, IL-5, *re/ A*, TNF- α , or RSV by administering to a patient an enzymatic nucleic acid molecule of claim 1 or 2.
16. A method for treatment of a pathological condition related to the mRNA level of ICAM-1, IL-5, *re/ A*, TNF- α , or RSV by administering to a patient an expression vector of claim 12.
17. The method of claims 15 or 16, wherein said patient is a human.
18. The method of claim 17 wherein said condition is selected from the group consisting of atherosclerosis, myocardial infraction, stroke, restenosis, heart diseases, cancer, rheumatoid arthritis, asthma, reperfusion injury, inflammatory or autoimmune disorders, transplant rejection, myocardial ischemia, stroke, psoriasis, Kawasaki disease, HIV and AIDS, and septic shock.
19. A nucleoside selected from the group consisting of 5'-C-alkylnucleoside, 2'-deoxy-2'-alkylnucleoside, nucleoside 5'-deoxy-5'-dihalo-methylphosphonate, nucleoside 5'-deoxy-5'-difluoro-methylphosphonate, nucleoside 3'-deoxy-3'-dihalo-methylphosphonate, and 5',3'-dideoxy-5',3'-bis(dihalo)-methylphosphonate.
20. A nucleotide selected from the group consisting of 5'-C-alkylnucleotide, 2'-deoxy-2'-alkylnucleotide, 5'-deoxy-5'-dihalo-methylnucleotide, 5'-deoxy-5'-difluoro-methylnucleotide, 3'-deoxy-3'-dihalo-methylnucleotide, and 5',3'-dideoxy-5',3'-bis(dihalo)-methylphosphonate.

21. A nucleotide triphosphate comprising a nucleotide selected from the group consisting of 5'-C-alkylnucleotide, 2'-deoxy-2'-alkylnucleotide, 5'-deoxy-5'-dihalo-methylnucleotide, 5'-deoxy-5'-difluoro-methylnucleotide, 3'-deoxy-3'-dihalo-methylnucleotide, and 5',3'-dideoxy-5',3'-bis(dihalo)-methylphosphonate.
22. The 5'-C-alkylnucleoside of claim 19, wherein the sugar portion is in a talo configuration.
23. The 5'-C-alkylnucleoside of claim 19, wherein the sugar portion is in an allo configuration.
24. An oligonucleotide comprising a nucleotide selected from the group consisting of 5'-C-alkylnucleotide, 2'-deoxy-2'-alkylnucleotide, 5'-deoxy-5'-dihalo-methylnucleotide, 5'-deoxy-5'-difluoro-methylnucleotide, 3'-deoxy-3'-dihalo-methylnucleotide, and 5',3'-dideoxy-5',3'-bis(dihalo)-methylphosphonate.
25. An oligonucleotide comprising a moiety having the formula:
- wherein B is a nucleotide base or hydrogen; R1, R2 and R3 independently is selected from the group consisting of hydrogen, an alkyl group containing between 2 and 10 carbon atoms inclusive, an amine, an amino acid, and a peptide containing between 2 and 5 amino acids inclusive; and the zigzag lines are independently hydrogen or a bond.
26. An oligonucleotide comprising a 3'-amido or peptido group.
27. An oligonucleotide comprising a 5'-amido or peptido group.
28. The oligonucleotide of claim 24, 25, 26, or 27 having enzymatic activity.
29. Method for producing an enzymatic nucleic acid molecule having activity to cleave an RNA or single-stranded DNA molecule, comprising the step of forming said enzymatic molecule with at least one nucleotide having an alkyl group at its 5'-position or 2'-position.

- 5 30. Method for conversion of a protected allo sugar to a protected talo sugar, comprising the step of contacting said protected allo sugar with triphenyl phosphine, diethylazodicarboxylate, p-nitrobenzoic acid under inversion causing conditions to provide said protected talo sugar.
- 10 31. Method for the synthesis of a nucleoside 5' or a 3'-dihalo-methylphosphonate comprising the step of condensing a difluoromethylphosphonate-containing sugar with a pyrimidine or purine under conditions suitable for forming a nucleoside 5'- or 3'-difluoromethylphosphonate.
32. The oligonucleotide of claim 3, wherein the normal hammerhead U4 and/or U7 positions are substituted with 2'-NH-amino acid.
- 15 33. A method for the synthesis of RNA comprising the step of providing 5-S-alkyltetrazole at a delivered 0.1-1.0 M concentration for the activation of a RNA amidite during a coupling step for less than or equal to 10 minutes.
- 20 34. A method for the synthesis of RNA comprising the step of providing 5-S-alkyltetrazole at 0.15-0.35 M effective, or final, concentration for the activation of a RNA amidite during a coupling step for less than or equal to 10 minutes.
- 25 35. A method for the deprotection of RNA comprising the step of providing alkylamine (MA) or NH₄OH/alkylamine (AMA) at between 60°C - 70°C for 5 to 15 minutes to remove any exocyclic amino protecting groups from protected RNA; wherein said alkyl is selected from the group consisting of methyl, ethyl, propyl and butyl.
- 30 36. A method for the deprotection of RNA alkylsilyl protecting groups comprising, contacting said groups with anhydrous triethylamine-hydrogen fluoride (aHF•TEA) trimethylamine or diisopropylethylamine at between 60 °C-70 °C for 0.25-24 h.
37. A method for the purification of an RNA molecule by passing said enzymatic RNA molecule over an HPLC column, wherein said HPCC column is an anion exchange chromatography column.

38. Method for one pot deprotection of RNA comprising, contacting a protected base with anhydrous methyl amine at between 60 °C-70 °C for at least 5 min; cooling the resulting mixture and contacting said mixture with TEA-3HF reagents under conditions which remove a protecting group of the 2'-hydroxyl position.
39. Method for synthesizing RNA containing a phosphorothioate linkage comprising the step of contacting 6-10 equivalents of 3H-1,2-benzodithiole-3-one 1,1-dioxide (Beaucage reagent) with the growing RNA chain for 5 seconds with a reaction time of at least 300 seconds.
40. Method of synthesizing RNA containing a phosphorothioate linkage comprising the step of achieving coupling with 5-S-ethyltetrazole or 5-S-methyltetrazole prior to sulfurization.
41. Method of claims 38, 39 or 40 wherein said RNA is enzymatically active.
42. Method for synthesizing 2'-deoxy-2'-amino-nucleoside phosphoramidite, comprising the step of protecting the 2'-amino group with a N-phtaloyl group.
43. The method of claim 42 wherein the said nucleoside lacks a base.
44. Method for synthesis of RNA comprising the step of: protecting the 2'-position of a nucleotide during said synthesis with a (trimethylsilyl)ethoxymethyl (SEM) group.
45. Method for covalently linking a SEM group to the 2'-position of a nucleotide, comprising the step of: contacting a nucleoside with an SEM-containing molecule under SEM bonding conditions.
46. The method of claim 45, wherein said conditions comprise dibutyltin oxide and tetrabutylammonium fluoride and SEM-Cl.
47. Method for removal of an SEM group from a nucleoside molecule or an oligonucleotide, comprising the step of: contacting said molecule or oligonucleotide with boron trifluoride etherate (BF₃•OEt₂) under SEM removing conditions.

48. The method of claim 57 wherein said $(\text{BF}_3 \cdot \text{OEt}_2)$ is provided in acetonitrile.
49. One or more vectors comprising
- 5 a first nucleic acid sequence encoding a first ribozyme having intramolecular or intermolecular cleaving activity, said first ribozyme being selected from the group consisting of a hammerhead, hairpin, hepatitis delta virus, *Neurospora* VS RNA, Group I, and RNaseP motif;
- 10 and a second nucleic acid sequence encoding a second ribozyme having intermolecular cleaving activity, said second ribozyme being selected from the group consisting of a hammerhead, hairpin, hepatitis delta virus, *Neurospora* VS RNA, Group I, and RNaseP motif and said second nucleic acid being flanked by other
- 15 nucleic acid sequences encoding RNA which is cleaved by said first ribozyme to release said second ribozyme from RNA encoded by said vector;
- 20 wherein said first and second nucleic acid sequences may be on the same or separate nucleic acid molecules, and said vector encodes mRNA or comprises RNA which lacks secondary structure which reduces release of said second ribozyme by more than 20%.
50. Cell comprising the vector of claim 49.
51. A transcribed non-naturally occurring RNA molecule, comprising a desired therapeutic RNA portion, wherein said molecule comprises an intramolecular stem formed by base-pairing interactions
- 25 between a 3' region and 5' complementary nucleotides in said RNA, wherein said stem comprises at least 8 base pairs.
52. The RNA molecule of claim 51, wherein said molecule is transcribed by a RNA polymerase III based promoter system.
53. The RNA molecule of claim 51, wherein said molecule is transcribed
- 30 by a type 2 pol III promoter system.
54. The RNA molecule of claim 51, wherein said molecule is a chimeric tRNA.

55. The RNA molecule of claim 53, said RNA having A and B boxes of a type 2 pol III promoter separated by between 0 and 300 bases.
56. The RNA molecule of claim 53, wherein said desired RNA molecule is at the 3' end of said B box.
- 5 57. The RNA molecule of claim 53, wherein said desired RNA molecule is in between the said A and the B box.
58. The RNA molecule of claim 53, wherein said desired RNA molecule includes said B box.
- 10 59. The RNA molecule of claim 51, wherein said desired RNA molecule is selected from the group consisting of antisense RNA, decoy RNA, therapeutic editing RNA, enzymatic RNA, agonist RNA and antagonist RNA.
60. The RNA molecule of claim 51, wherein said 5' terminus is able to base-pair with at least 12 bases of said 3' region.
- 15 61. The RNA molecule of claim 51, wherein said 5' terminus is able to base-pair with at least 15 bases of said 3' region.
62. DNA vector encoding the RNA molecule of claim 51
63. The vector of claim 62, wherein said vector is derived from an AAV or adeno virus.
- 20 64. RNA vector encoding the RNA molecule of claim 51.
65. The vector of claim 64, wherein said vector is derived from an alpha virus or retro virus.
66. The vector of claim 62 wherein the portions of the vector encoding said RNA function as a RNA pol III promoter.
- 25 67. Cell comprising the vector of claim 62.
68. Cell comprising the vector of claim 53.
69. Cell comprising the RNA of claim 51.

70. Method to provide a desired RNA molecule in a cell, comprising introducing said molecule into said cell a RNA comprising a desired RNA molecule, having a 5' terminus able to base pair with at least 8 bases of a 3' region of said RNA molecule.
- 5 71. The method of claim 70, wherein said introducing comprises providing a vector encoding said RNA molecule.
72. Hammerhead ribozyme having 2 or 3 base pairs in stem II with an interconnecting loop of 4 or more bases between said base pairs.
- 10 73. Hairpin ribozyme lacking a substrate moiety, comprising at least six bases in helix 2 and able to base-pair with a separate substrate RNA, wherein the said ribozyme comprises one or more bases 3' of helix 3 able to base-pair with the said substrate RNA to form a helix 5 and wherein the said ribozyme can cleave and/or ligate said separate RNA(s) in *trans*.
- 15 74. The ribozyme of claim 73, wherein said ribozyme comprises six bases in helix 2.
- 20 75. The ribozyme of claim 73, having the structure of Fig. 3, wherein each N and N' is independently any base and each dash may represent a hydrogen bond, r is 1-20, q is 2-20, o is 0 - 20, n is 1 - 4, and m is 1 - 20.
- 25 76. Method for increasing the activity of a hairpin ribozyme by providing one or more bases 3' of helix 3 able to base-pair with a substrate RNA to form a helix 5.
77. Trans-cleaving Hairpin ribozyme comprising at least 6 base pairs in helix 2 lacking a substrate RNA moiety.
78. Trans-ligating Hairpin ribozyme comprising at least 6 base pairs in helix 2 lacking a substrate RNA moiety.
79. The ribozyme of claim 73 having the structure of Fig. 73.
80. The ribozyme of claim 73 having the structure of Fig. 74.
- 30 81. A cell including the ribozyme of any of claims 73-80.

82. An expression vector comprising nucleic acid encoding the ribozyme of any of claims 73-80, in a manner which allows expression of that ribozyme within a cell.
83. A cell including an expression vector of claim 82.
- 5 84. Method for altering in vivo the nucleotide base sequence of a naturally occurring mutant nucleic acid molecule, comprising the steps of:
- 10 contacting said nucleic acid molecule in vivo with an oligonucleotide or peptide nucleic acid able to form a duplex or triplex molecule with said nucleic acid molecule, wherein formation of said duplex or triplex molecule directly, or after nucleic acid repair *in vivo*, causes at least one base in said nucleic acid molecule to be chemically modified to functionally alter the nucleotide base sequence of said nucleic acid sequence.
- 15 85. The method of claim 84, wherein said oligonucleotide is of a length sufficient to activate dsRNA deaminase in vivo to cause conversion of an adenine base to inosine in an RNA molecule.
- 20 86. The method of claim 84, wherein said oligonucleotide comprises an enzymatic nucleic acid molecule which is active to chemically modify a base.
87. The method claim 84, wherein said nucleic acid molecule is DNA or RNA.
88. The method of claim 84, wherein said oligonucleotide comprises a chemical mutagen.
- 25 89. The method of claim 88, wherein said mutagen is nitrous acid.
90. The method of claim 84 wherein said oligonucleotide causes deamination of 5-methylcytosine to thymidine, cytosine to uracil, or adenine to inosine, or methylation of cytosine to 5-methylcytosine.
- 30 91. The method of claim 84, wherein an endogenous mammalian editing system is co-opted to cause said chemical modification.

92. Method for introduction of enzymatic nucleic acid into a cell or tissue, comprising the steps of;

5 providing a complex of a first nucleic acid molecule encoding said enzymatic nucleic acid associated with a second nucleic acid molecule having sufficient complementarity with said first nucleic acid molecule so that it is able to form an R-loop base-paired structure under physiological conditions with said first nucleic acid molecule; wherein said R-loop is formed in a region of said first nucleic acid molecule at a location which promotes expression of
10 RNA from said first nucleic acid under said conditions;

and contacting said complex with said cell or tissue under conditions in which said enzymatic nucleic acid molecule is produced in said cell or tissue.

- 15 93. Method for introduction of a desired nucleic acid into a cell or tissue, comprising the steps of;

20 providing a complex of a first nucleic acid molecule encoding said desired nucleic acid associated with a second nucleic acid molecule having sufficient complementarity with said first nucleic acid molecule so that it is able to form an R-loop base-paired structure under physiological conditions with said first nucleic acid molecule; wherein said first nucleic acid molecule lacks a promoter region and said R-loop is formed in a region of said first nucleic acid molecule at a location which promotes expression of RNA from said first nucleic acid under said conditions;

25 and contacting said complex with said cell or tissue under conditions in which said desired acid molecule is produced in said cell or tissue.

- 94 Method for introduction of a desired nucleic acid into a cell or tissue, comprising the steps of;

30 providing a complex of a first nucleic acid molecule encoding said enzymatic nucleic acid associated with a second nucleic acid molecule having sufficient complementarity with said first nucleic acid molecule so that it is able to form an R-loop base-paired

structure under physiological conditions with said first nucleic acid molecule; wherein said R-loop is formed in a region of said first nucleic acid molecule at a location which promotes expression of RNA from said first nucleic acid under said conditions;

5 and wherein said second nucleic acid further comprises a localization factor;

and contacting said complex with said cell or tissue under conditions in which said desired nucleic acid molecule is produced in said cell or tissue.

- 10 95. Complex of a first nucleic acid molecule encoding an enzymatic nucleic acid associated with a second nucleic acid molecule having sufficient complementarity with said first nucleic acid molecule so that it is able to form an R-loop base-paired structure under physiological conditions with said first nucleic acid molecule;
- 15 wherein said R-loop is formed in a region of said first nucleic acid molecule at a location which promotes expression of RNA from said first nucleic acid under said conditions.
- 20 96. Complex of a first nucleic acid molecule encoding a desired nucleic acid associated with a second nucleic acid molecule having sufficient complementarity with said first nucleic acid molecule so that it is able to form an R-loop base-paired structure under physiological conditions with said first nucleic acid molecule;
- 25 wherein said first nucleic acid molecule lacks a promoter region and said R-loop is formed in a region of said first nucleic acid molecule at a location which promotes expression of RNA from said first nucleic acid under said conditions.
- 30 97. Complex of a first nucleic acid molecule encoding an enzymatic nucleic acid associated with a second nucleic acid molecule having sufficient complementarity with said first nucleic acid molecule so that it is able to form an R-loop base-paired structure under physiological conditions with said first nucleic acid molecule;
- wherein said R-loop is formed in a region of said first nucleic acid molecule at a location which promotes expression of RNA from said

first nucleic acid under said conditions, and wherein said second nucleic acid further comprises a localization factor.

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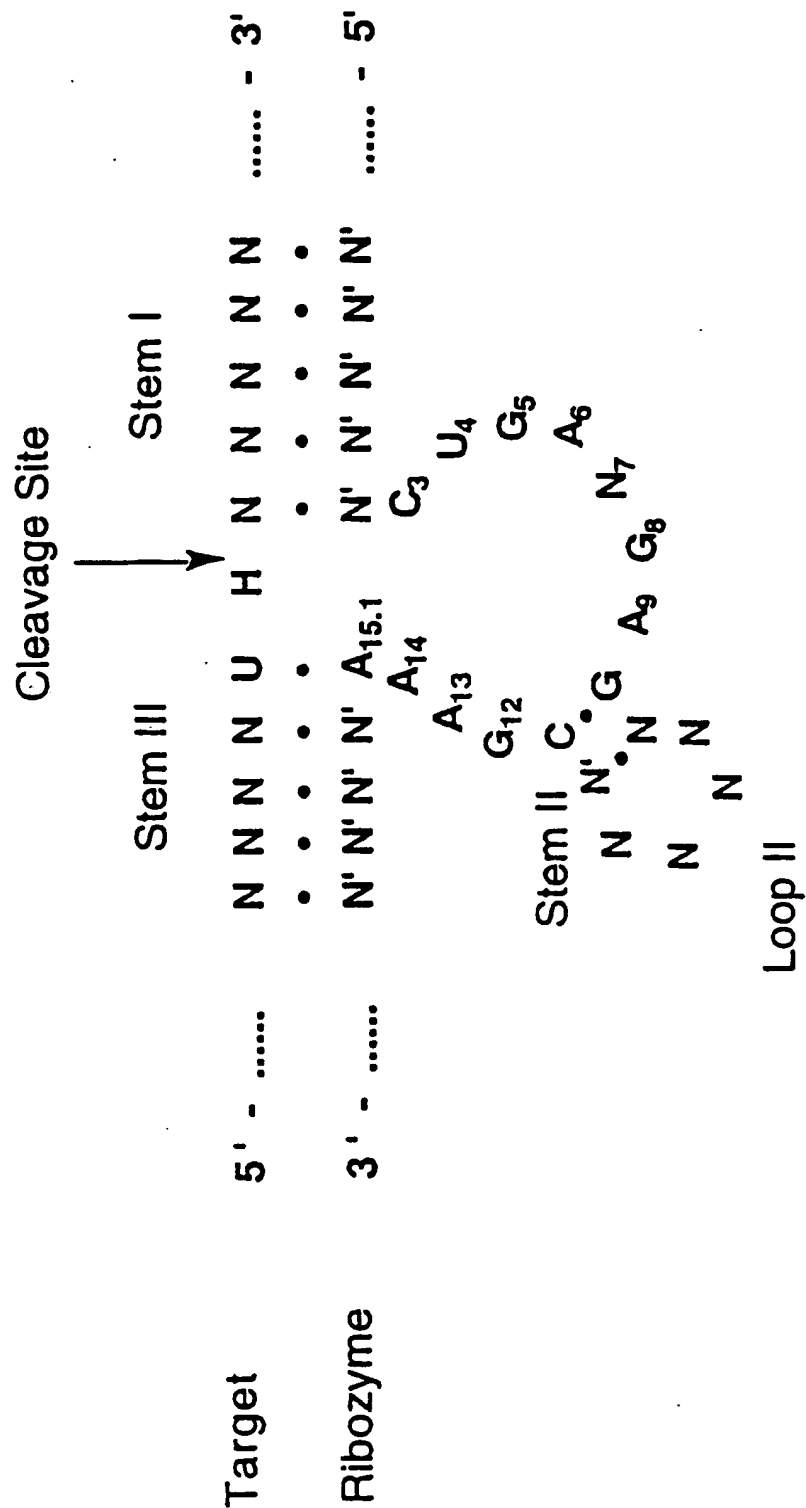
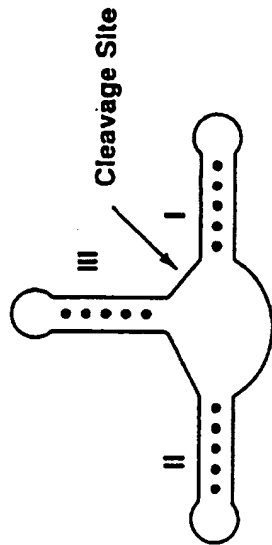


FIG. 1.

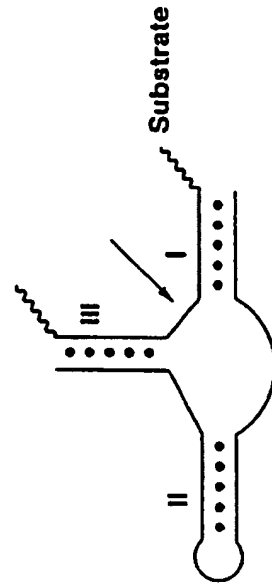
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FIG. 2a.



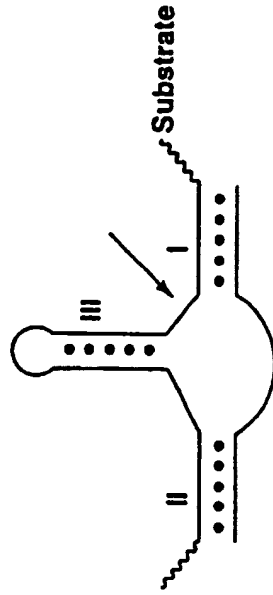
a

FIG. 2c.



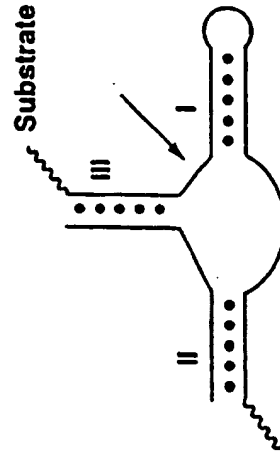
c

FIG. 2b.



b

FIG. 2d.



d

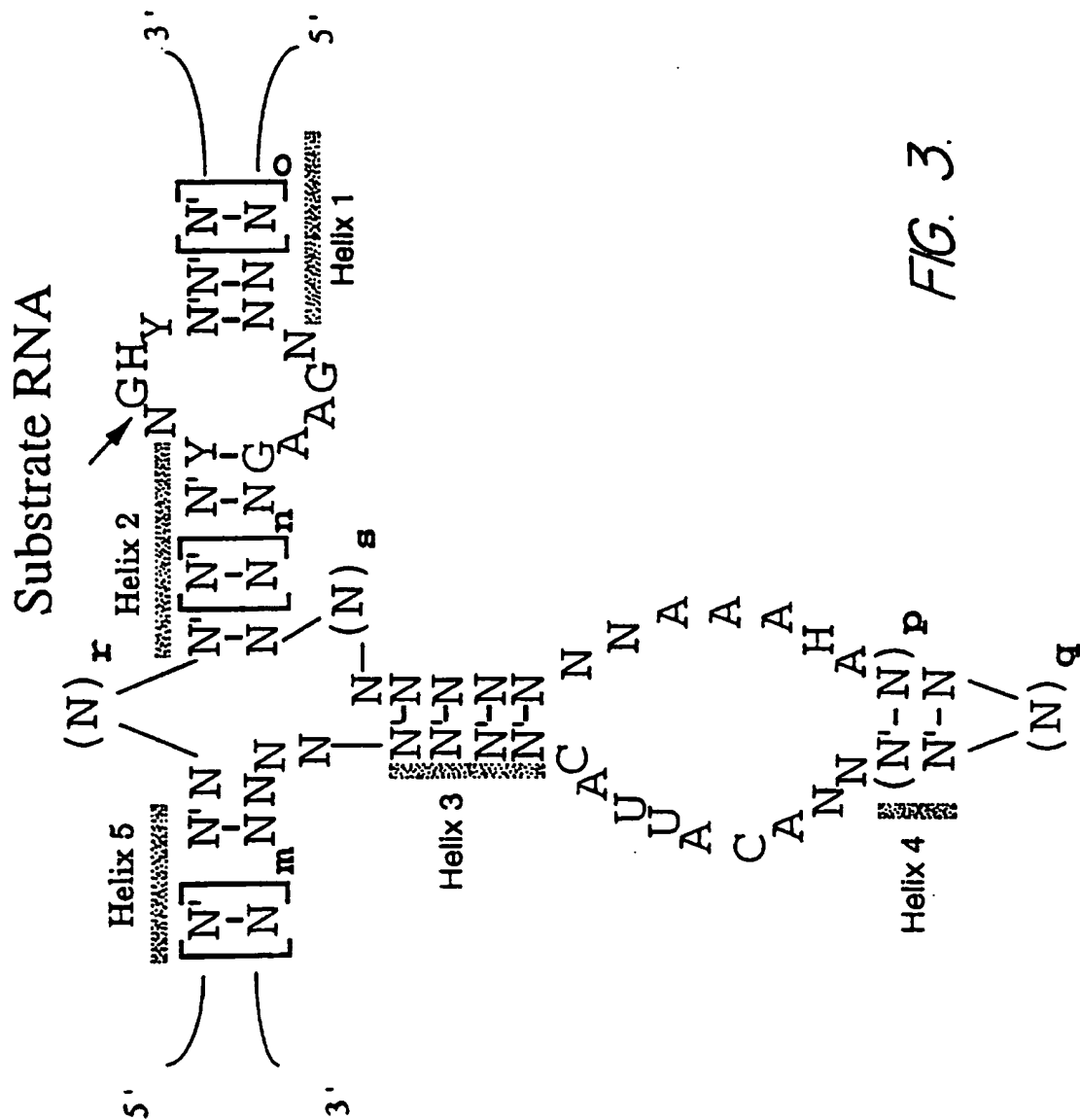
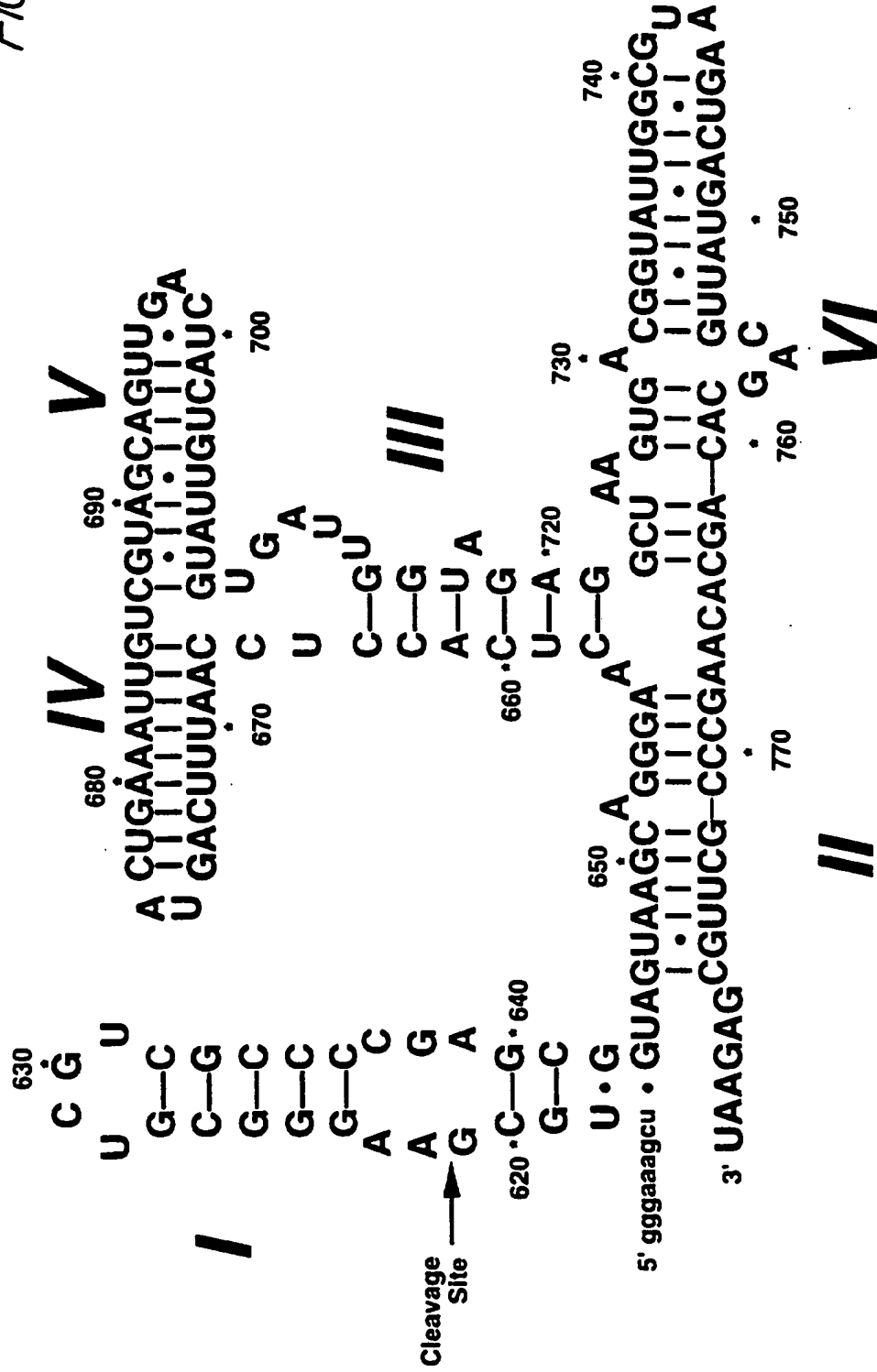


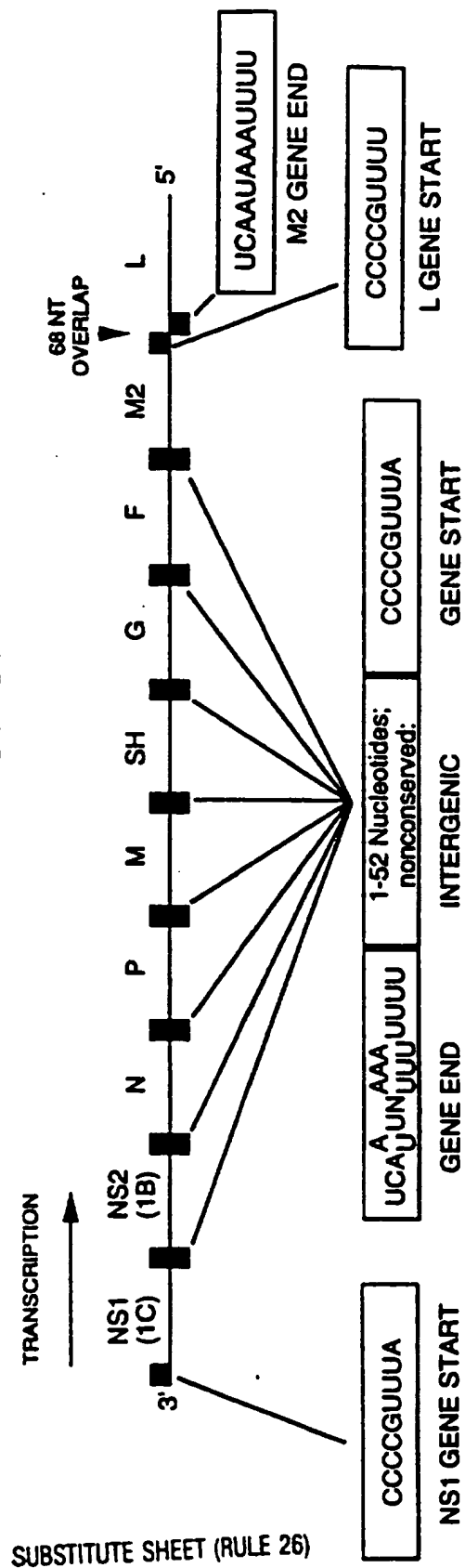
FIG. 3.



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FIG. 5.

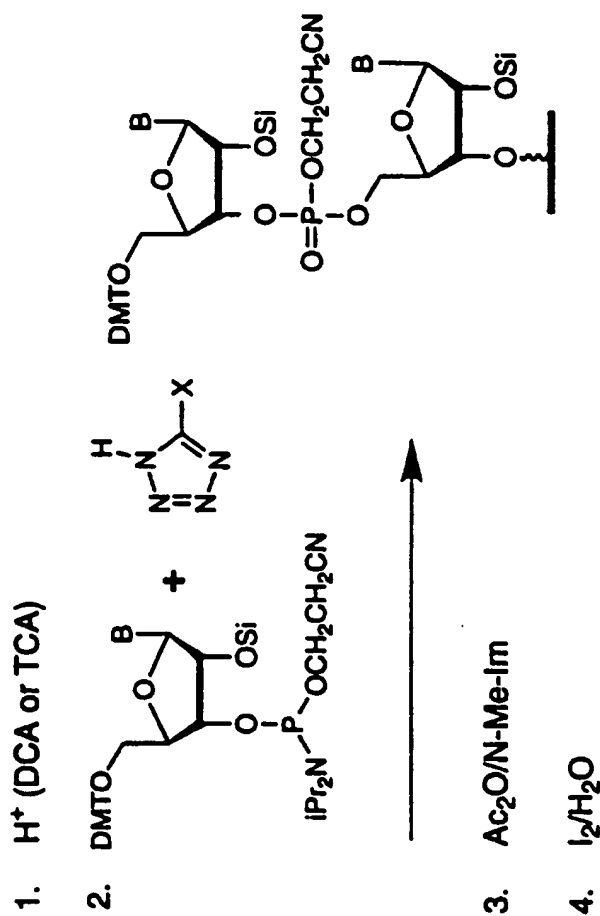




Adapted from Virology, Second Edition, Edited by B.N. Fields, 1990.

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FIG. 7.



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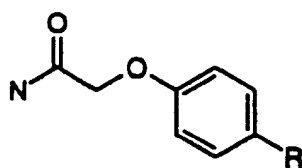
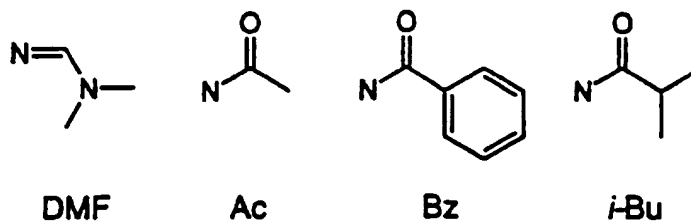


FIG. 8.

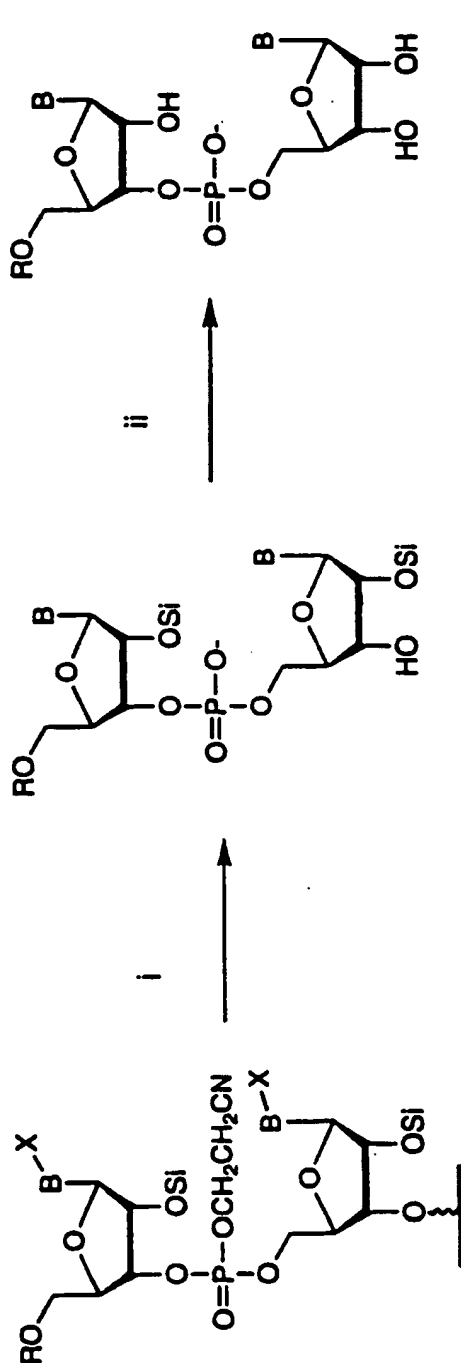
R = H = PAC

R = tBu = TAC

R = iPr = IPPAC

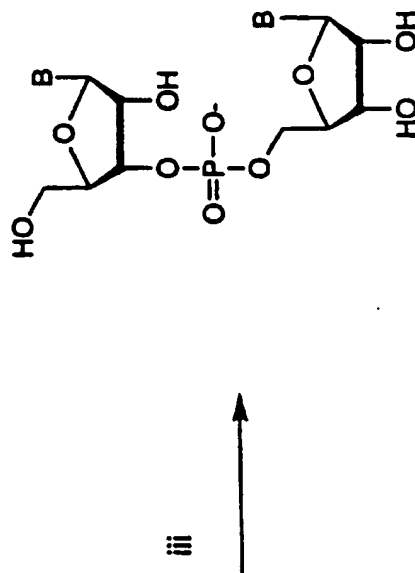
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FIG. 9.



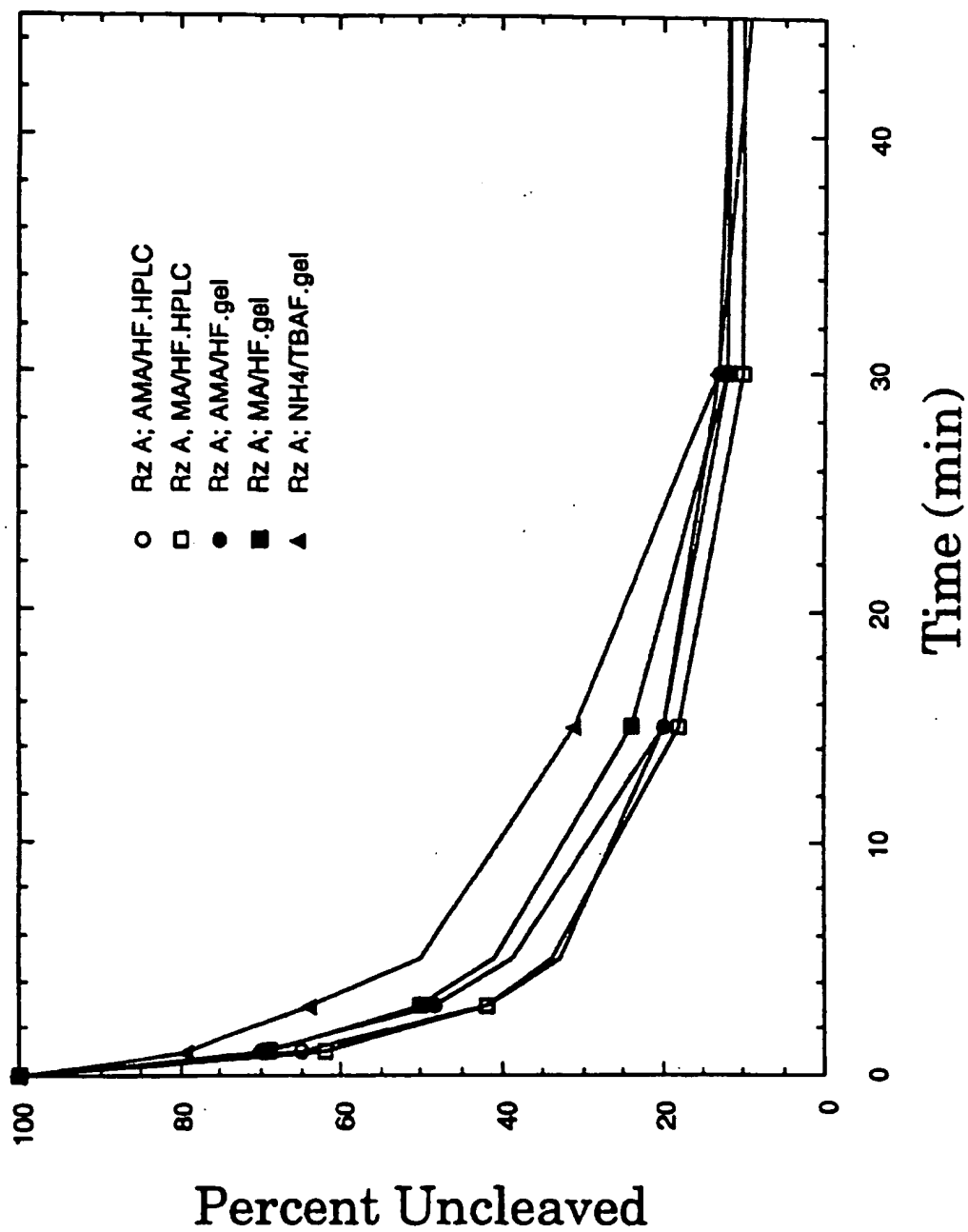
- i MA or AMA, 30 m @ 65 °C
 ii anhydrous TEA·HF, 30 m @ 65 °C
 iii H⁺

R = H or DMT or other hydroxyl protection
 X = Exocyclic Amino protection



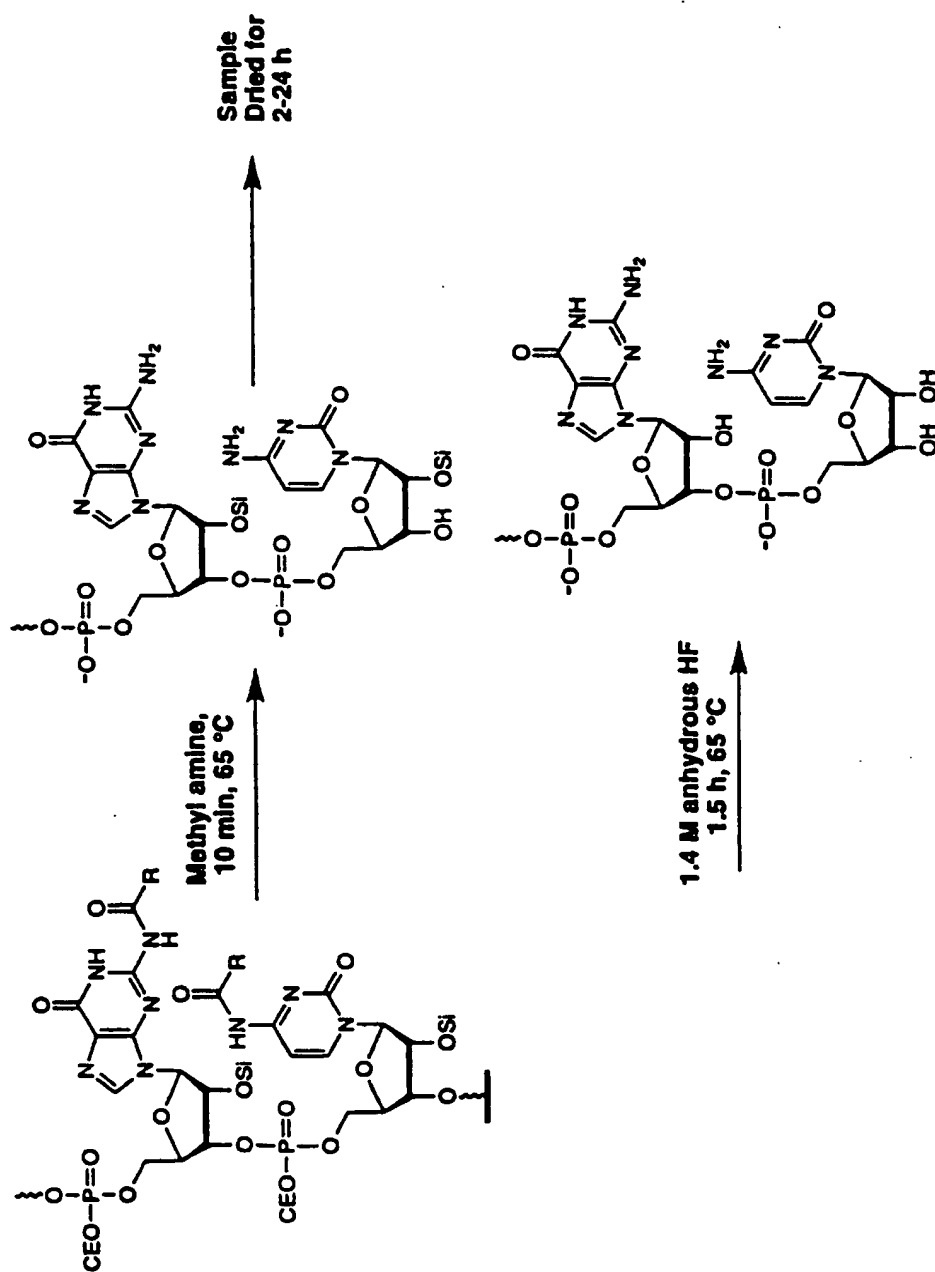
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FIG. 10.



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FIG. 11.



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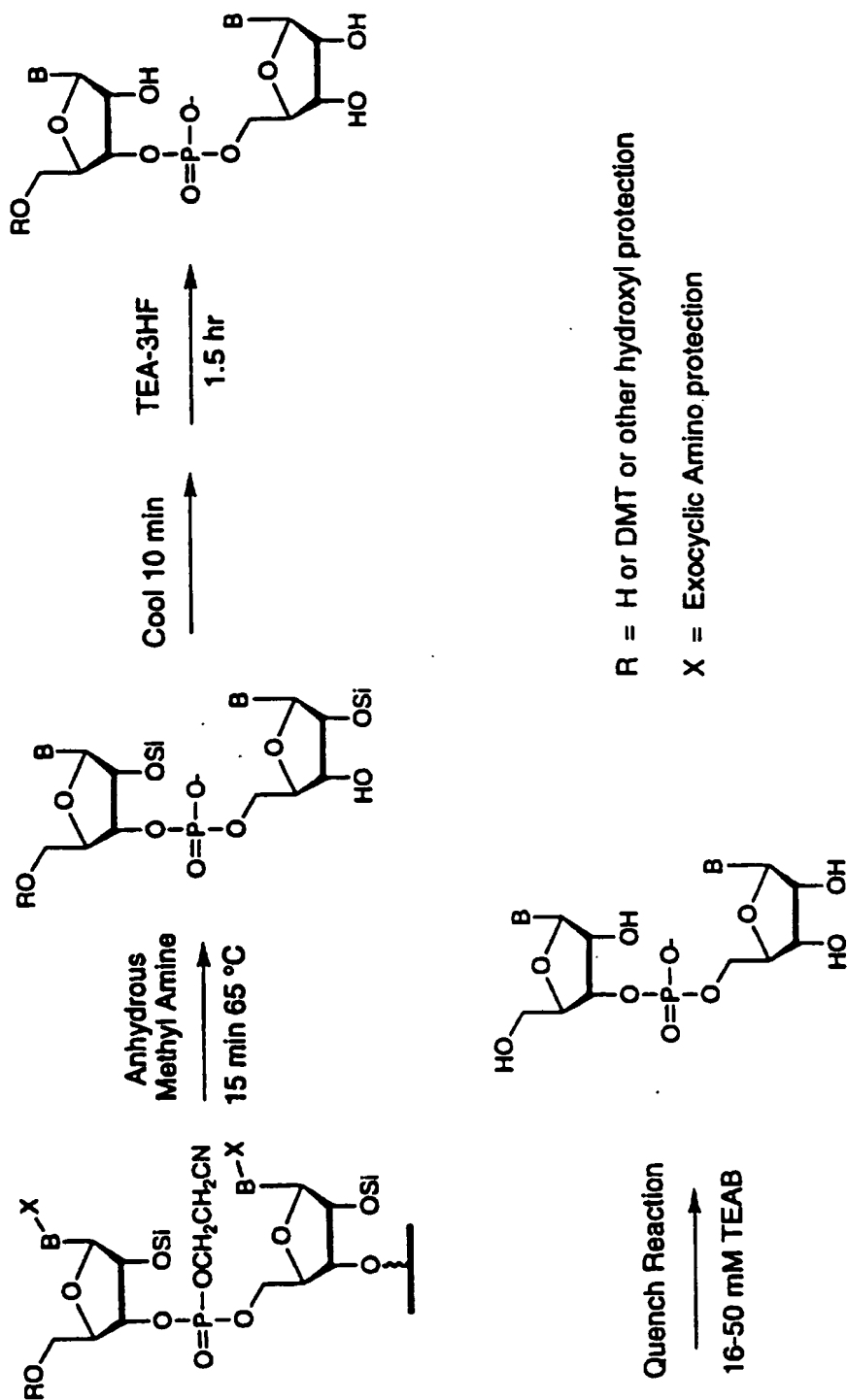
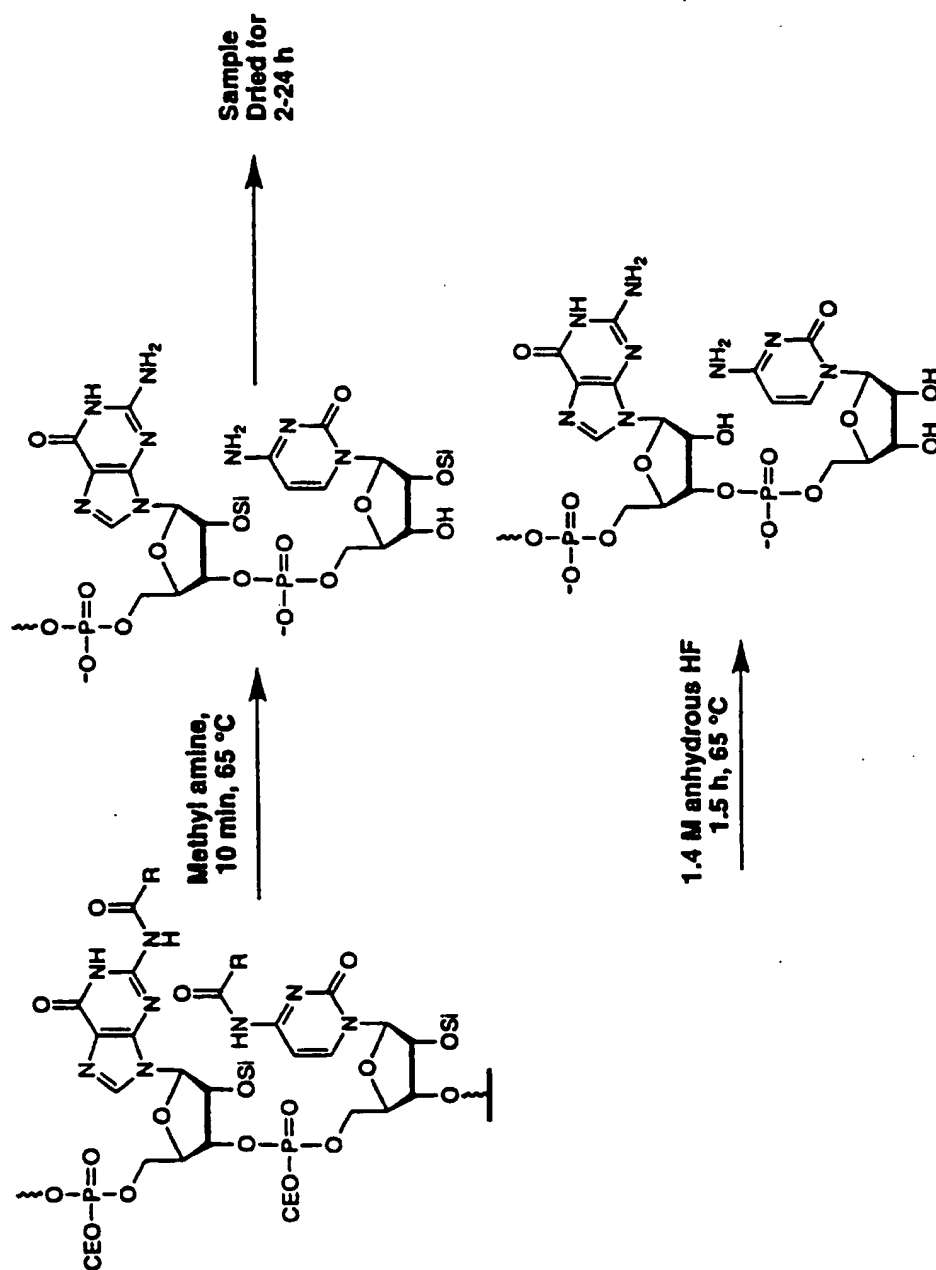


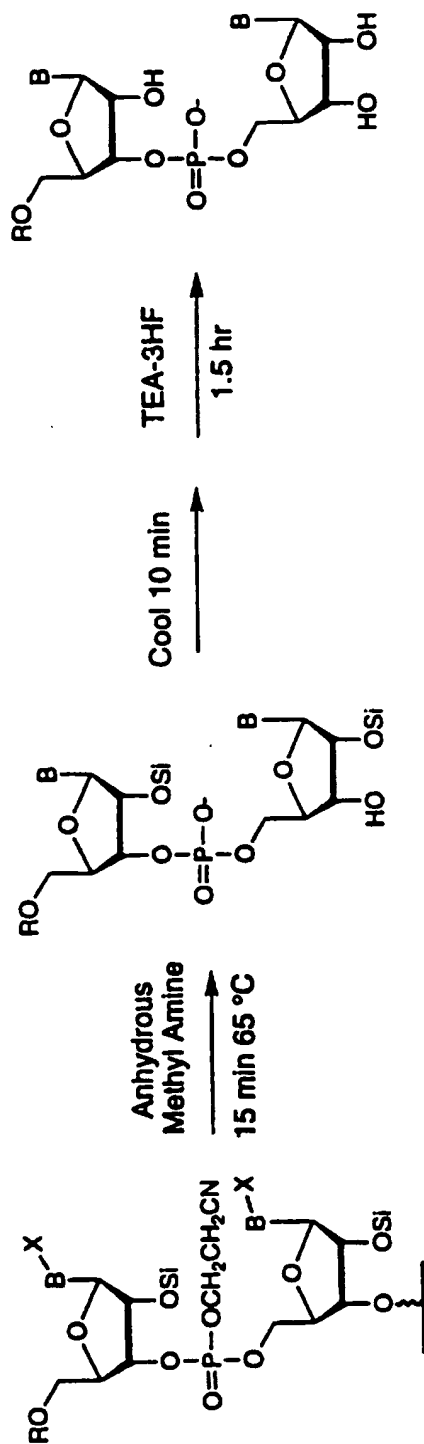
FIG. 12.

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FIG. 11.



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R = H or DMT or other hydroxyl protection

X = Exocyclic Amino protection

FIG. 12.

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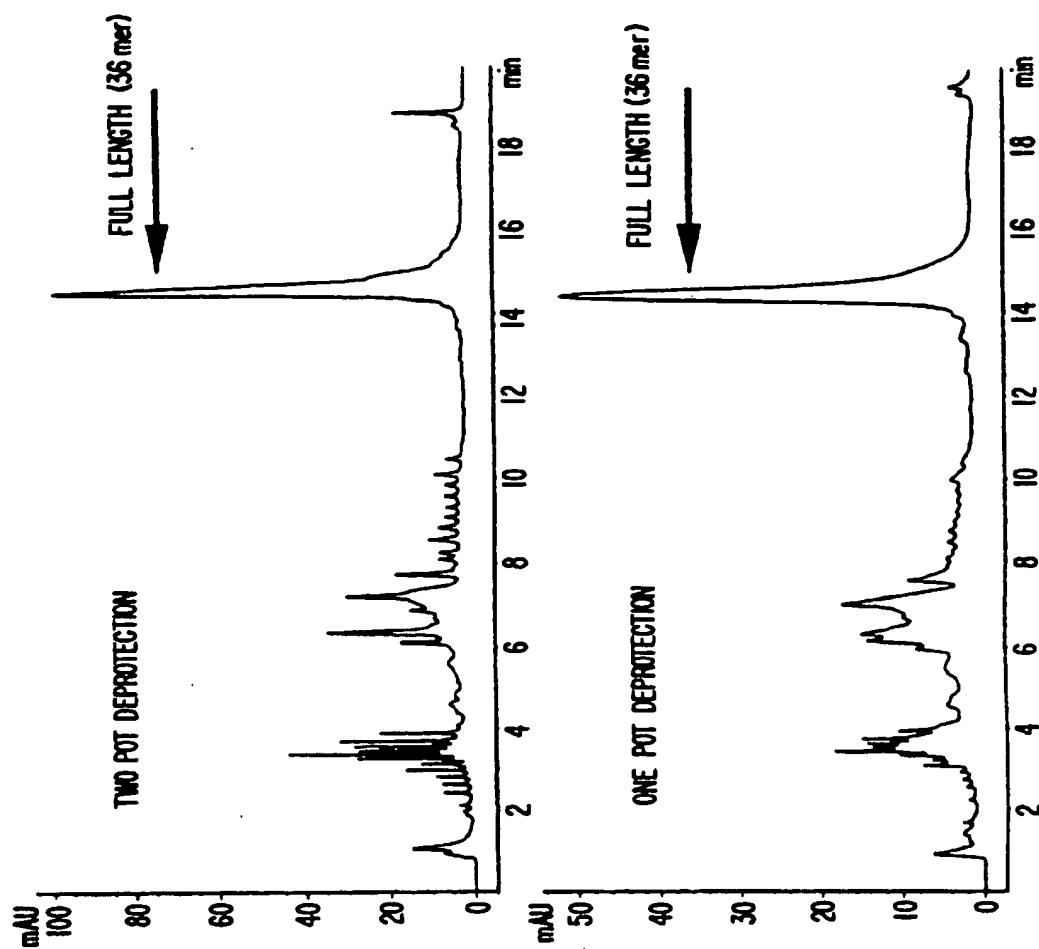
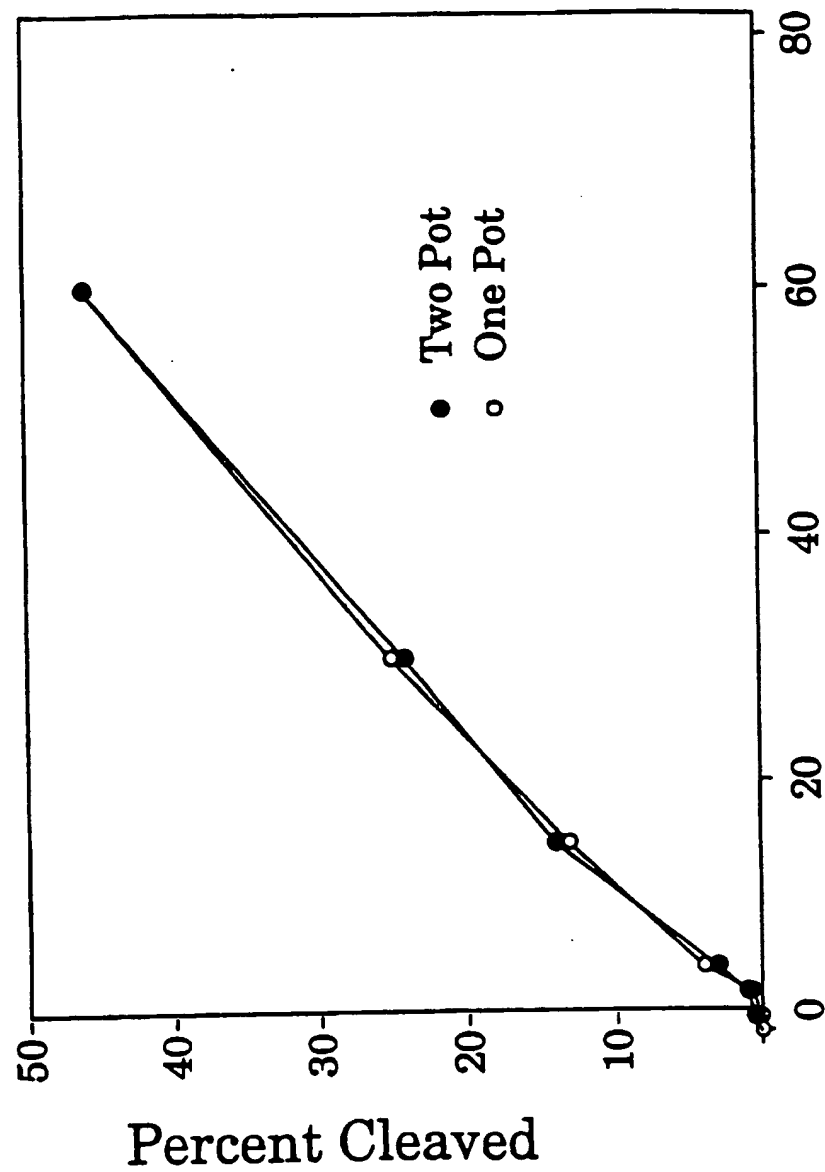


FIG. 13a.

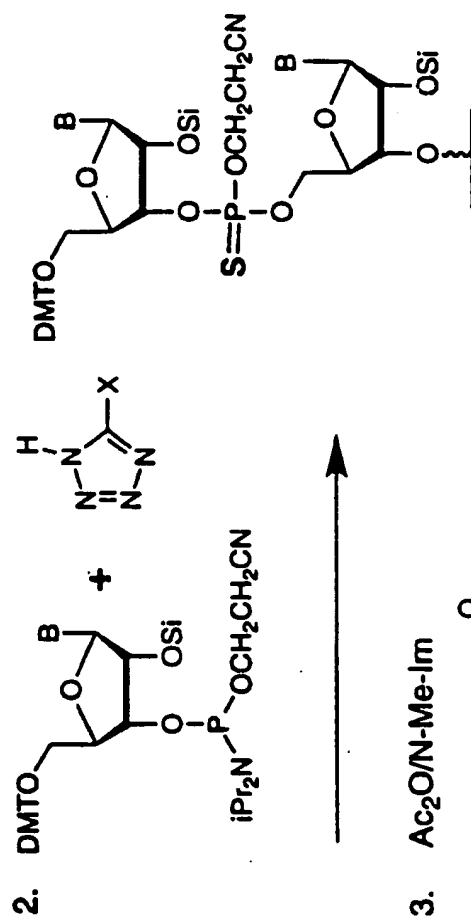
FIG. 13b.

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Time (min)
FIG. 14.

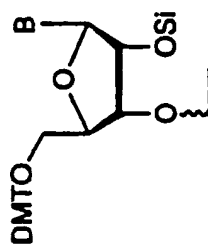
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FIG. 15.

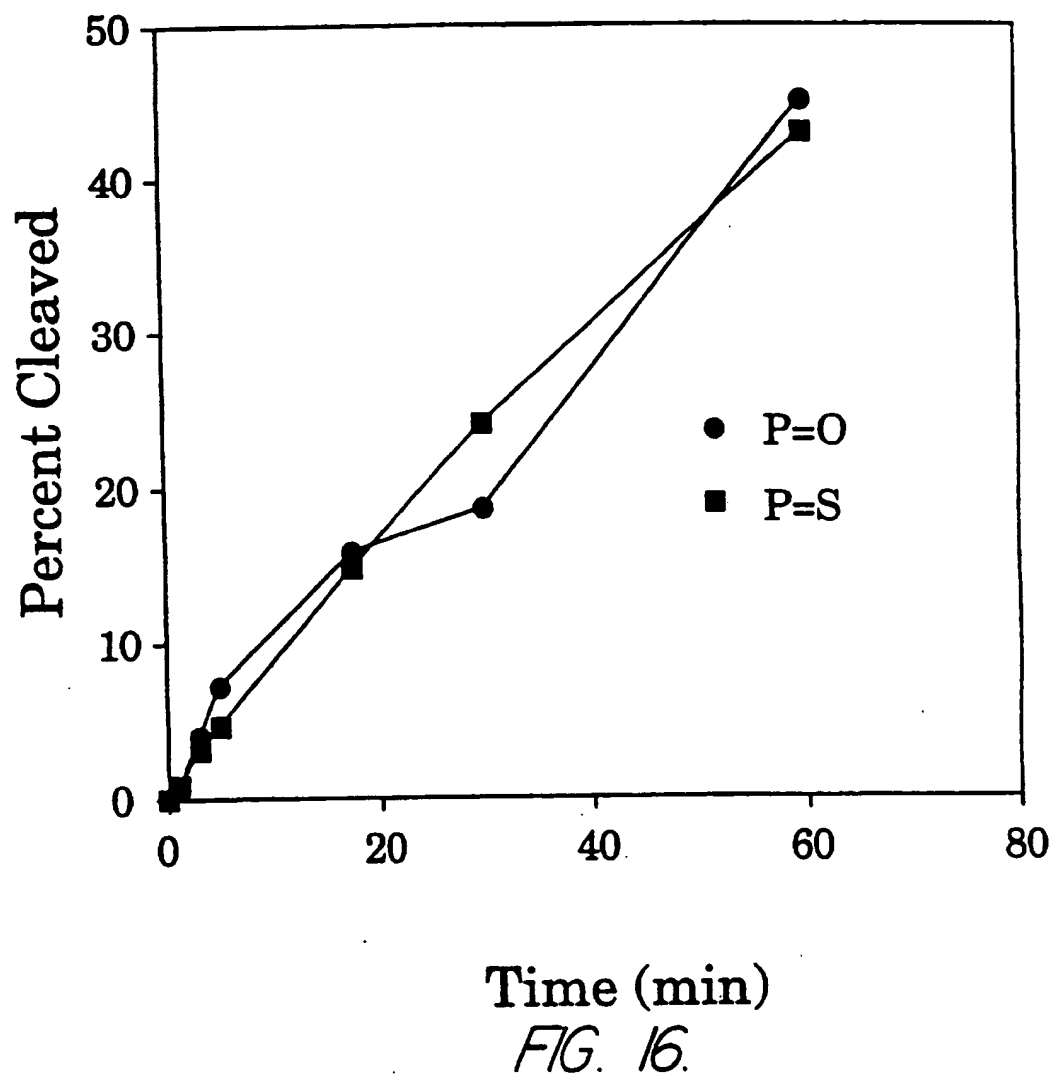
1. H^+ (DCA or TCA)3. $Ac_2O/N-Me-Im$

4.

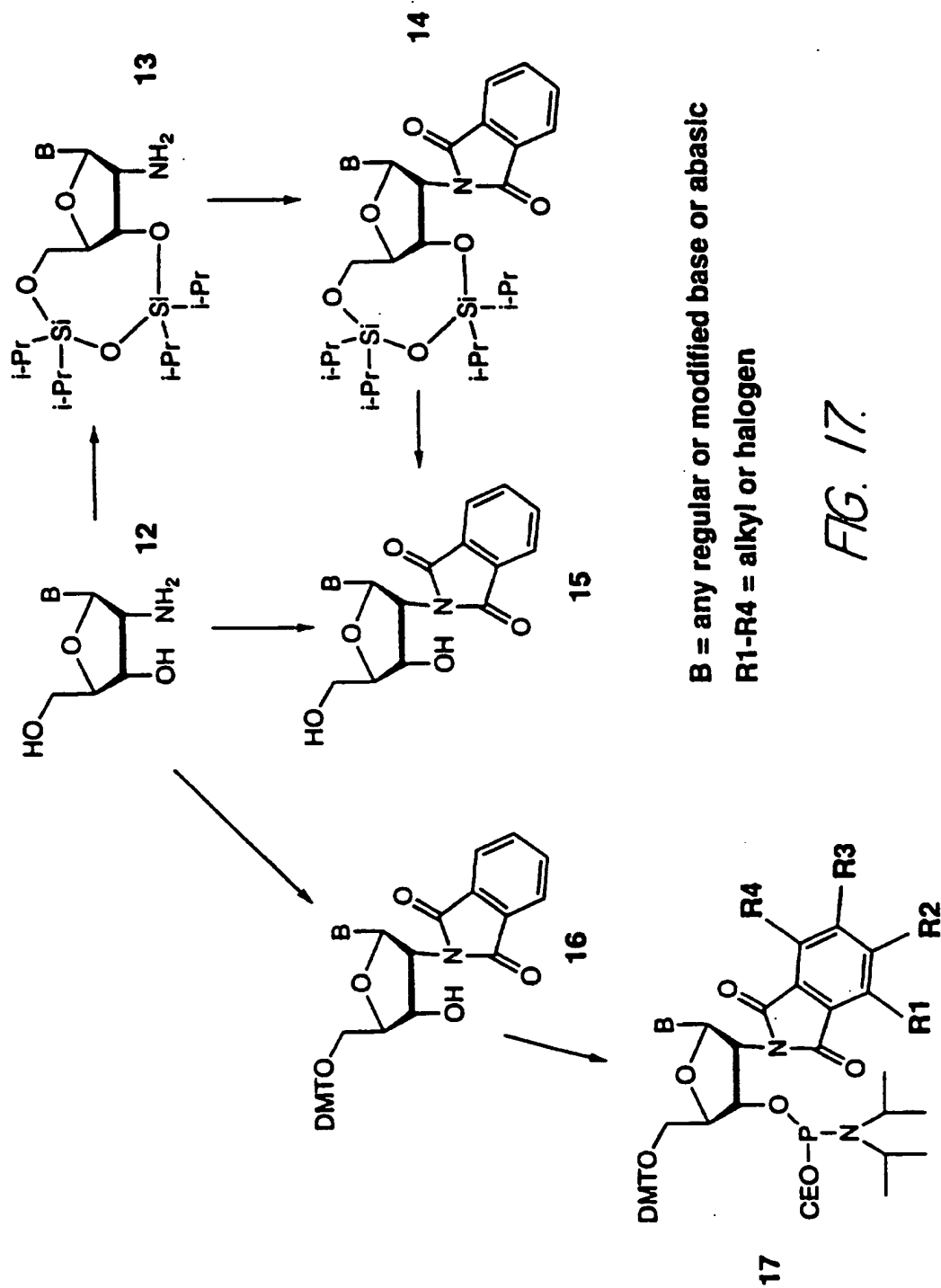
Beaucage Sulfurylating Reagent



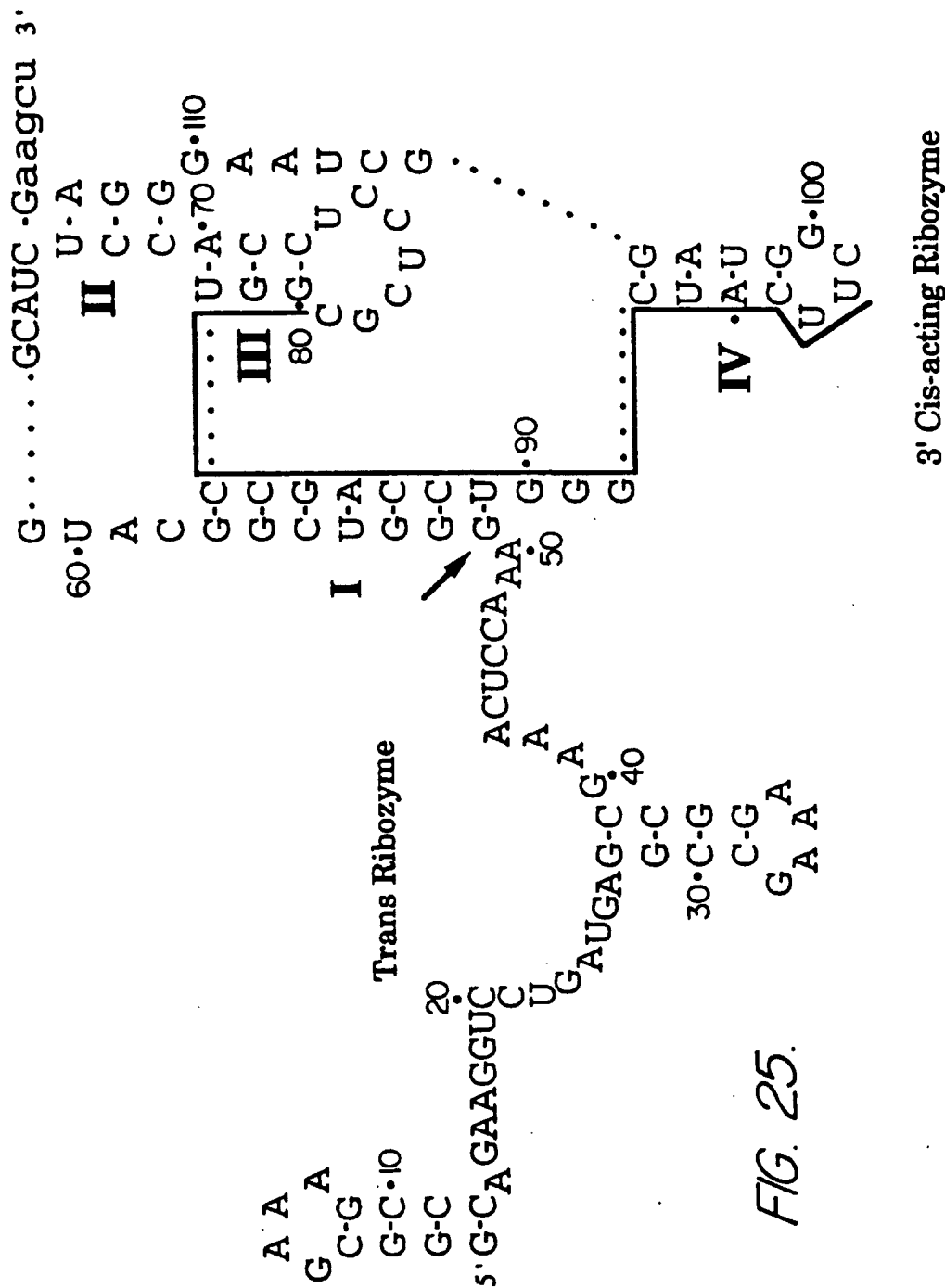
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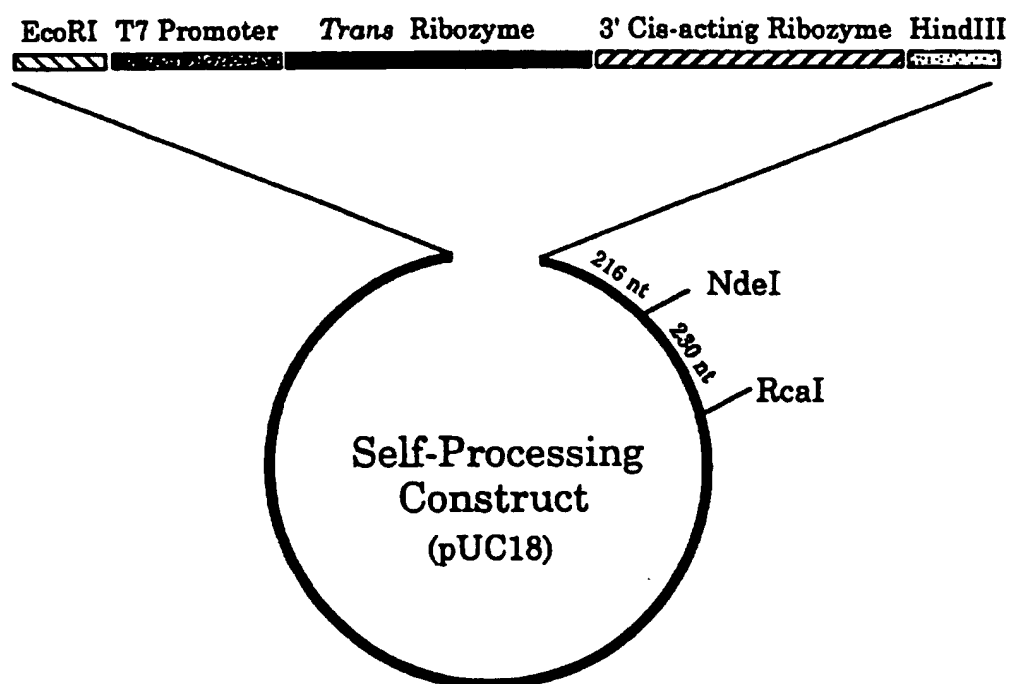


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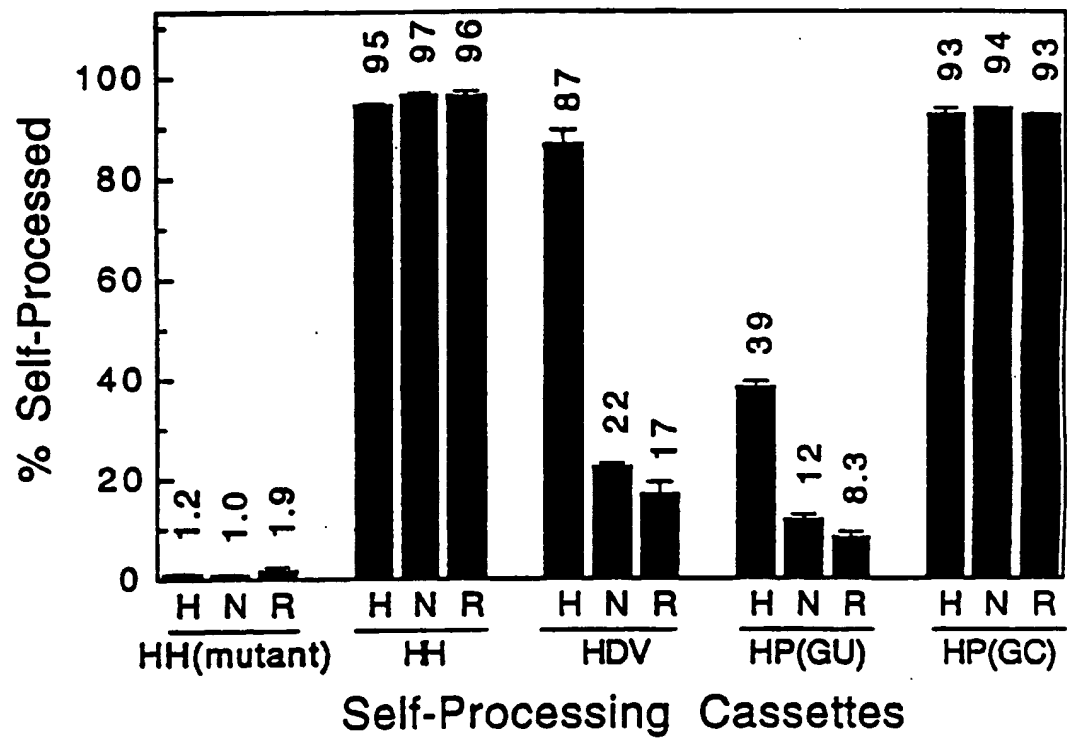
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FIG. 26.



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FIG. 27.



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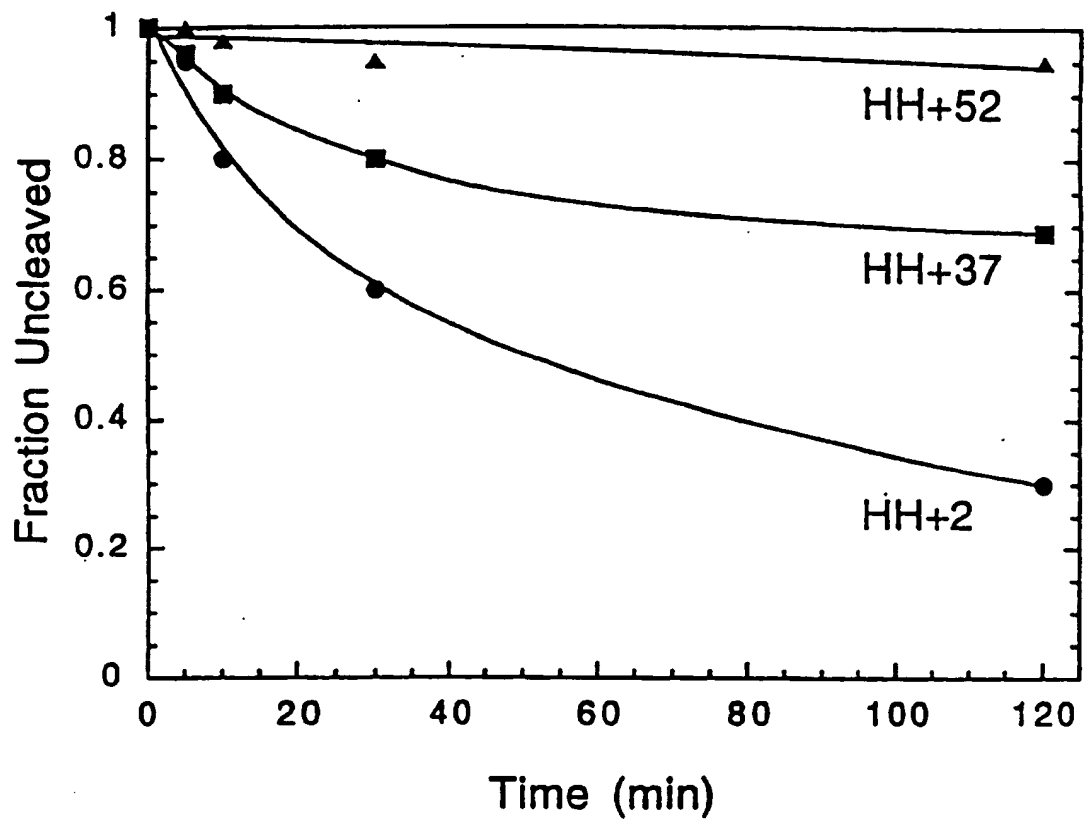


FIG. 28.

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FIG. 29.

Mutant										HP (G:C)		RNA	Preincubation with $MgCl_2$	Full Length RNA	3' Cleavage Products
HH		HH		HDV		HH		In Vitro	Cellular	In Vitro	Cellular				
+	-	+	-	+	-	+	-	+	-	+	-	↑	↑↑	↑	↑↑
+	-	+	-	+	-	+	-	+	-	+	-	↑	↑↑	↑	↑↑
+	-	+	-	+	-	+	-	+	-	+	-	↑	↑↑	↑	↑↑
+	-	+	-	+	-	+	-	+	-	+	-	↑	↑↑	↑	↑↑

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FIG. 30

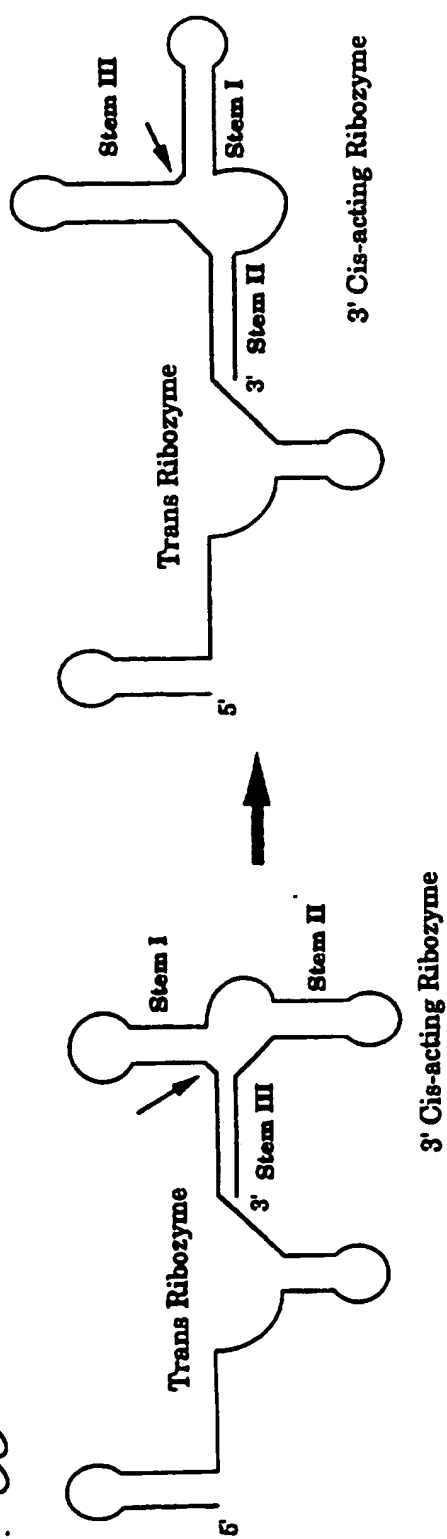
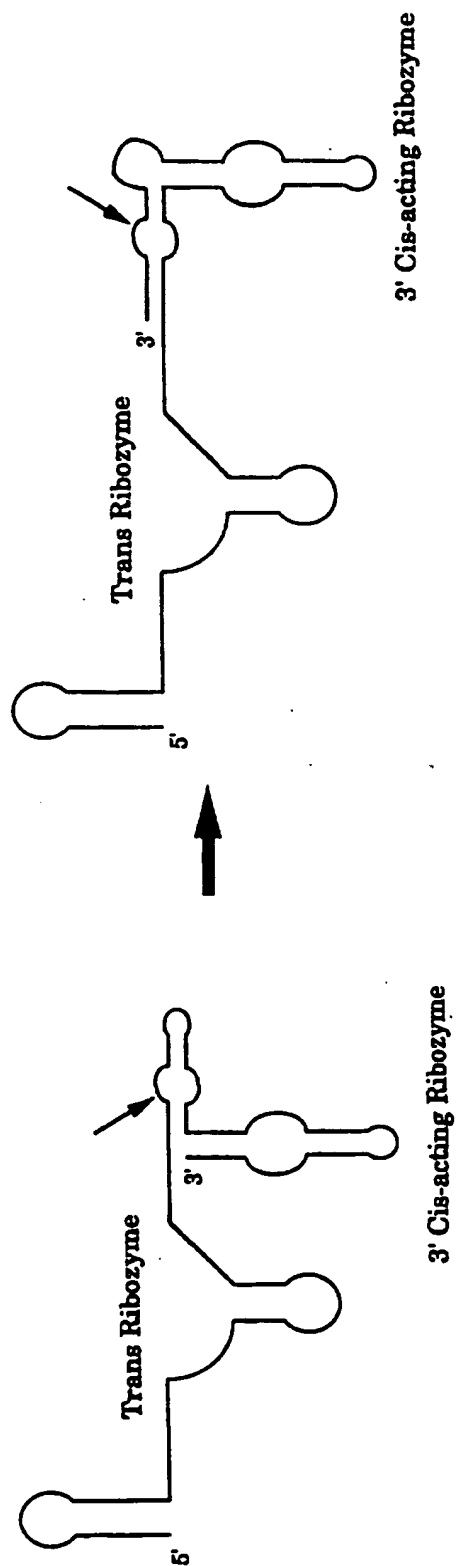
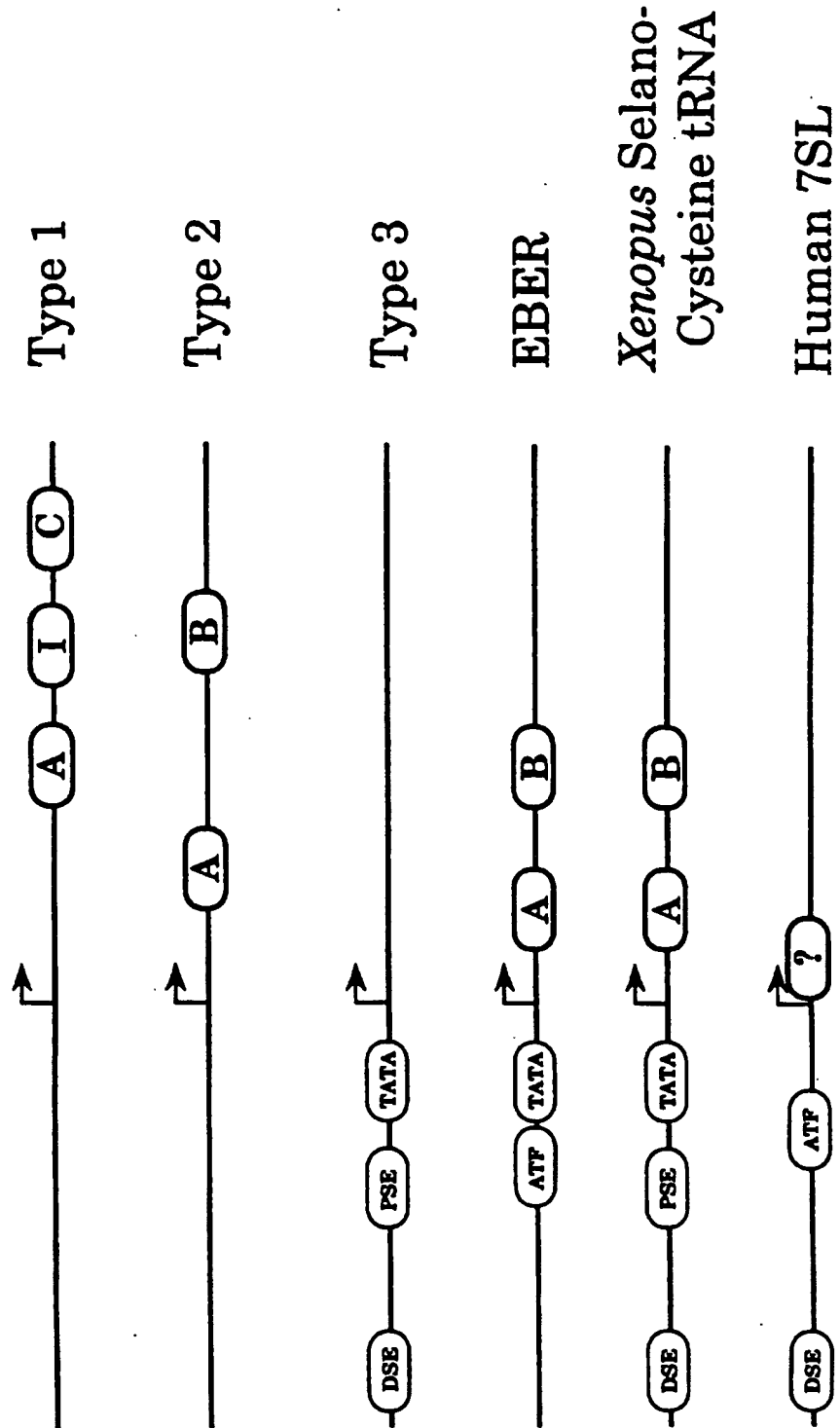


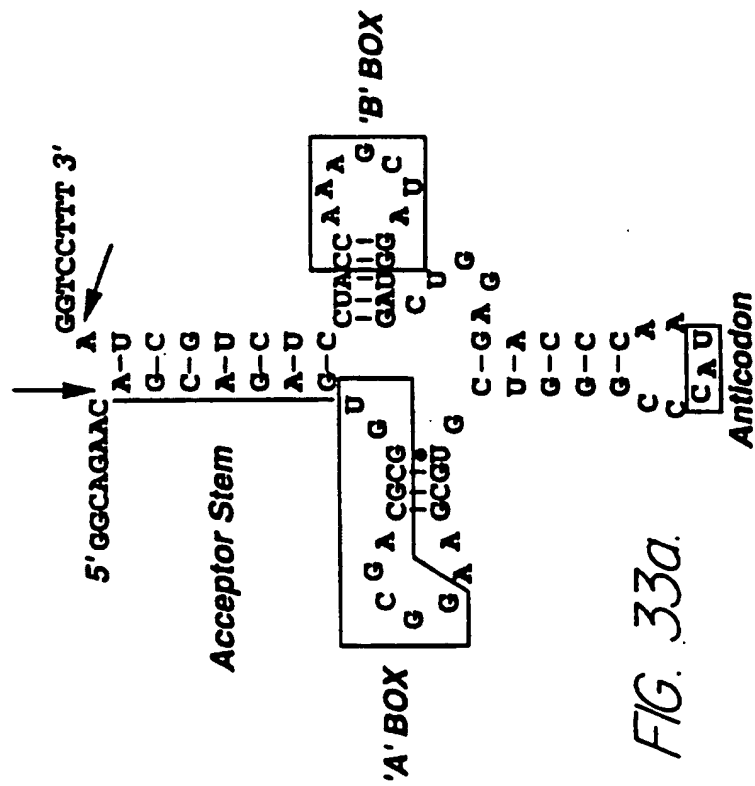
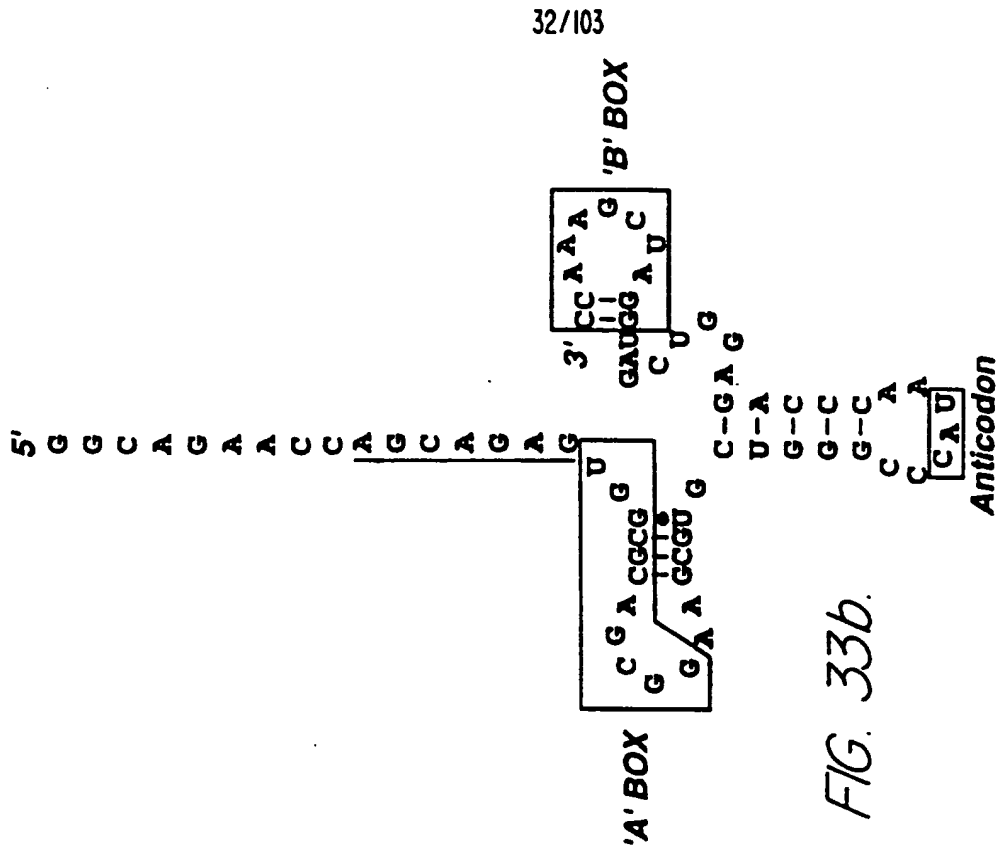
FIG. 31.



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FIG. 32.





met
tRNA_i

Δ 3-5

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FIG. 34a.

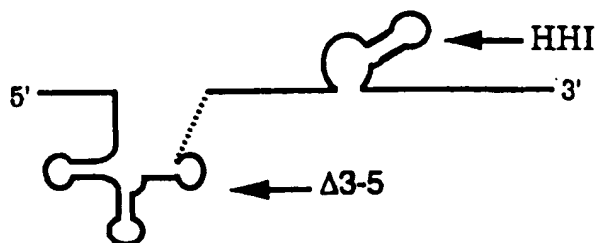
 $\Delta 3-5$ /HHI

FIG. 34b.

S3

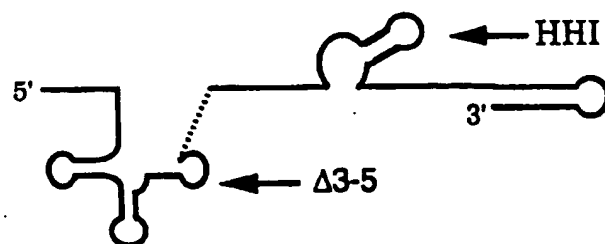


FIG. 34c.

S5

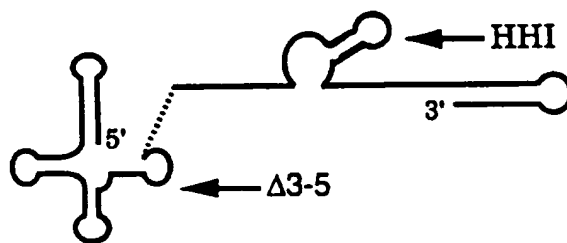


FIG. 34d.

S35

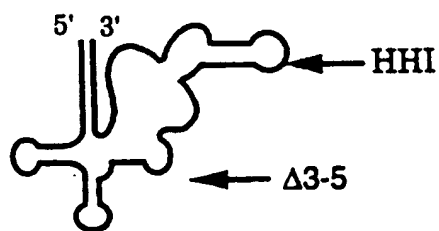
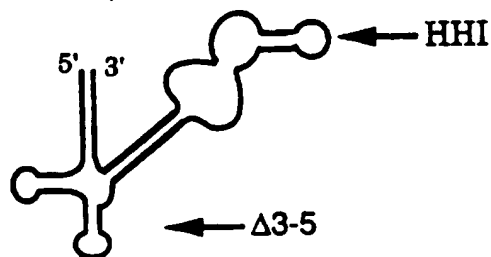


FIG. 34e.

S35Plus



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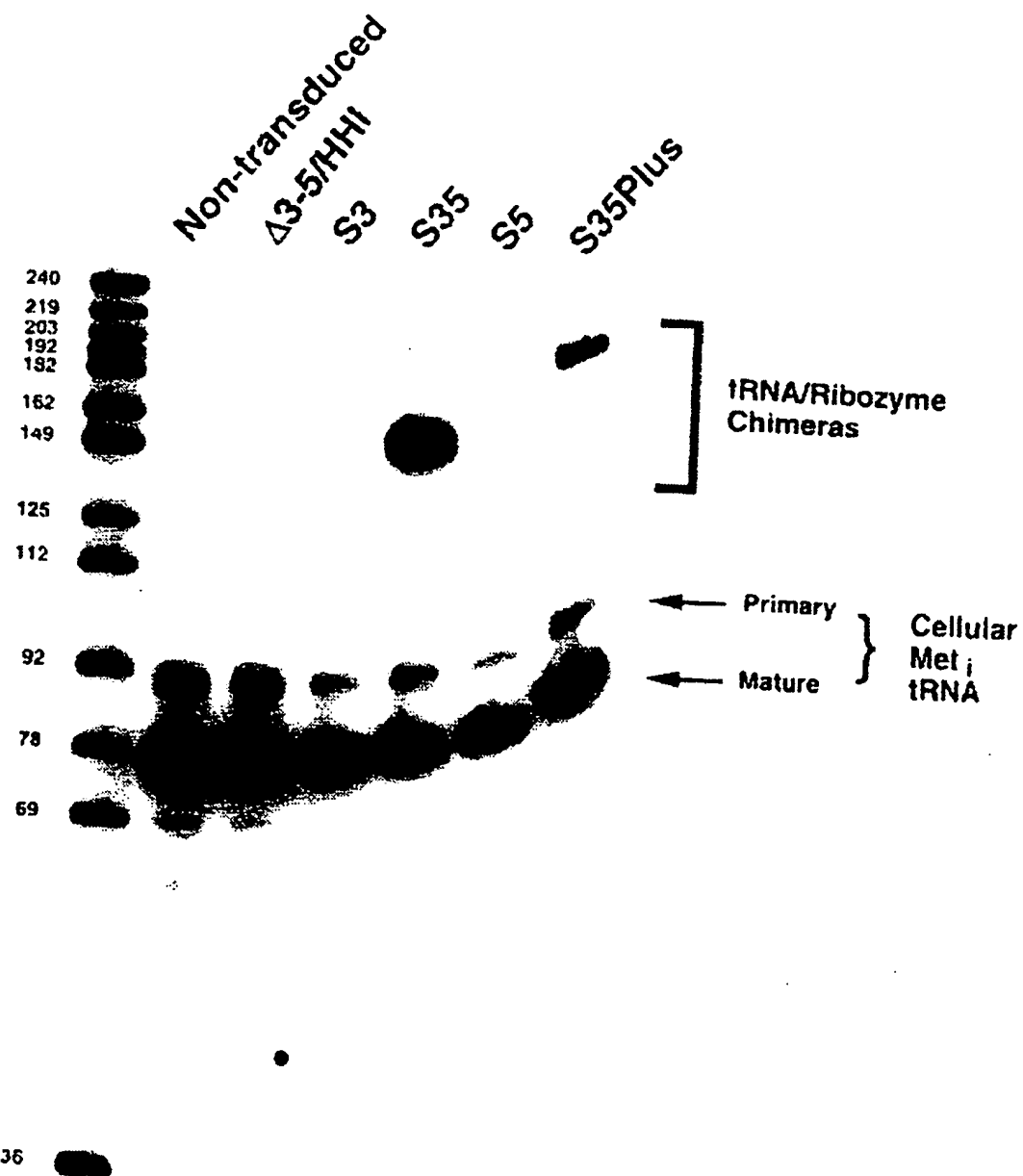


FIG. 35.

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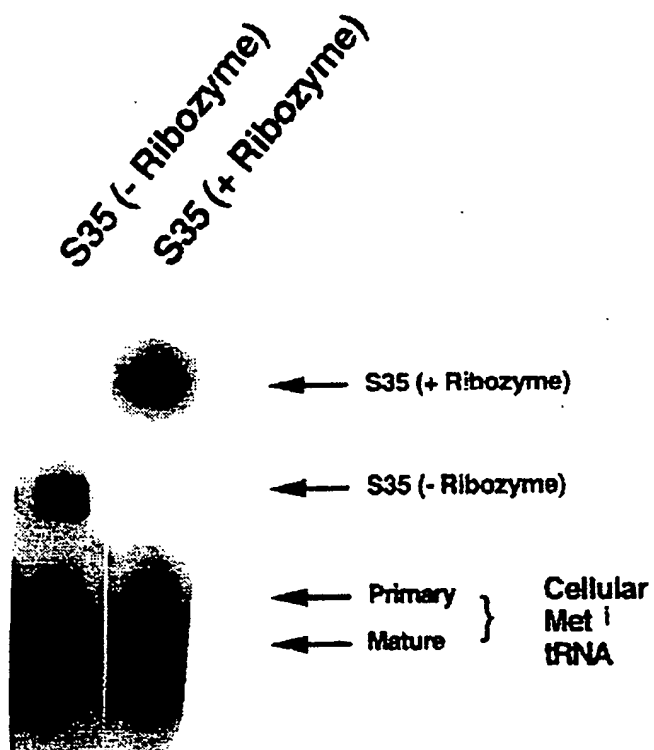


FIG. 36.

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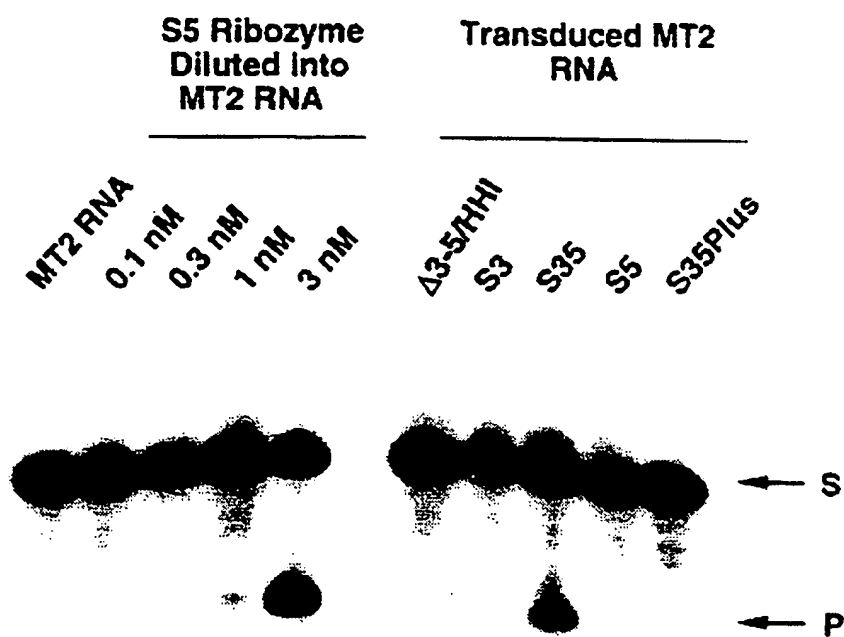
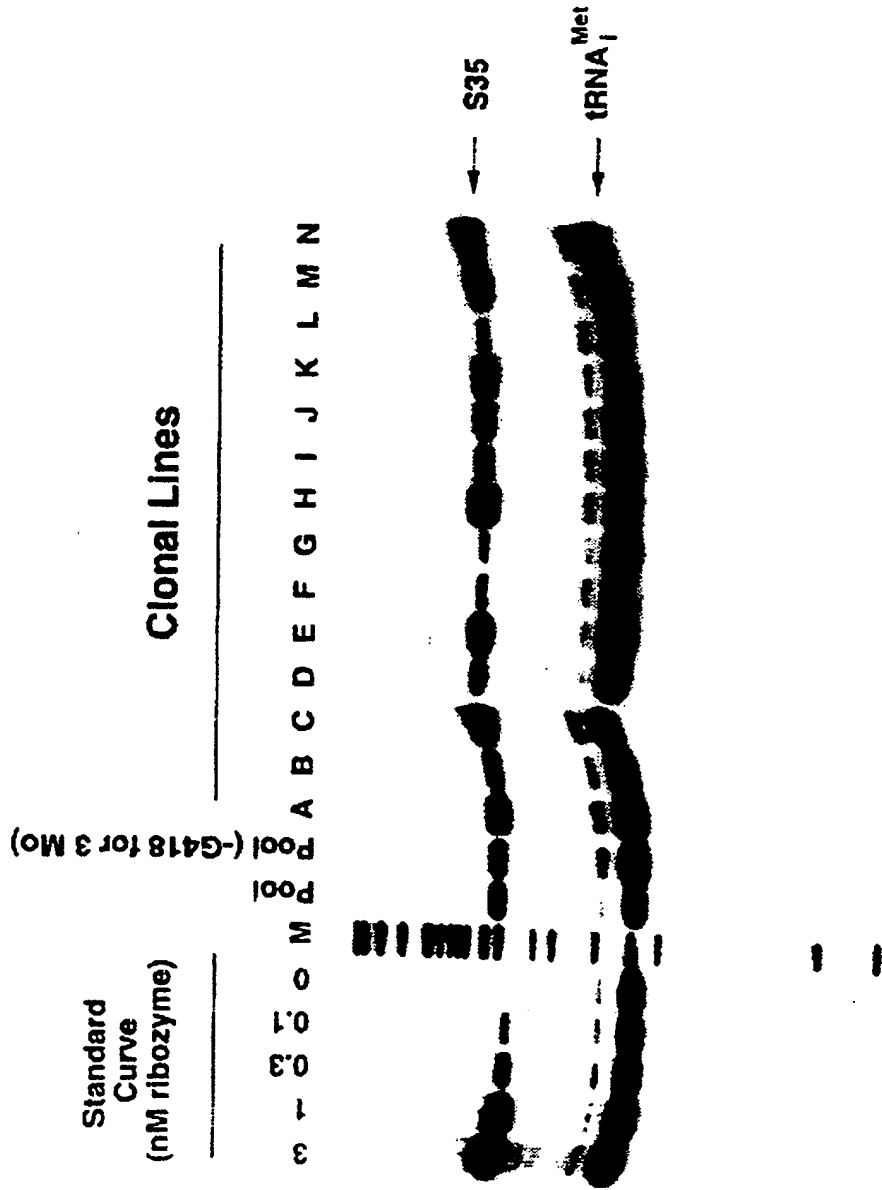


FIG. 37.

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FIG. 38.



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FIG. 39.

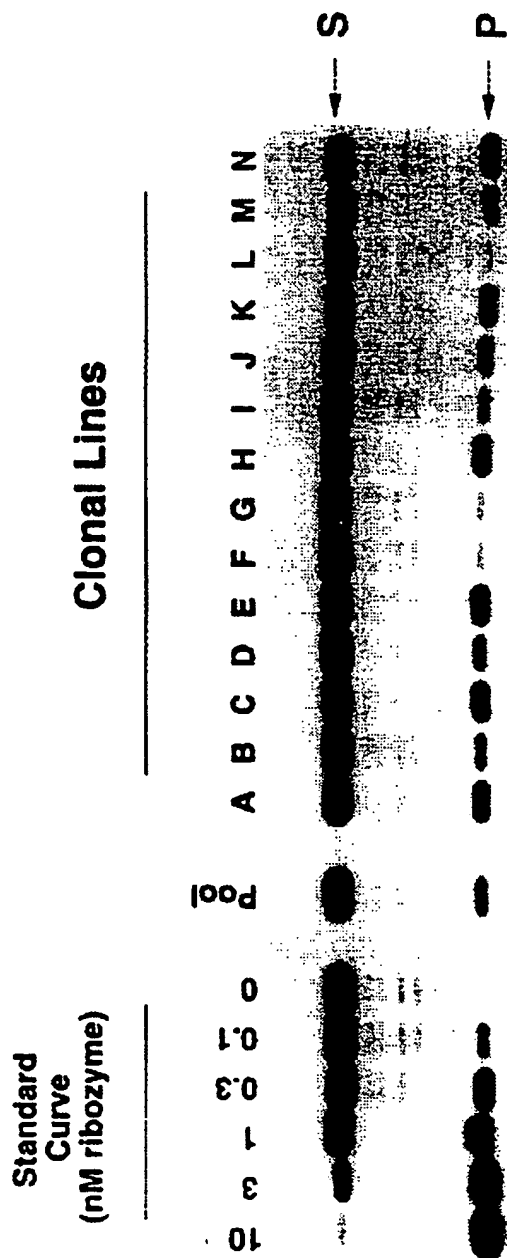




FIG. 40.

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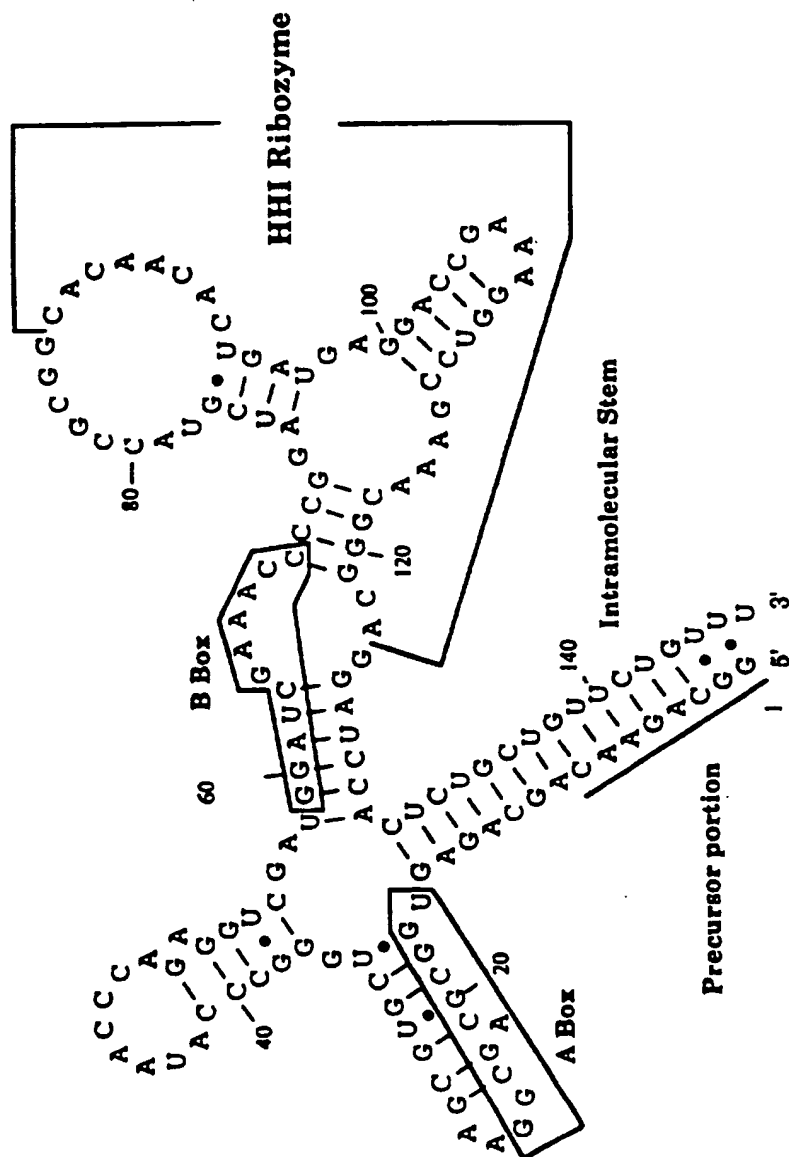


FIG. 41.

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Desired RNA

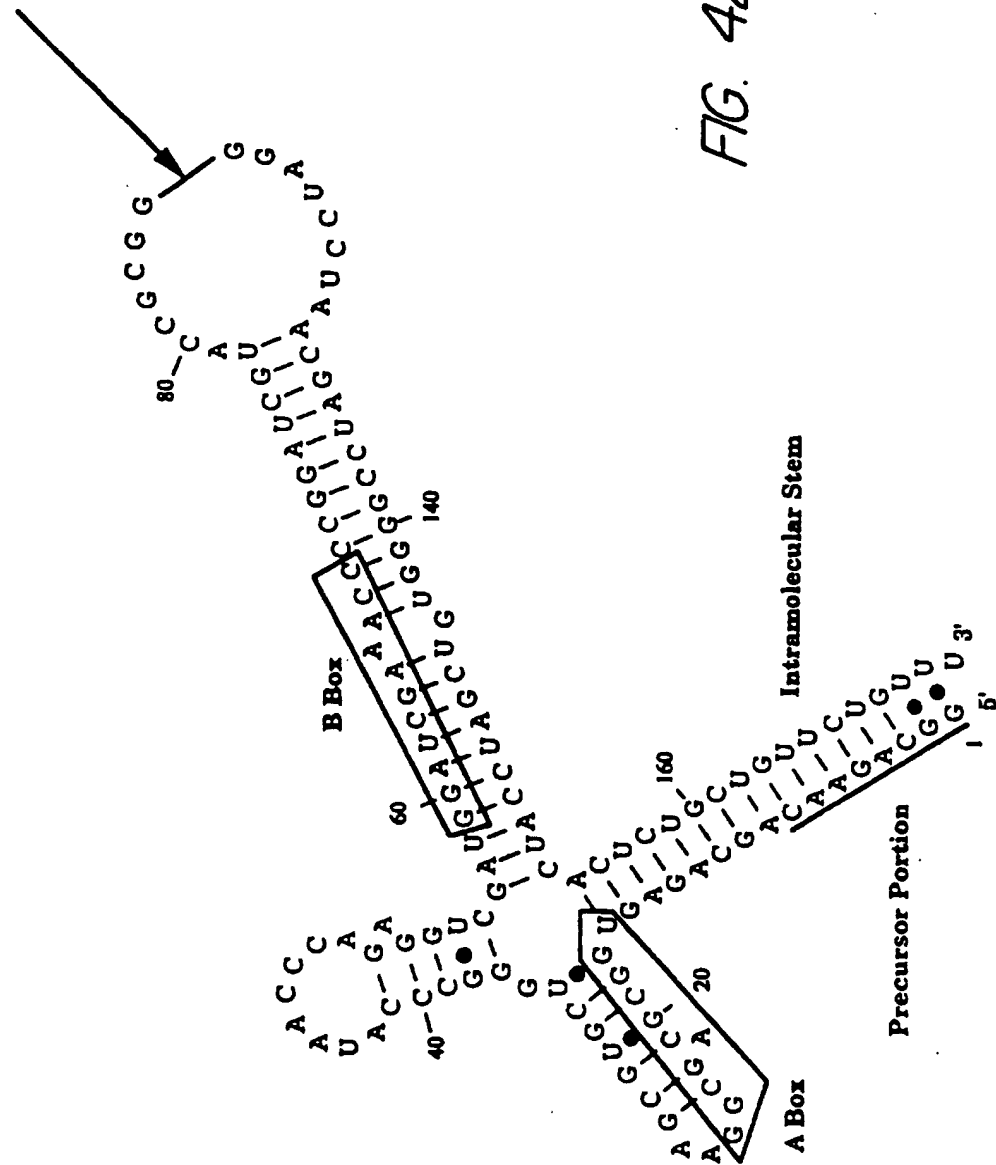


FIG. 42.

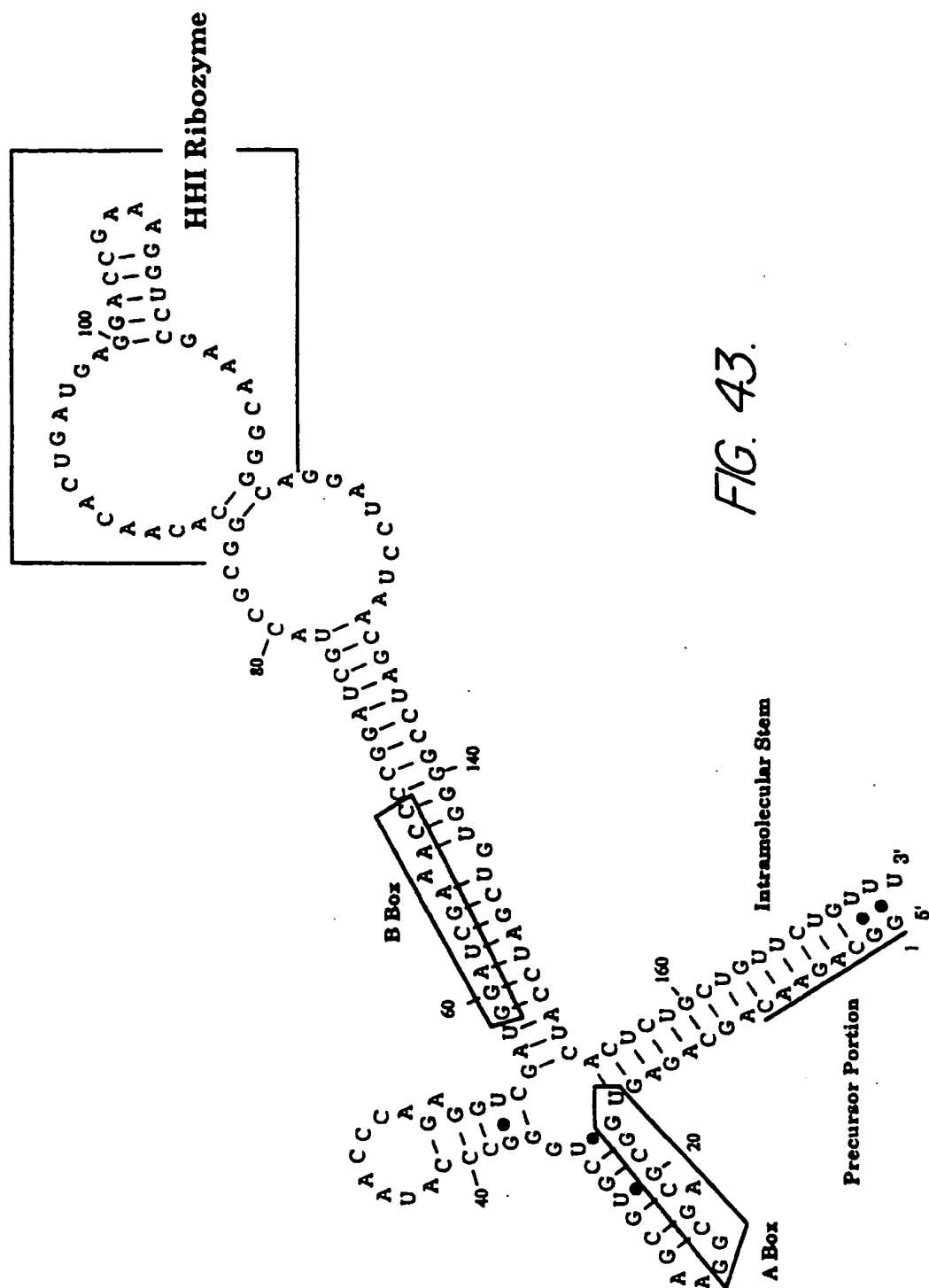


FIG. 43.

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*FIG. 44.***S35 Sequence**

GGCAGAACAG CAGAGUGGCG CAGCGGAAGC GUGCUGGGCC CAUAACCCAG 50
 AGGUCGAUGG AUCGAAACCC CGGAUCGUAC CGCGGUGGAU CCACUCUGCU 100
 GUUCUGUUU 109

*FIG. 45.***HHIS35**

GGCAGAACAG CAGAGUGGCG CAGCGGAAGC GUGCUGGGCC CAUAACCCAG 50
 AGGUCGAUGG AUCGAAACCC CGGAUCGUAC CGCGGCACAA CACUGAUGAG 100
GACCGAAAGG UCCGAAACGG GCAGGAUCCA CUCUGCUGUU CUGUUU 146

Underlined bases indicate the HHI ribozyme sequence

*FIG. 46.***S35 Plus Sequence**

GGCAGAACAG CAGAGUGGCG CAGCGGAAGC GUGCUGGGCC CAUAACCCAG 50
 AGGUCGAUGG AUCGAAACCC CGGAUCGUAC CGCGGGGAUC CUAACGAUCC 100
 GGGGUGUCGA UCCAUCACUC UGCUGUUCUG UU U 133

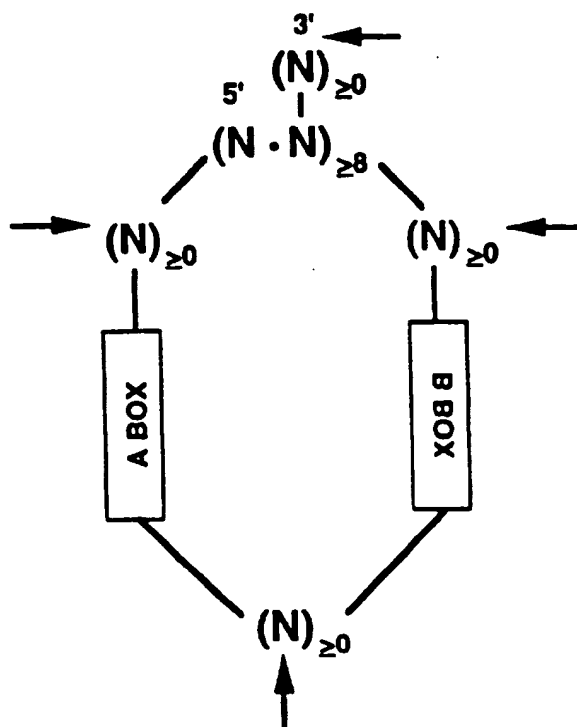
*FIG. 47.***HHIS35 Plus**

GGCAGAACAG CAGAGUGGCG CAGCGGAAGC GUGCUGGGCC CAUAACCCAG 50
 AGGUCGAUGG AUCGAAACCC CGGAUCGUAC CGCGGCACAA CACUGAUGAG 100
GACCGAAAGG UCCGAAACGG GCAGGAUCCU AACGAUCCGG GGUGUCGAUC 150
 CAUCACUCUG CUGUUCUGUU U 171

Underlined bases indicate the HHI ribozyme sequence
 SUBSTITUTE SHEET (RULE 26)

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FIG. 48.



A BOX = URGNNAGYGG

B BOX = GGUUCGANUCC

This is based on Geiduschek & Tocchini-Valentini, (1988) Annu. Review Biochem. 57, 873-914. However this consensus sequence is not meant to be limiting

N = A, U, G, or C

R = Purine

Y = Pyrimidine

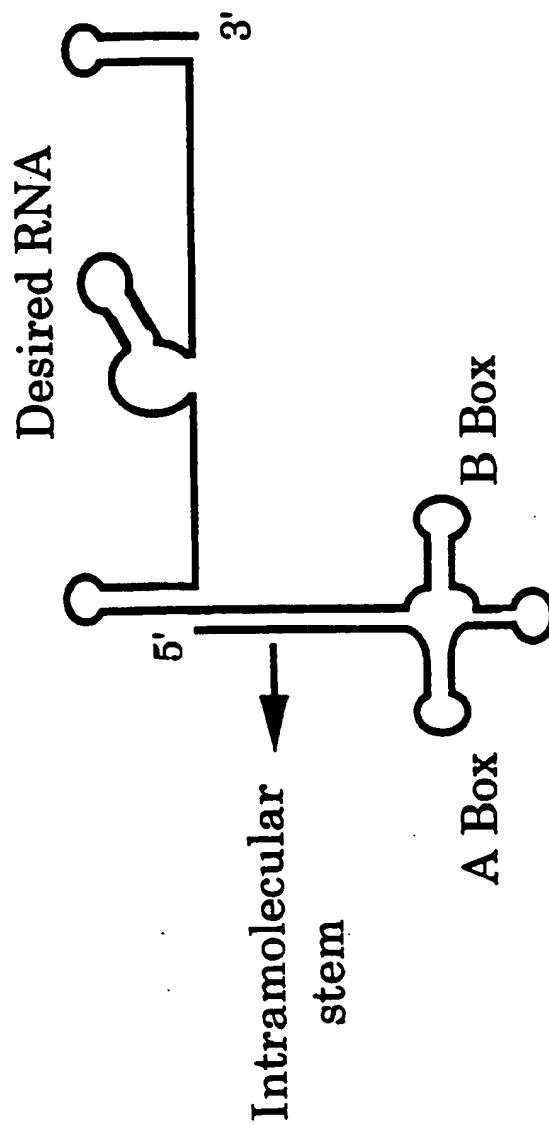
• = Indicates base-pairing

— = Indicates covalent linkage

➔ = Indicates sites at which desired RNAs can be cloned

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FIG. 49.



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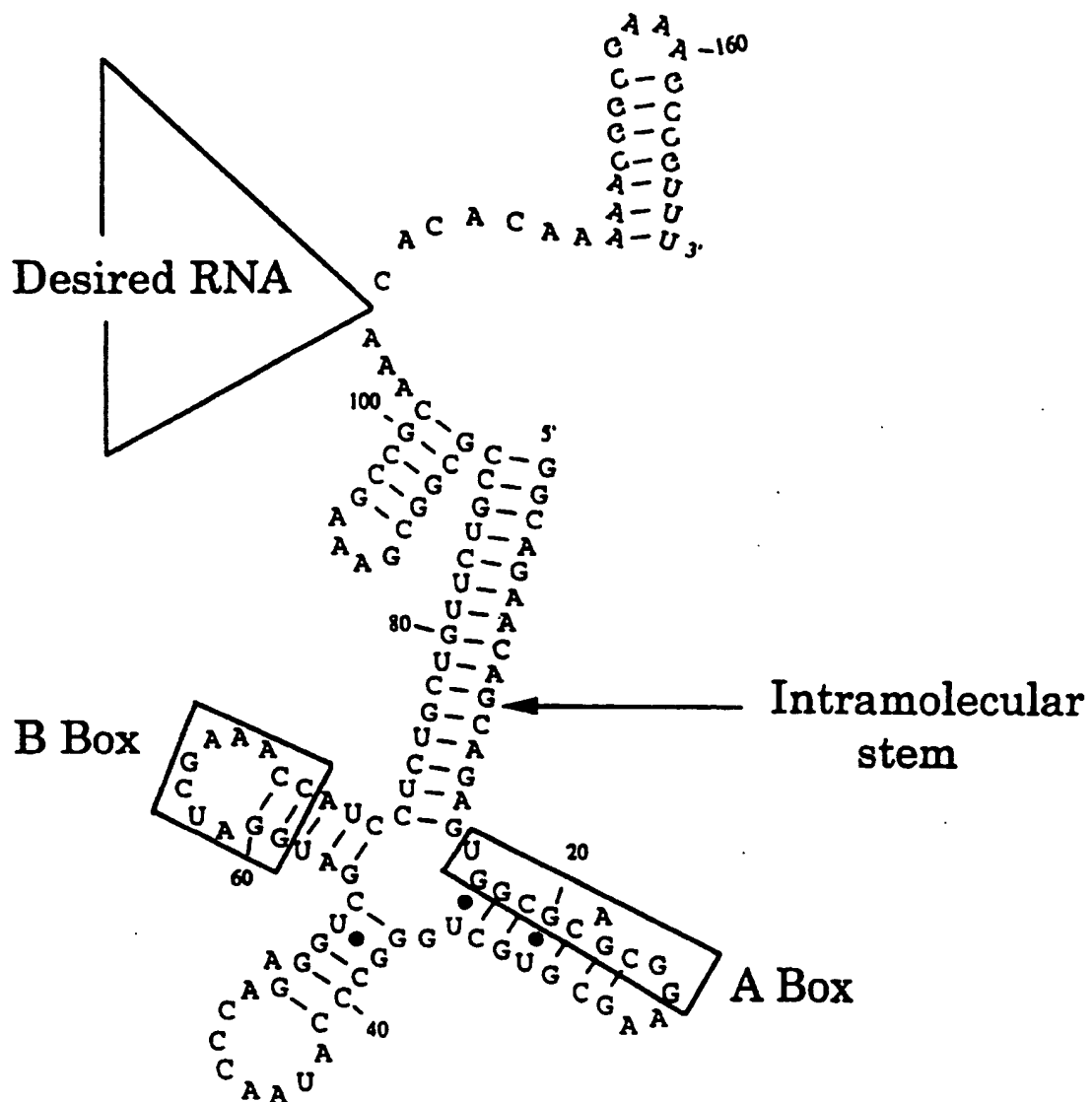


FIG. 50.

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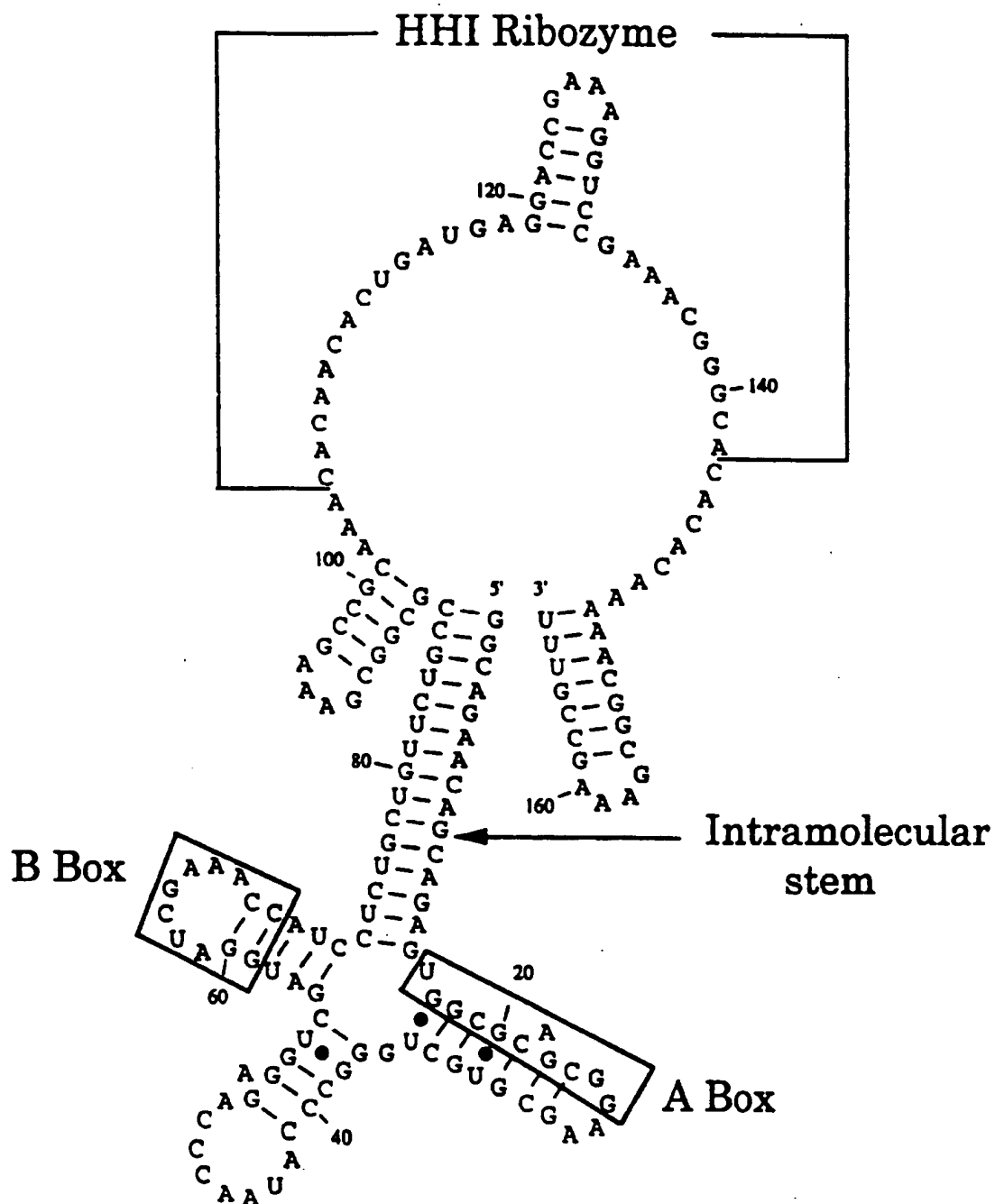


FIG. 52a.

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A: TRZ-A

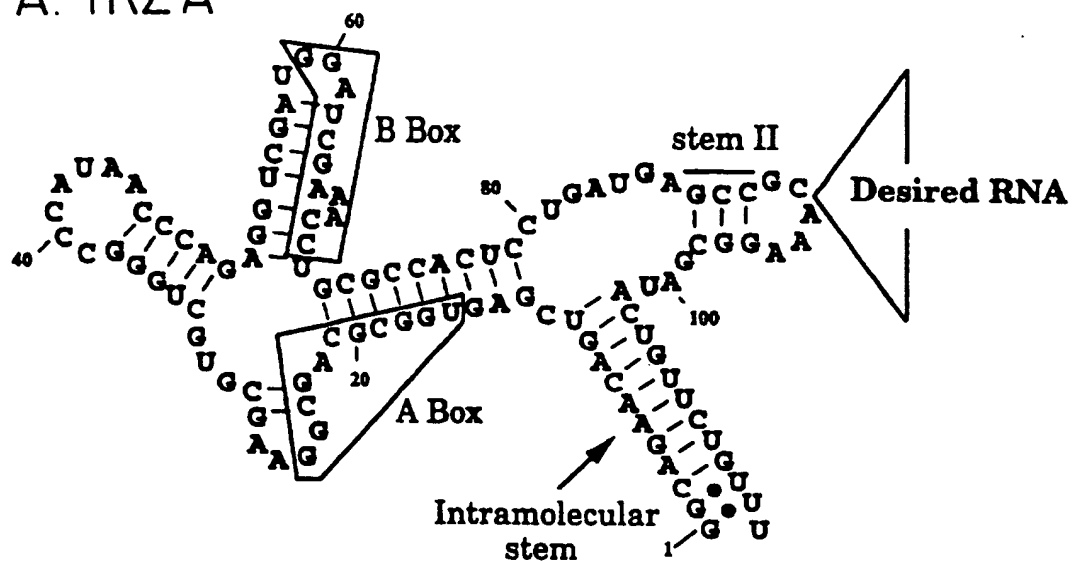
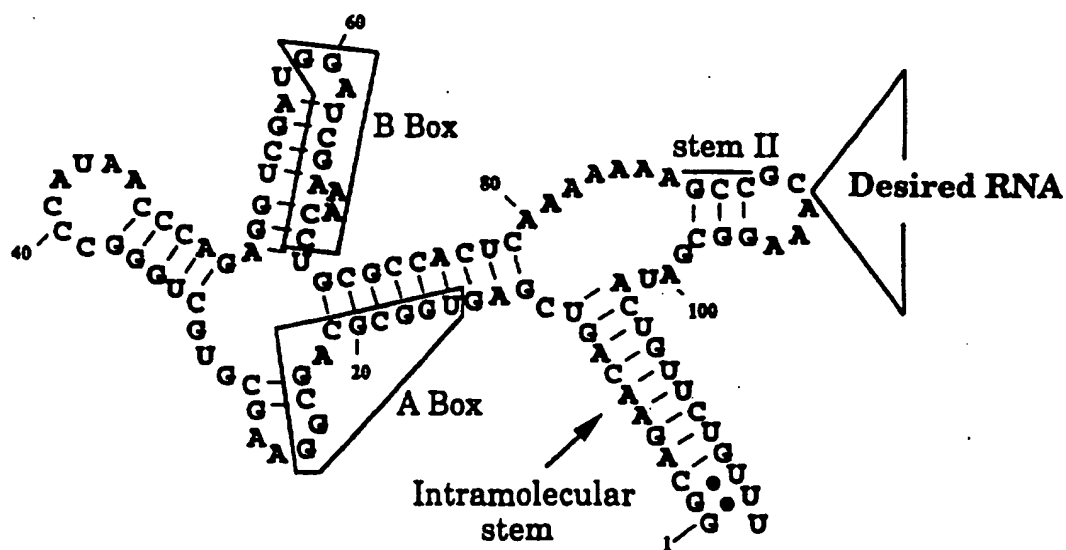
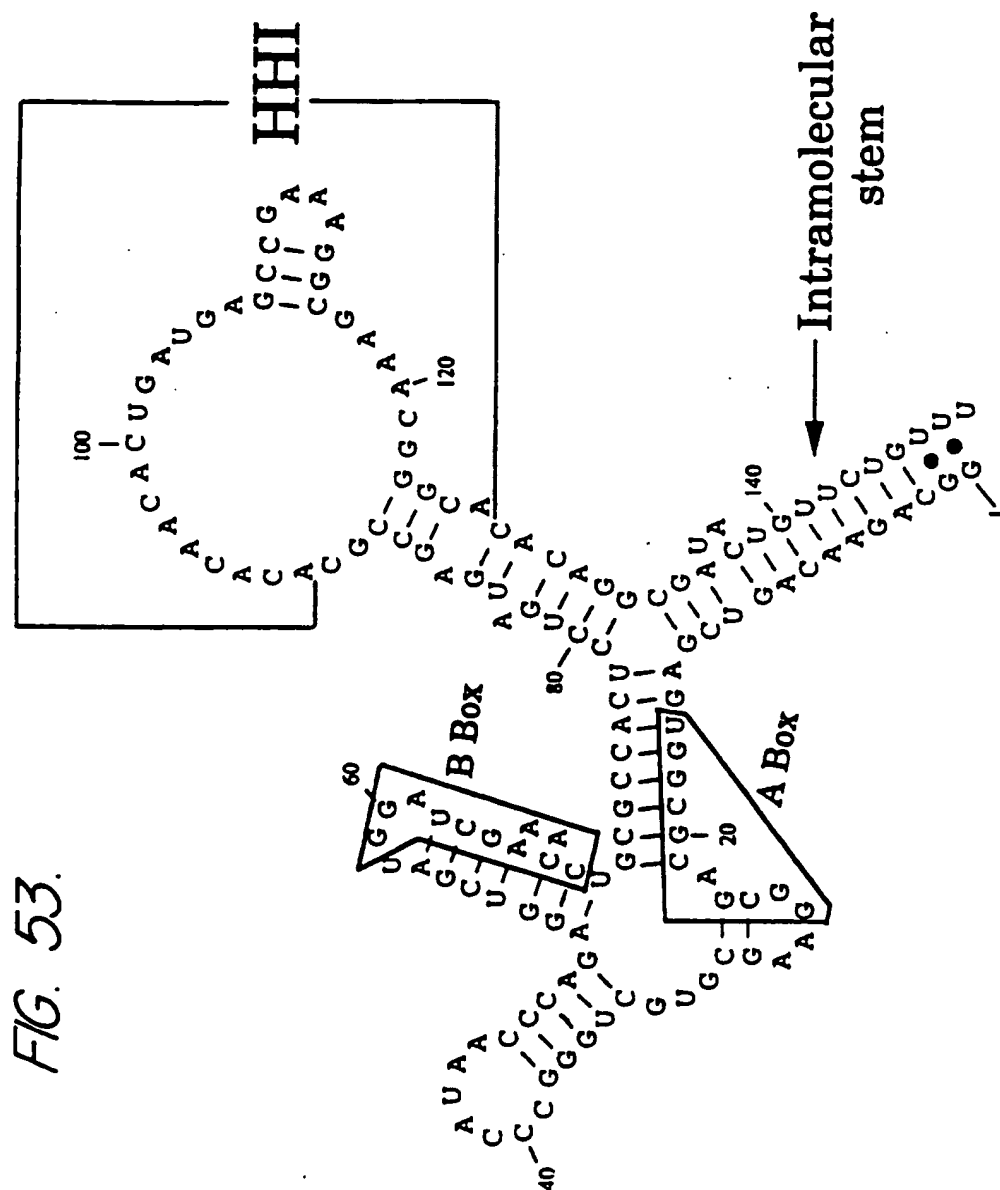


FIG. 52b.

B: TRZ-B





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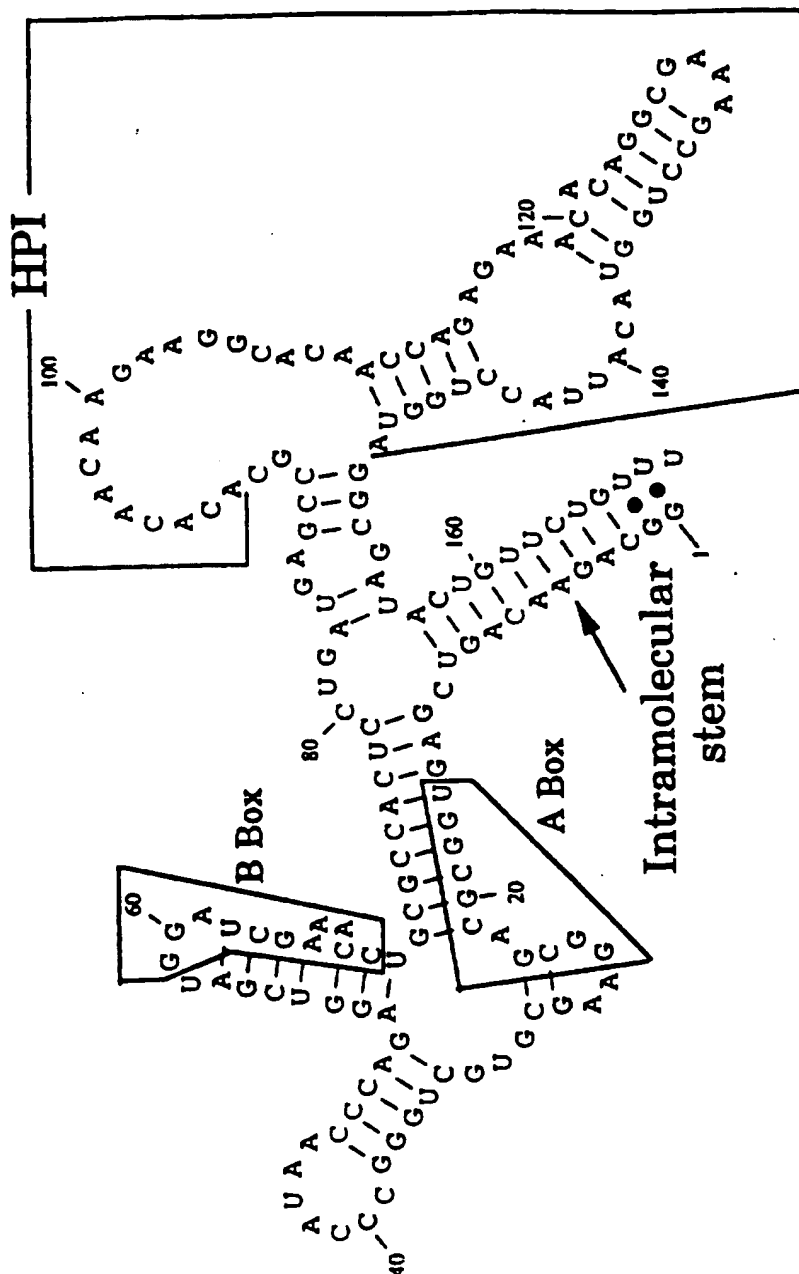


FIG. 54.

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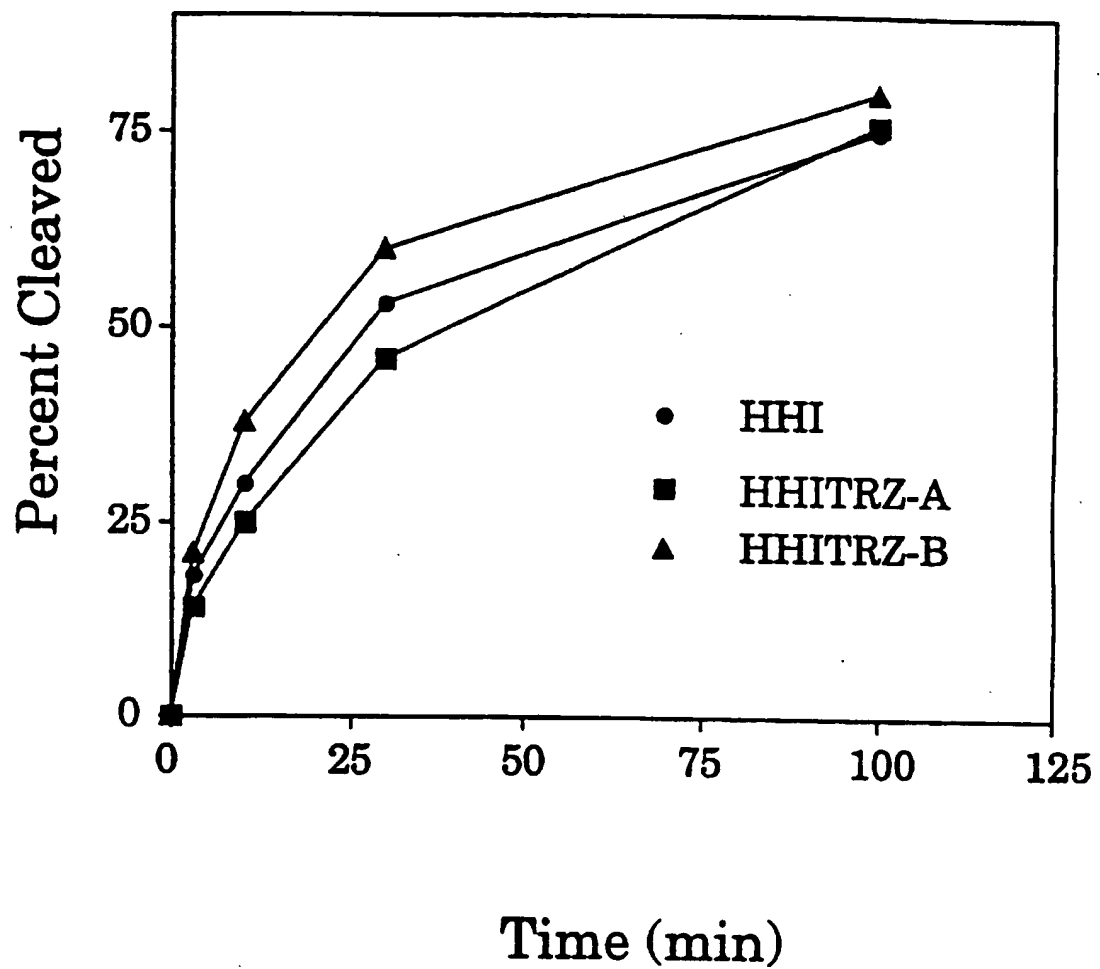


FIG. 55.

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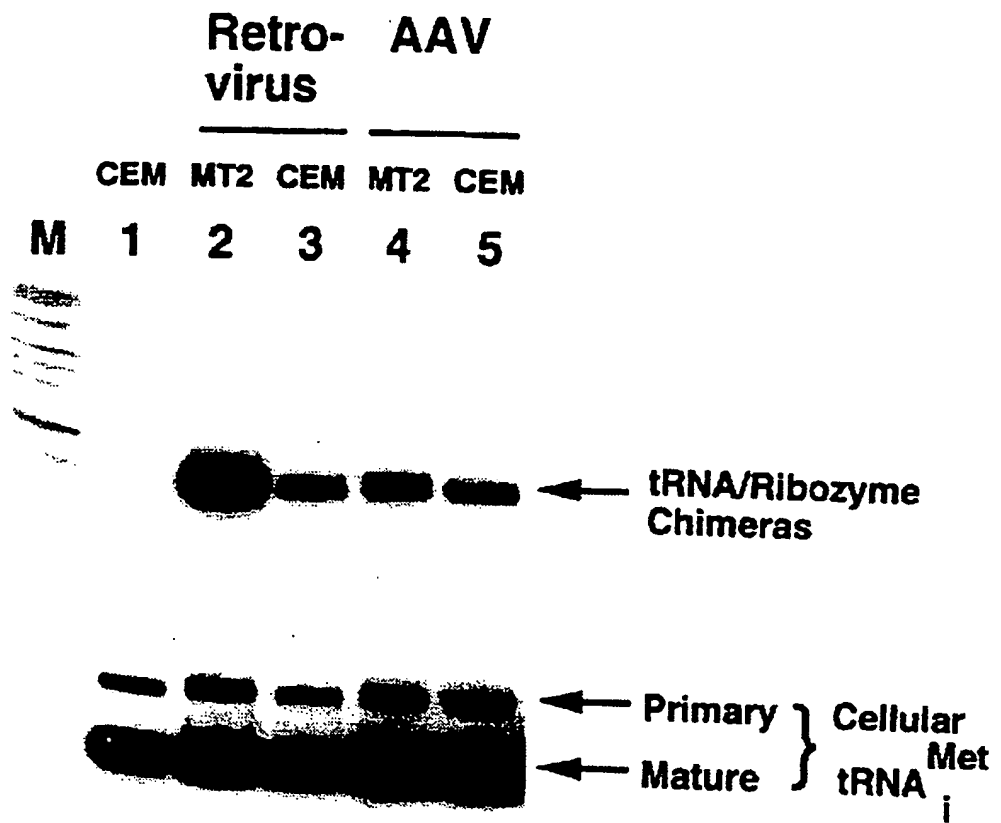


FIG. 56.

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FIG. 57a.

AAV Vector

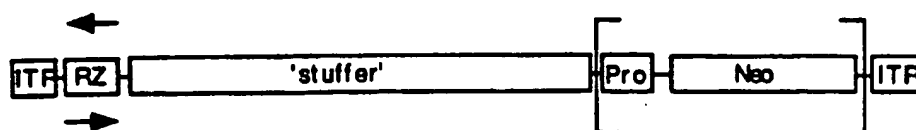
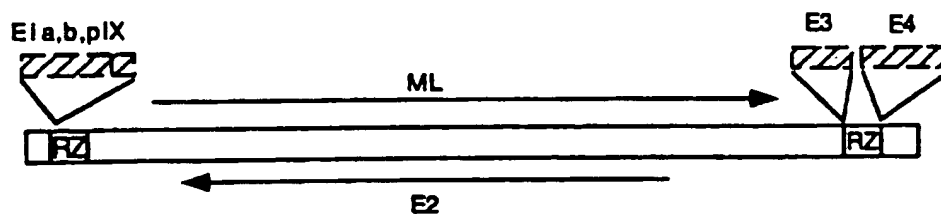


FIG. 57b.

Adenovirus Vector



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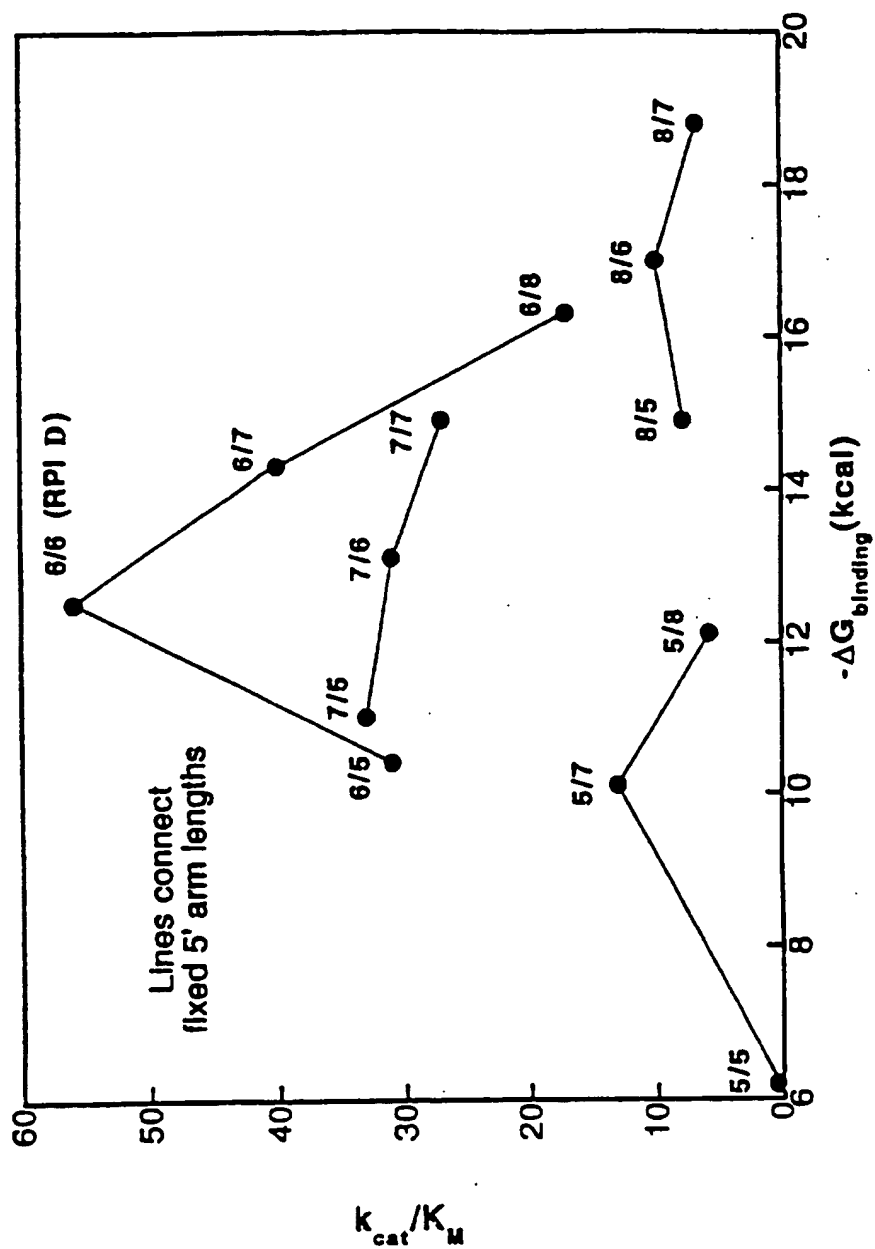
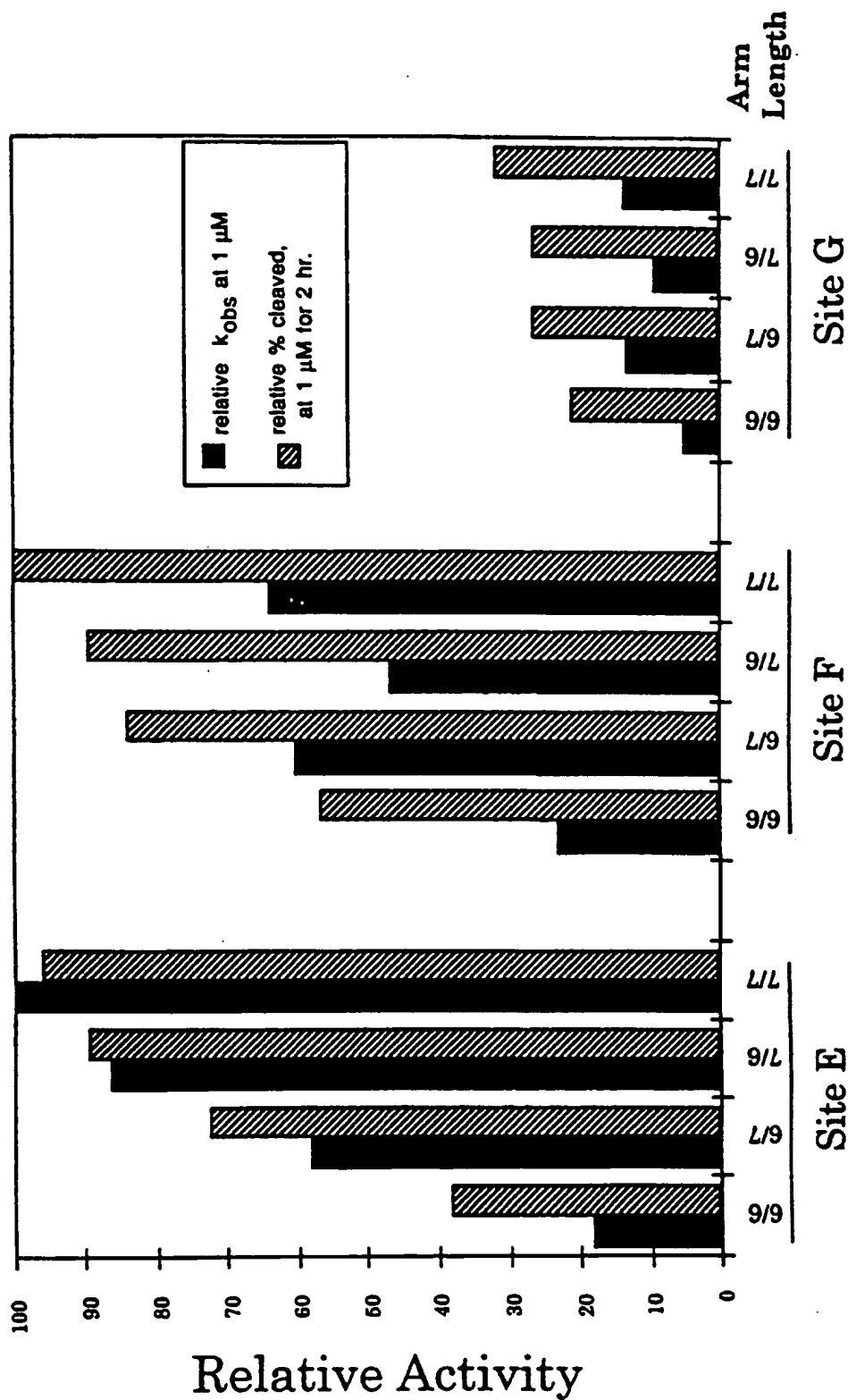


FIG. 58.

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Ribozyme

FIG. 59.

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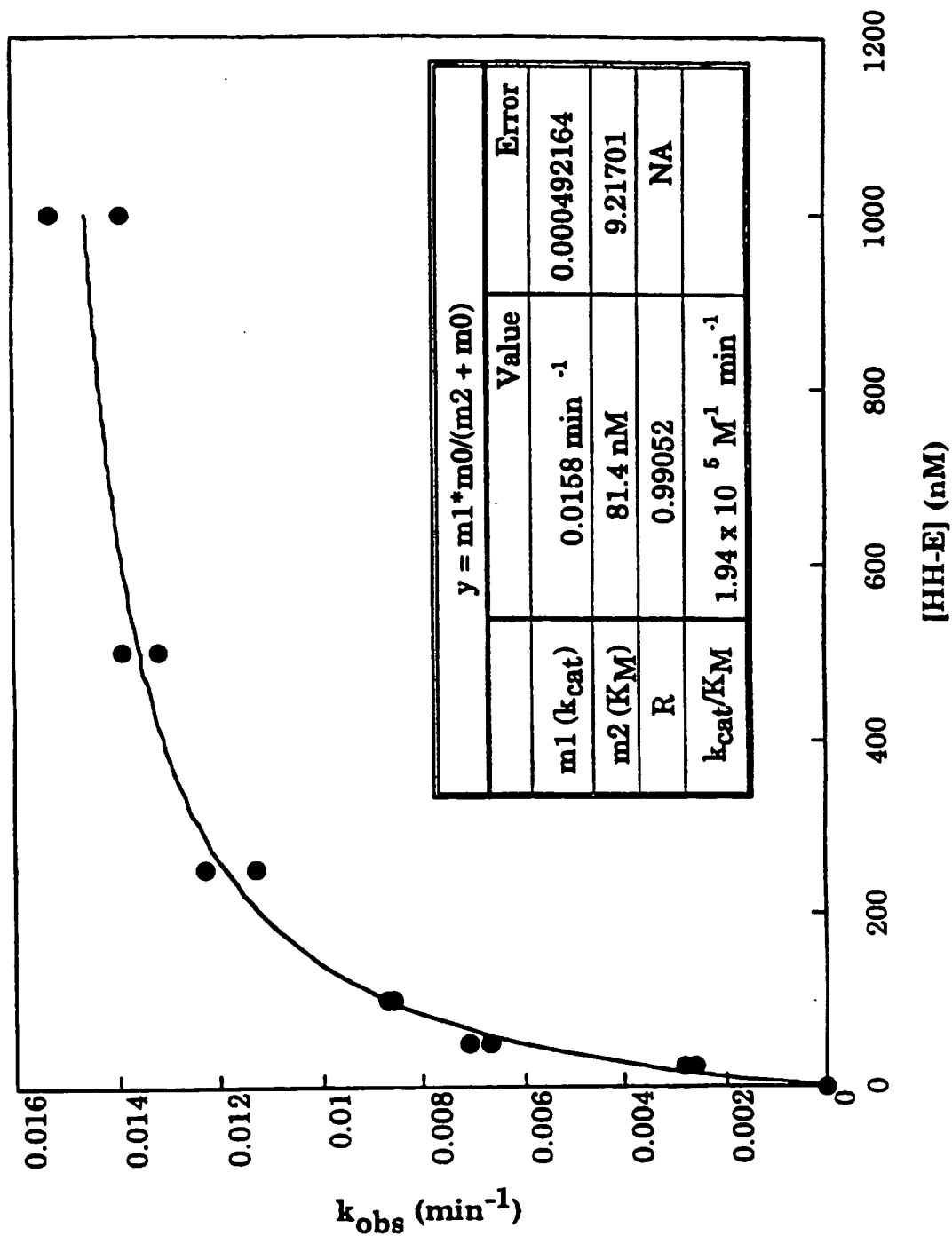
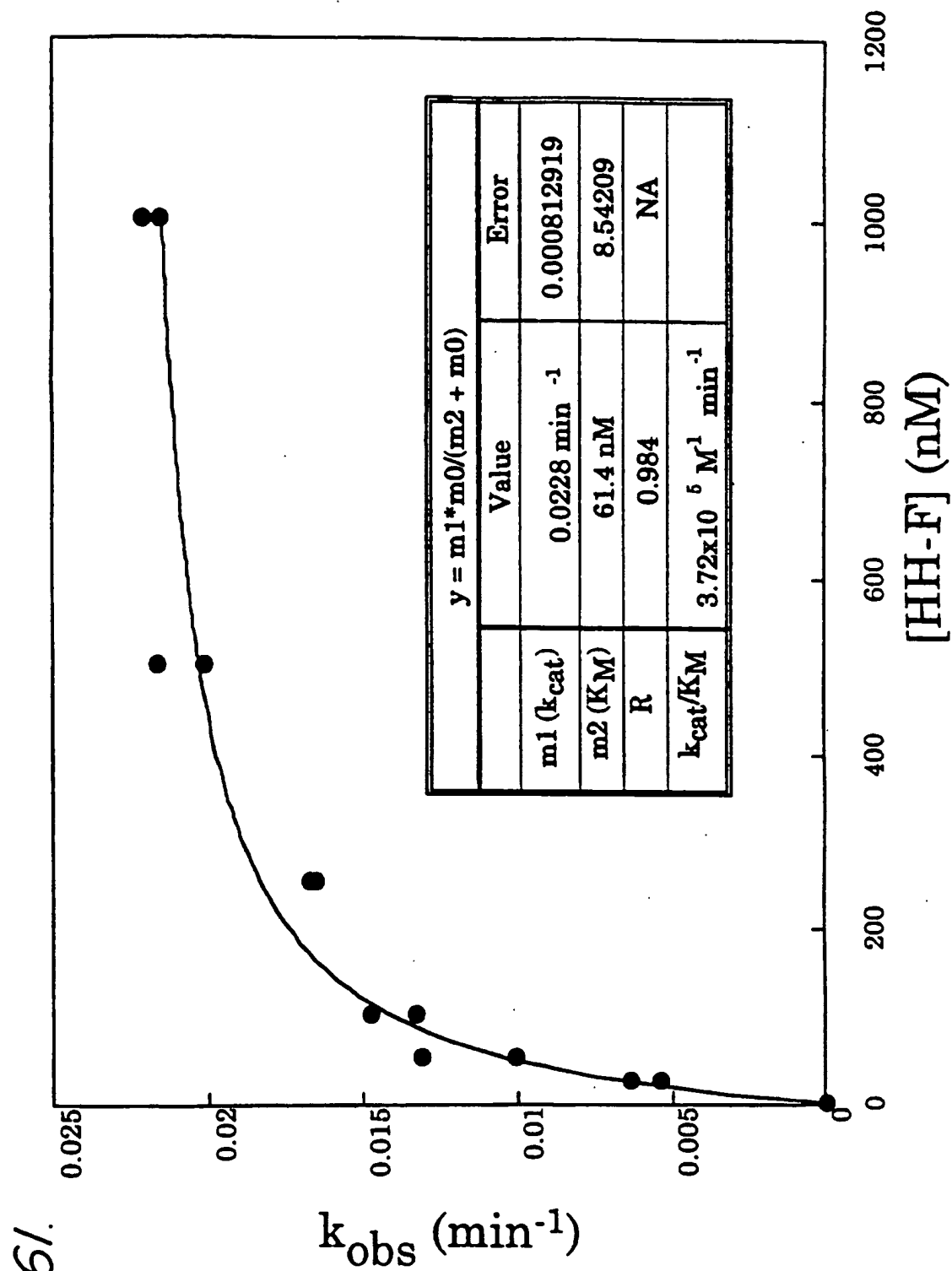


FIG. 60.

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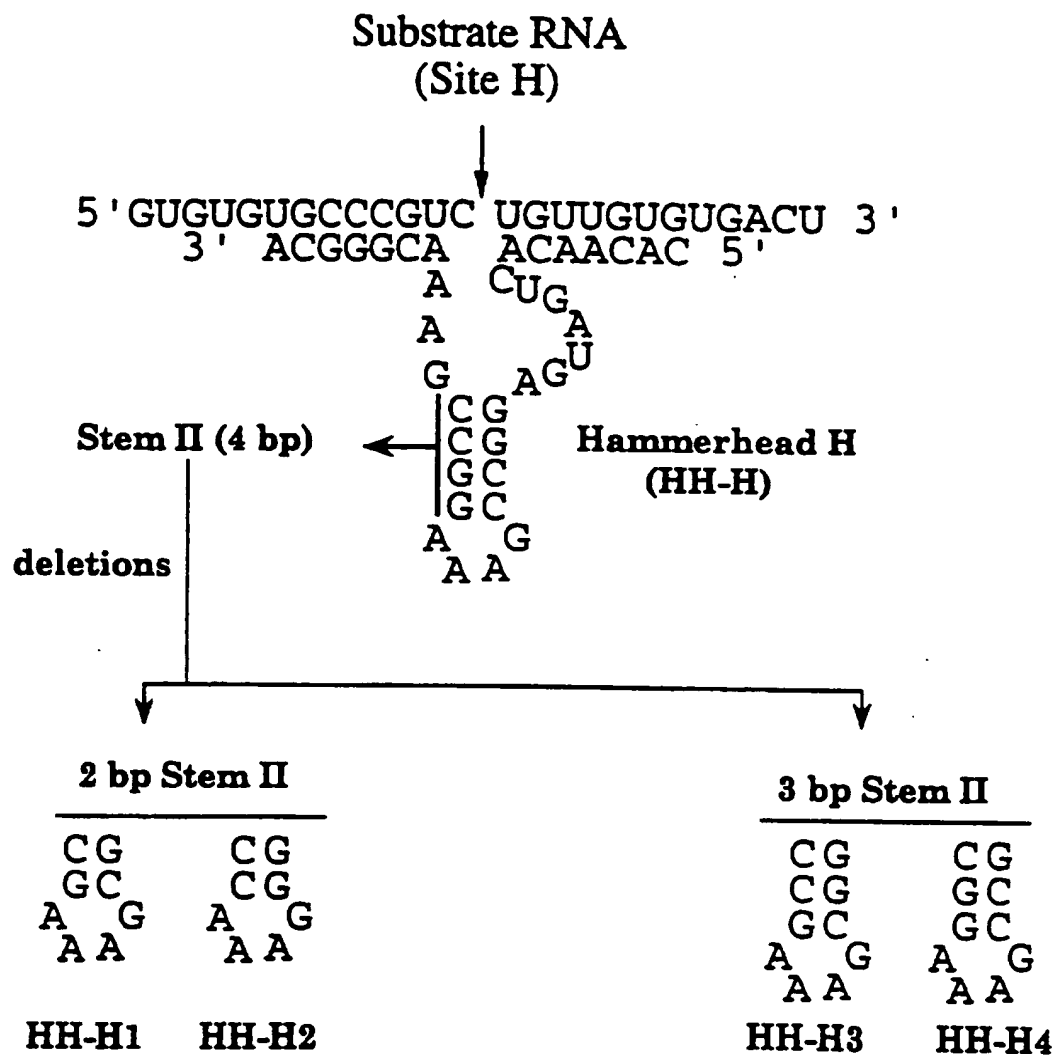


FIG. 62.

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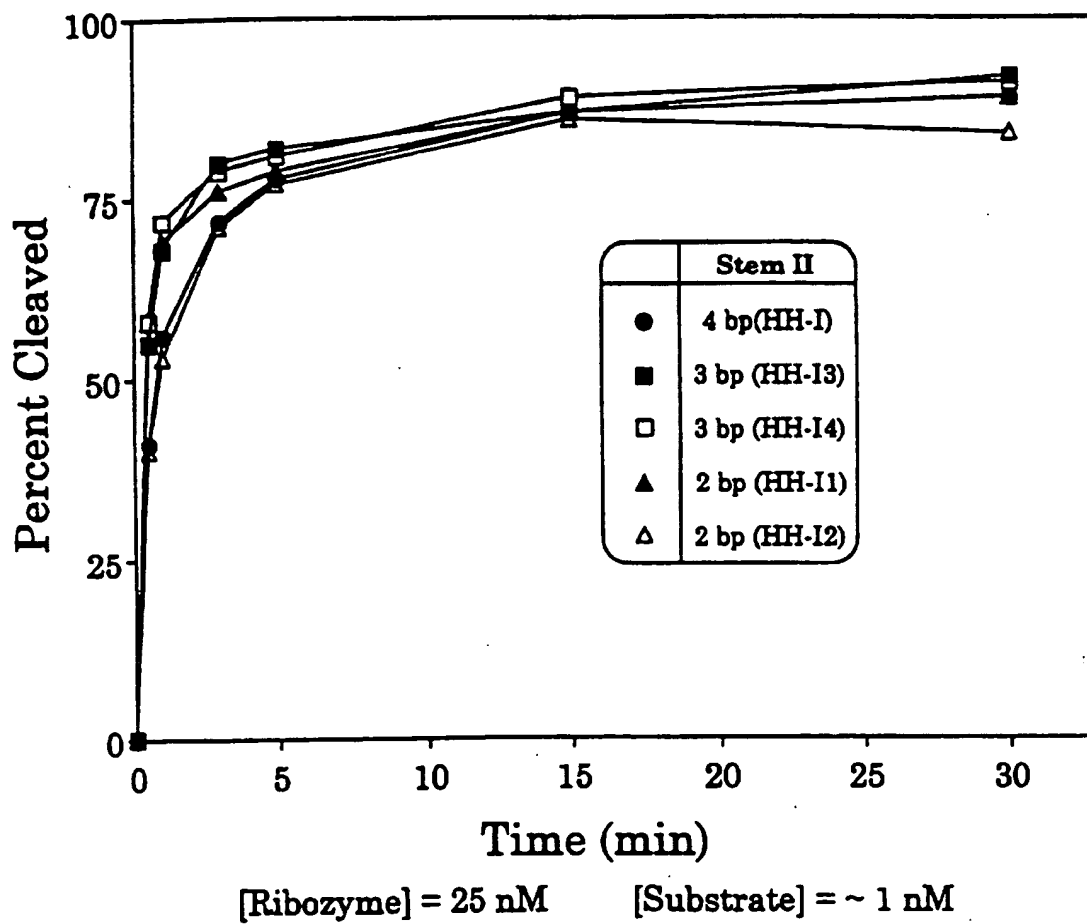


FIG. 63.

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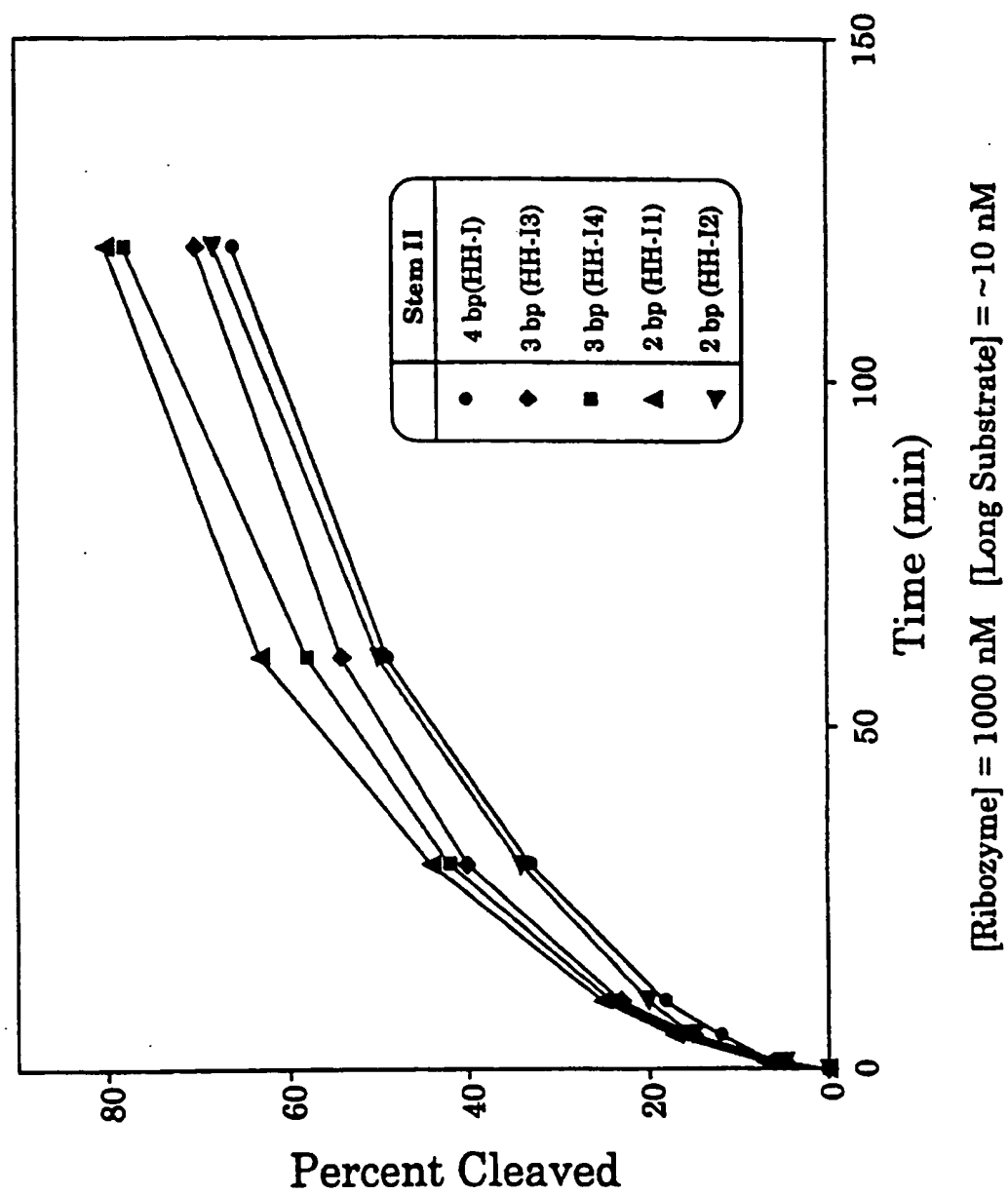
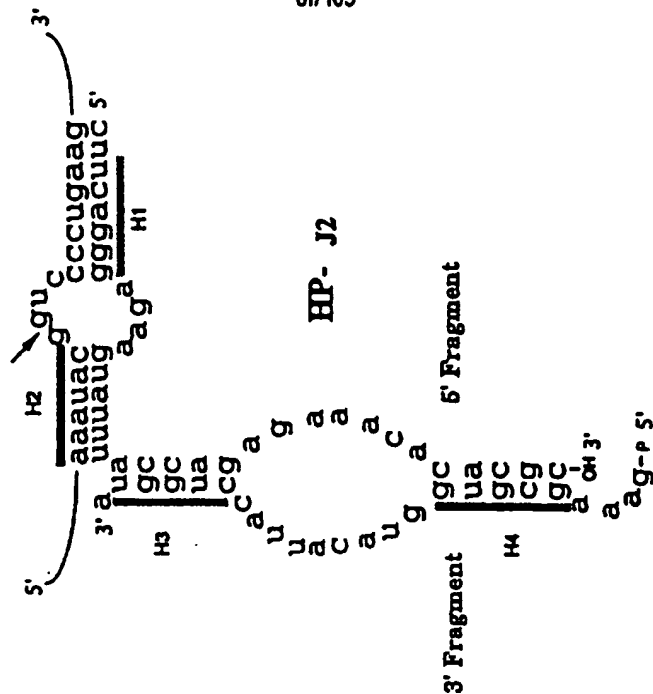


FIG. 65b.

Substrate RNA (site J)



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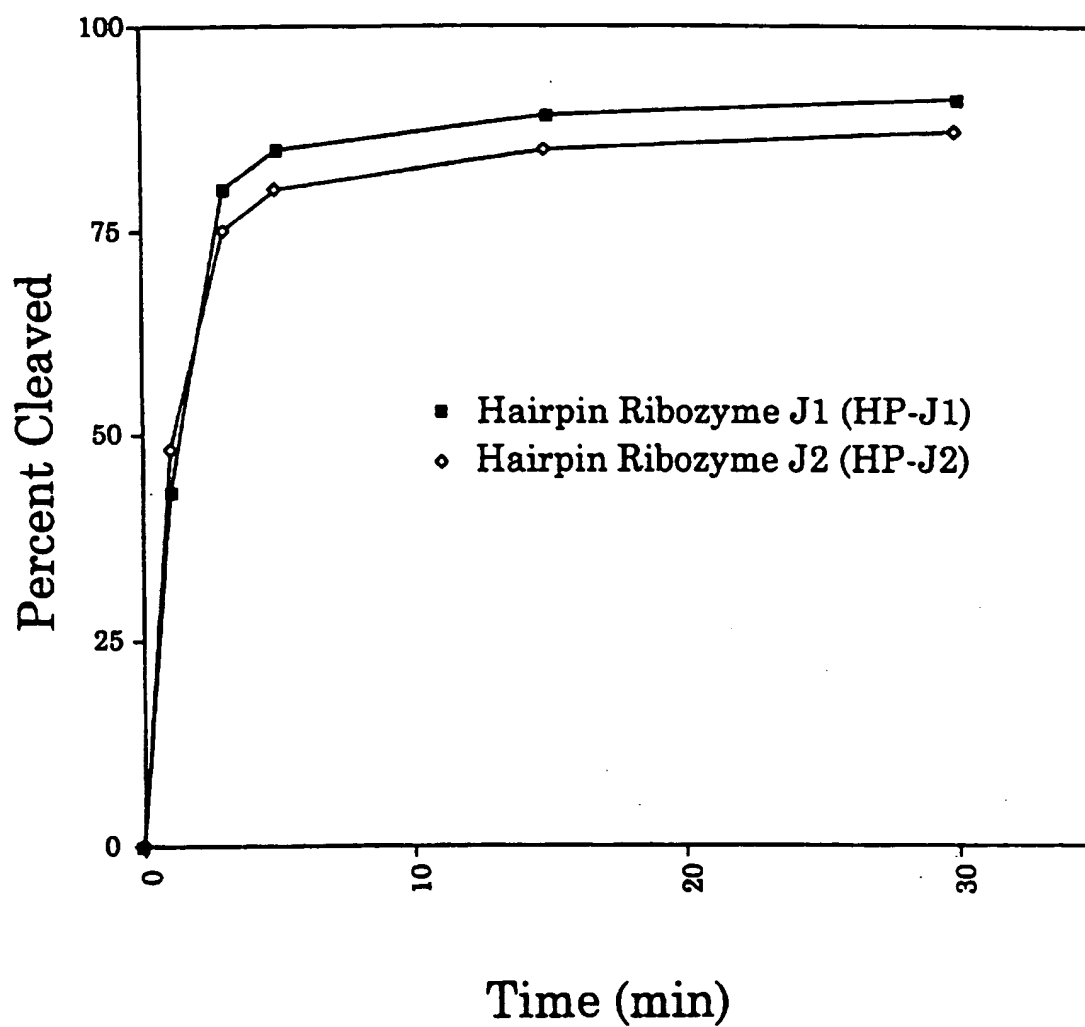


FIG. 66.

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FIG. 67b.

Substrate RNA

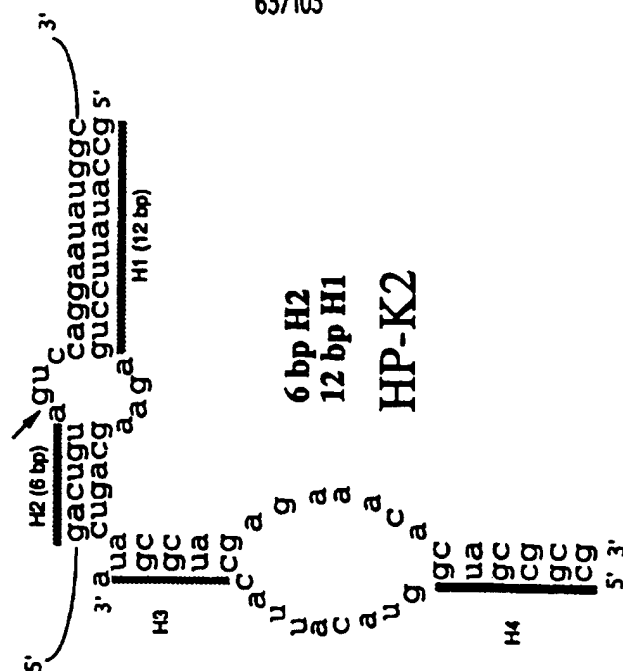
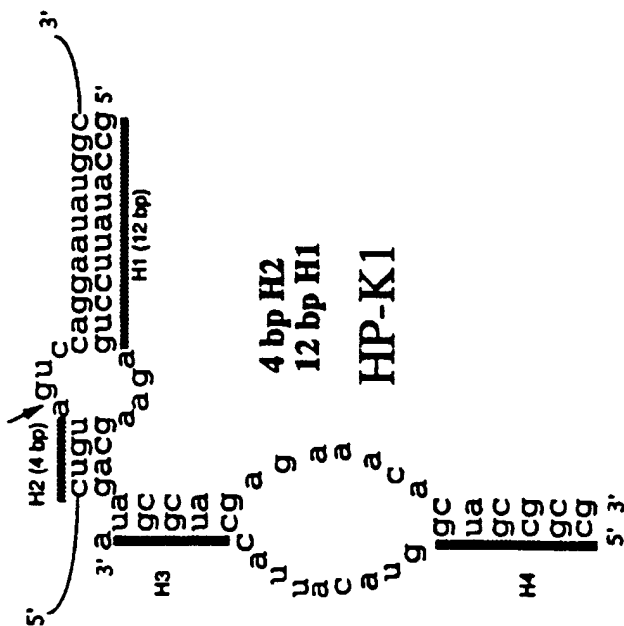


FIG. 67a.

Substrate RNA



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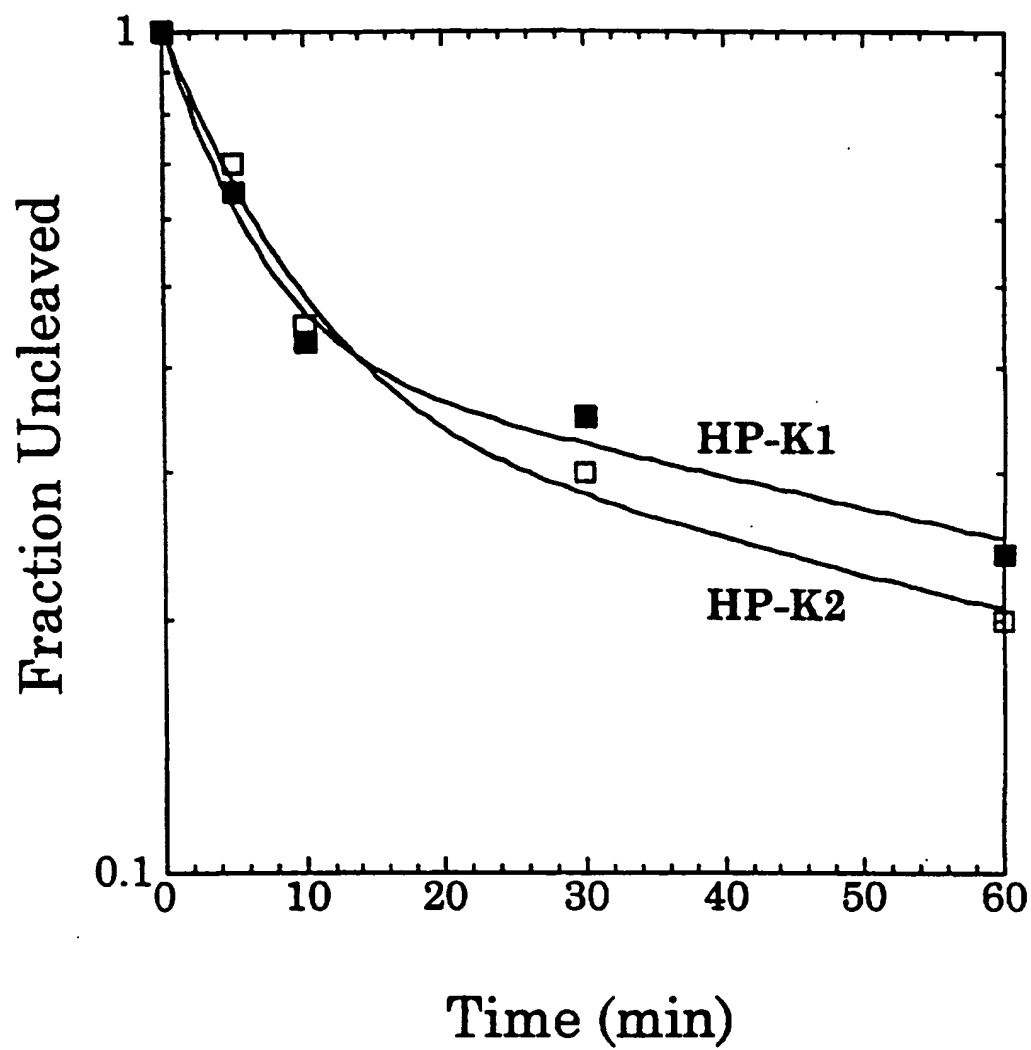


FIG. 68.

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FIG. 69b.

Substrate RNA

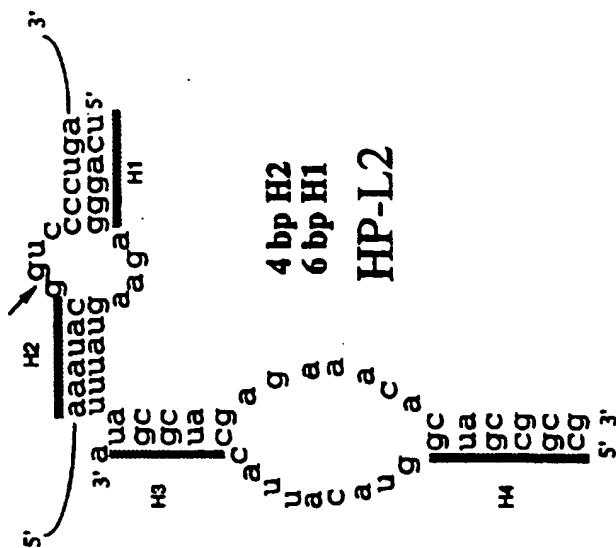
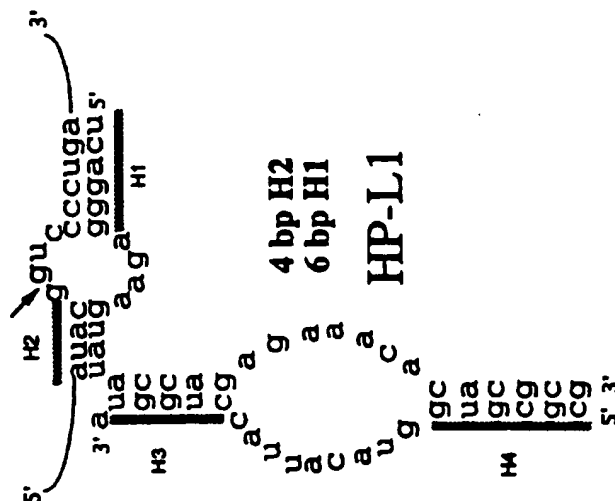


FIG. 69a.

Substrate RNA



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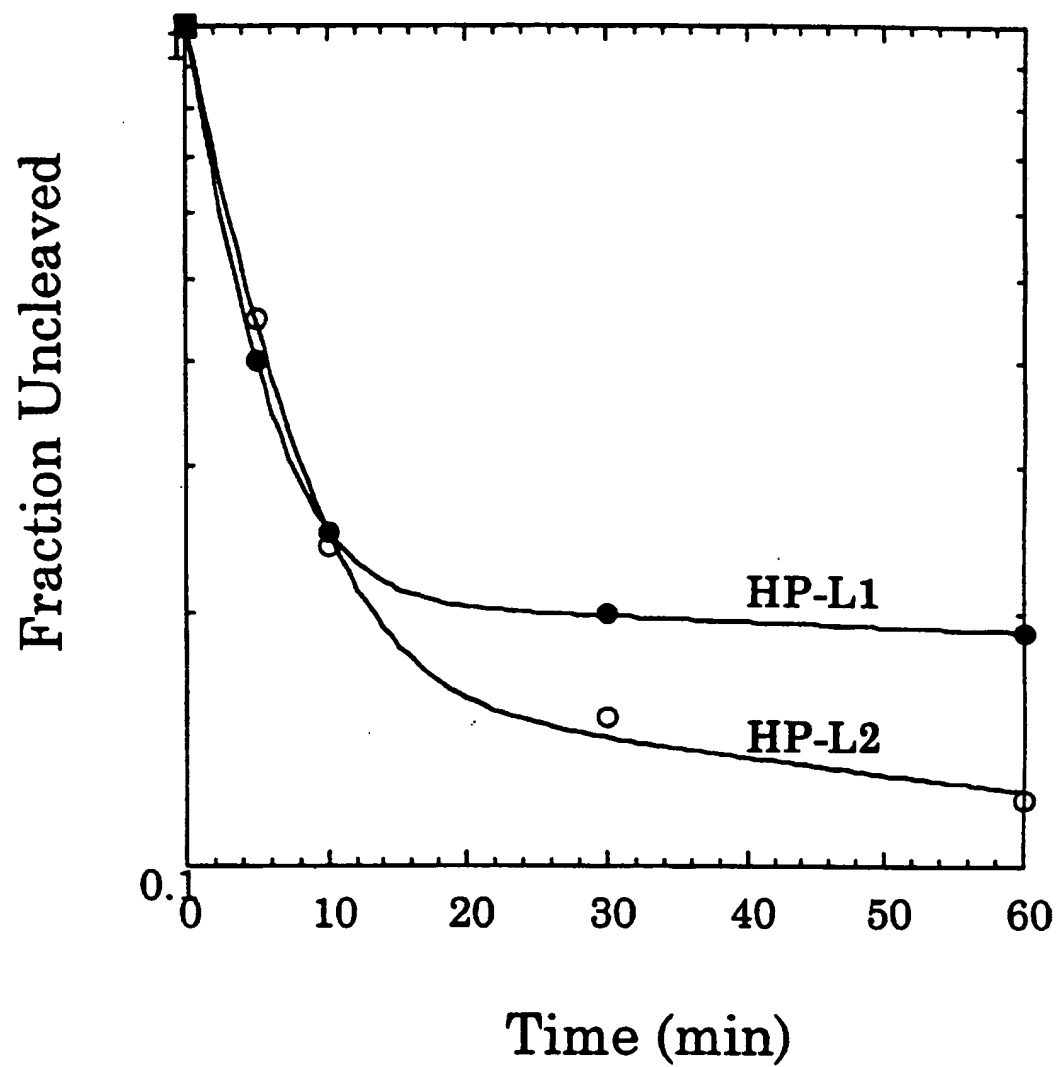


FIG. 70.

FIG. 71a.

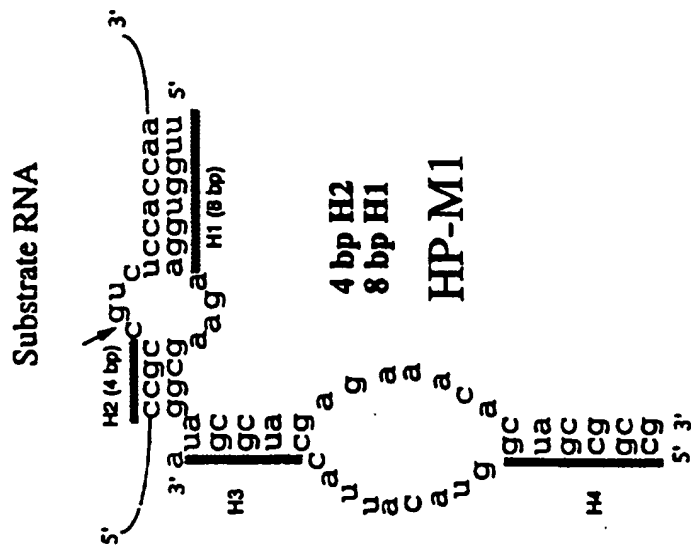
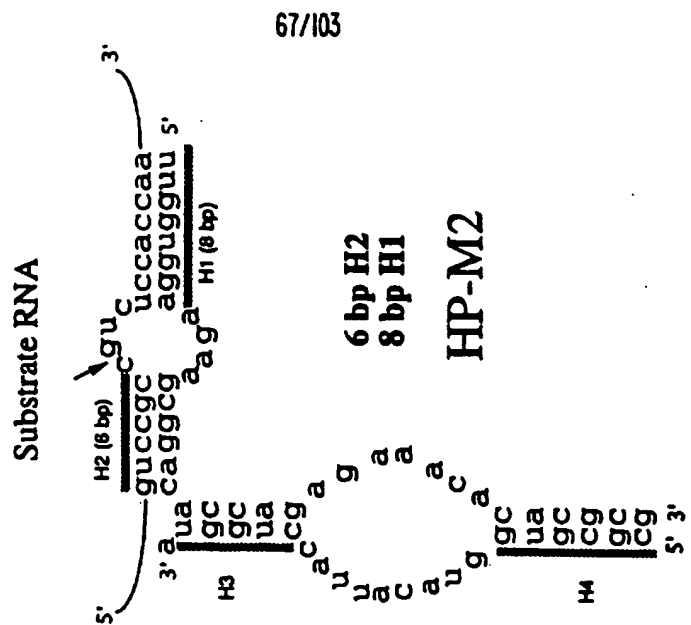


FIG. 71b.



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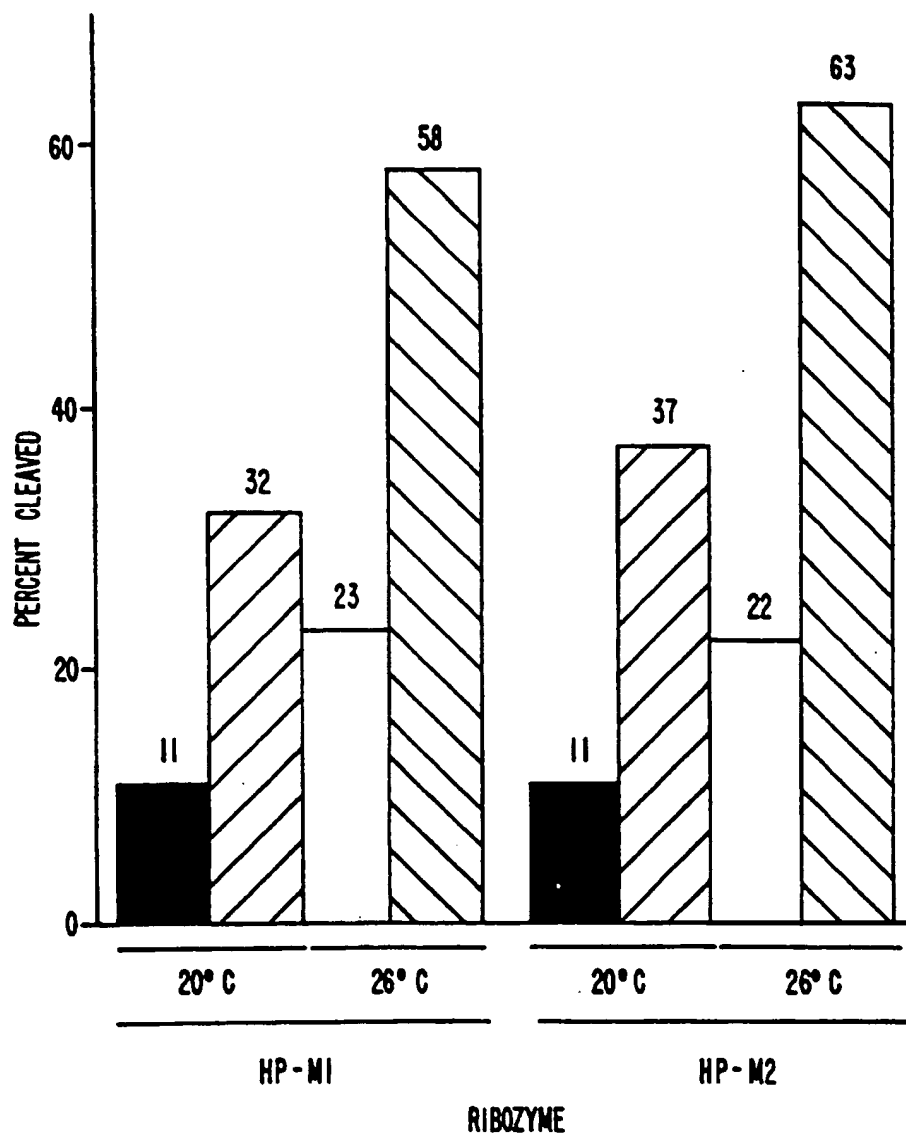


FIG. 72.

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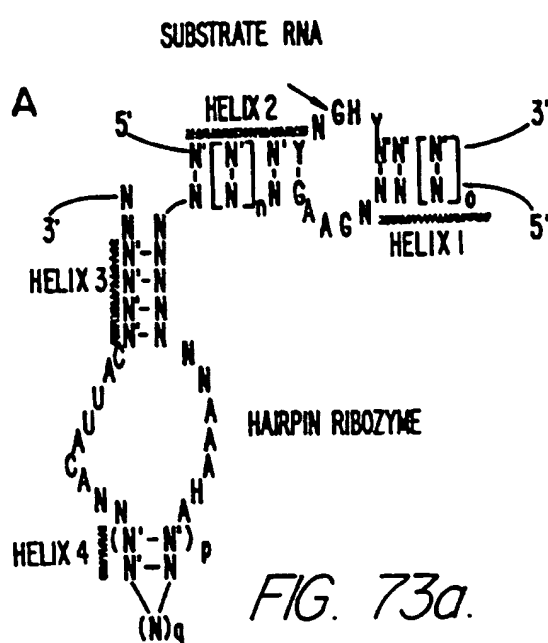


FIG. 73a.

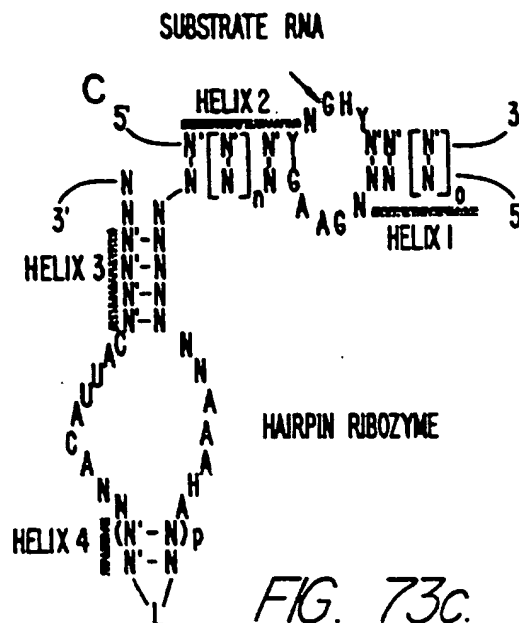


FIG. 73c.

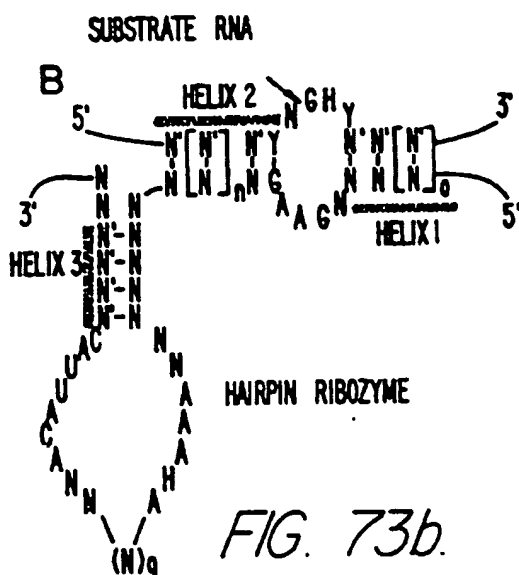


FIG. 73b.

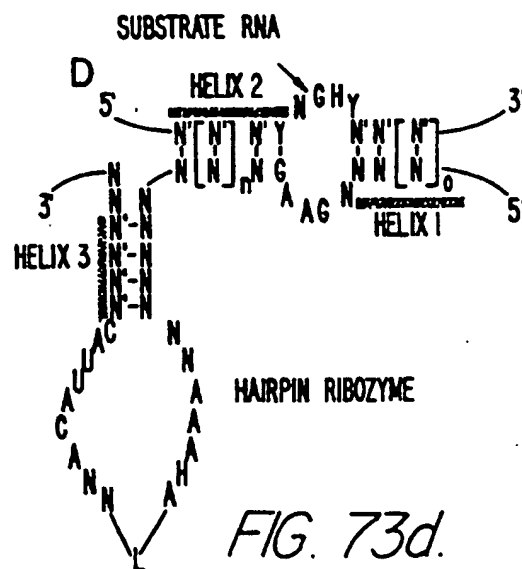


FIG. 73d.

FIG. 74a.

B

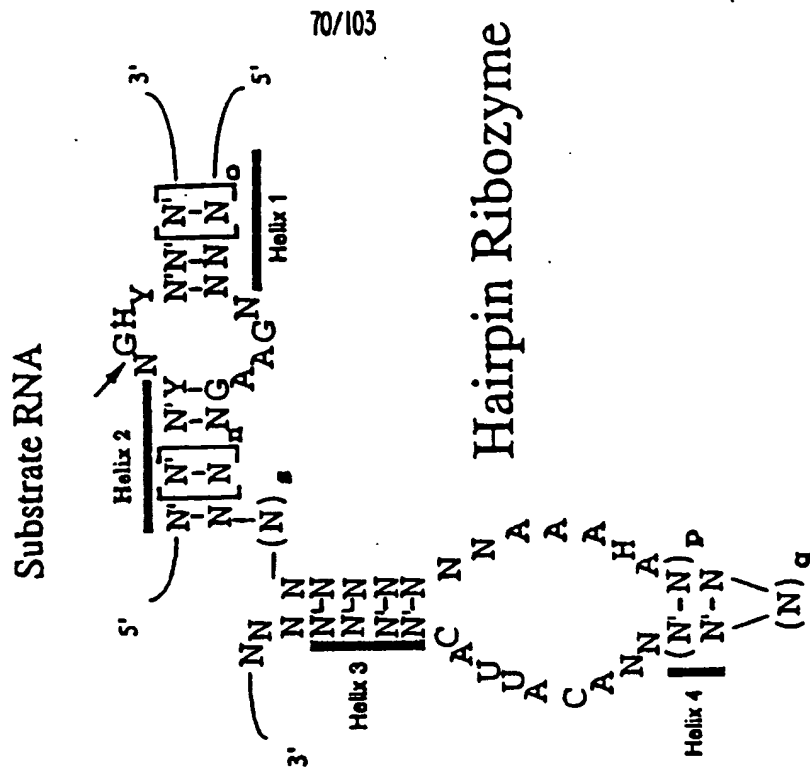


FIG. 74b.

A

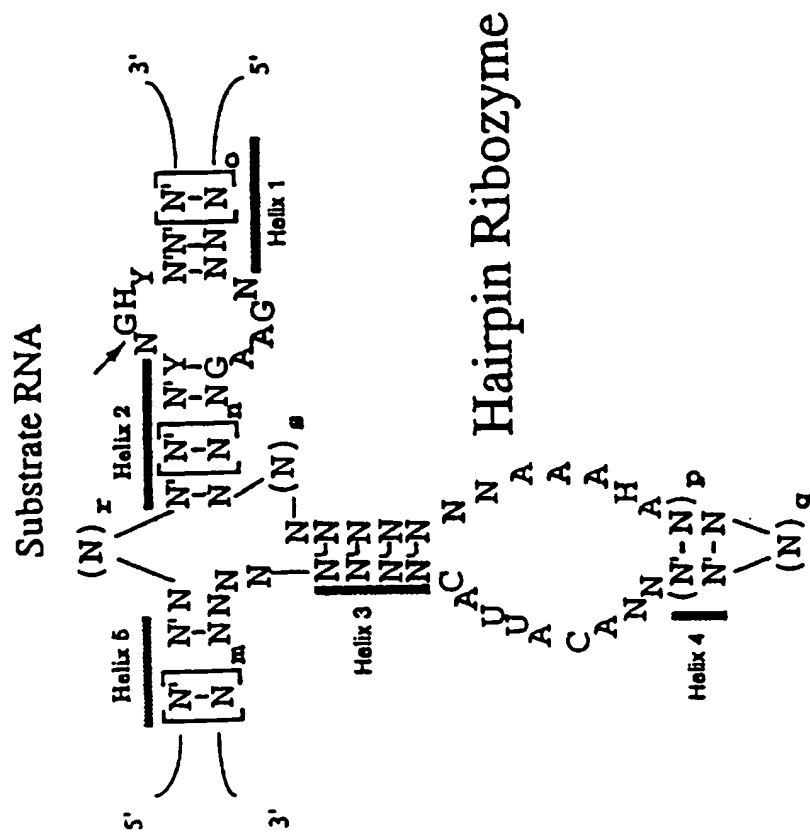
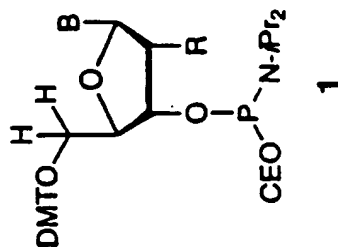
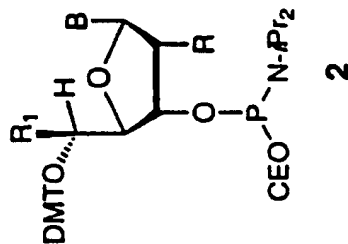


FIG. 75a.



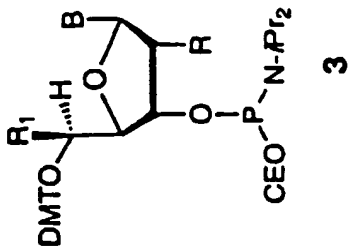
D-Ribose Family

FIG. 75b.



D-Allose Family

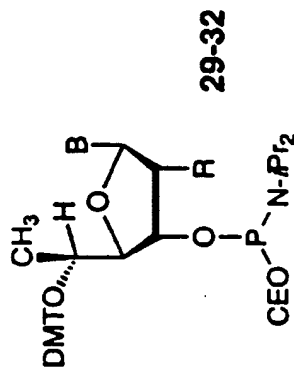
FIG. 75c.



L-Talose Family

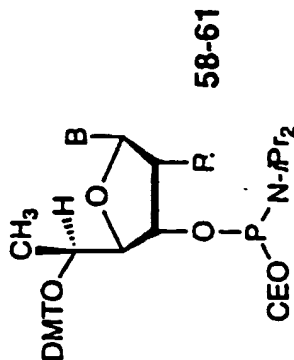
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FIG. 75d.



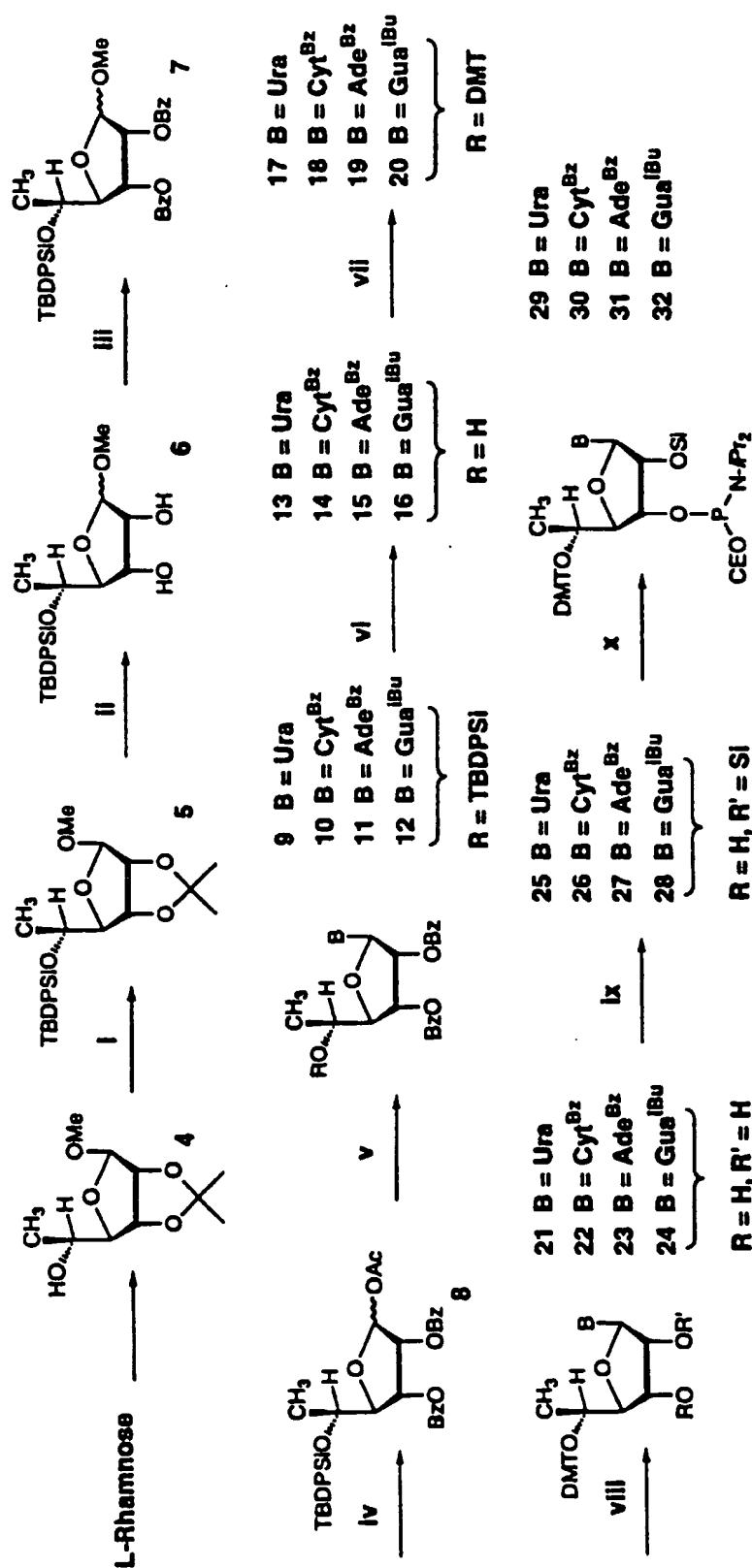
D-Allose

FIG. 75e.



L-Talose

B = Protected A, C, G, U, T, 2AP, I, DiAP, P etc.



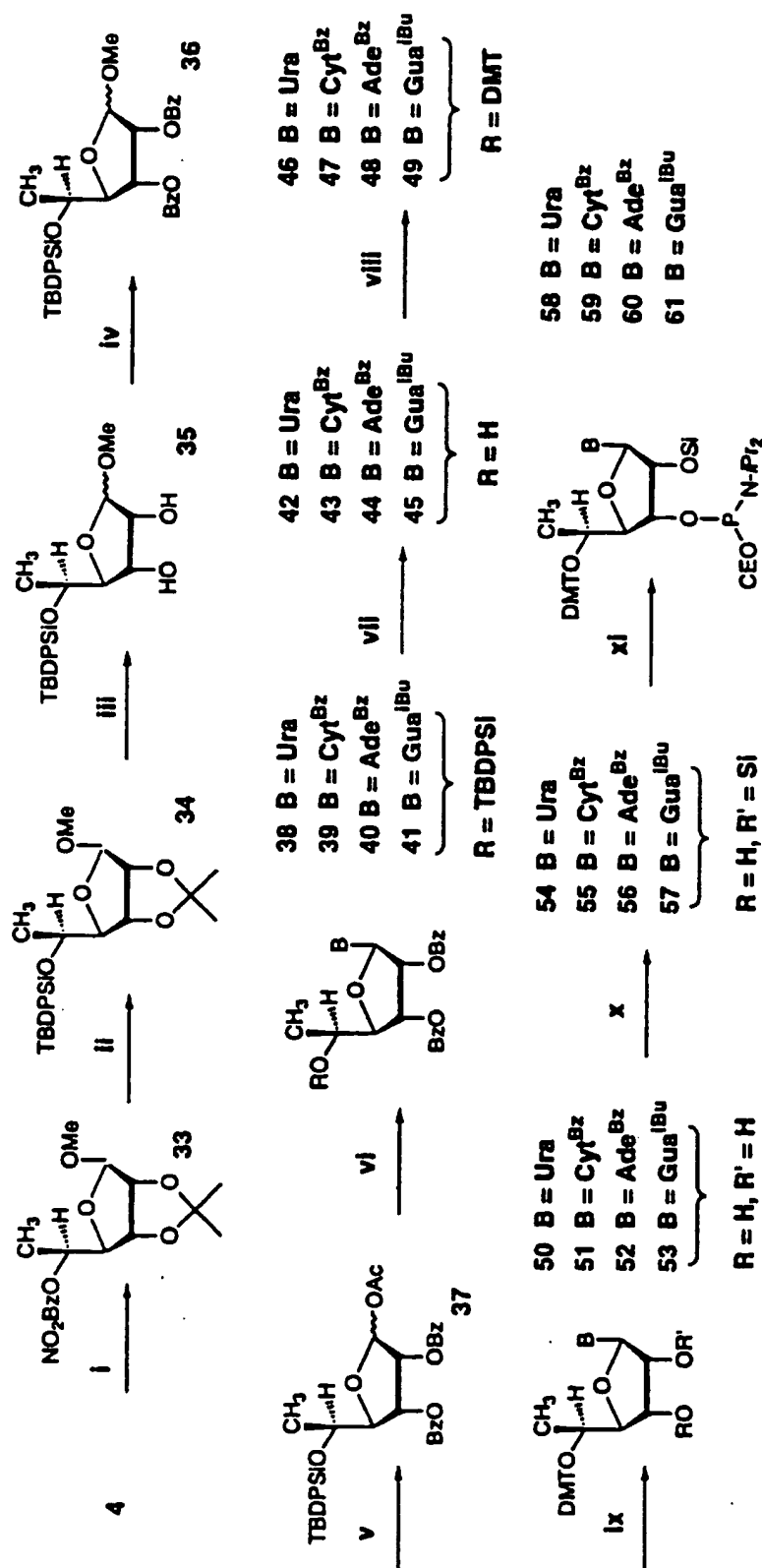
i) = TBDPSi-Cl
ii) = H^+
iii) = Bz-Cl/Pyr
iv) = $AcOH/Ac_2O/H^+$

v) = $\text{B}^{\text{TMS}}/\text{CF}_3\text{SO}_3\text{SiMe}_3$
vi) = TBAF
vii) = DMT-CI/AgNO₃
viii) = OH⁻

ix) = TBDMSi-Cl
x) = P(OCE)(N-IPr₂)Cl

FIG. 76.

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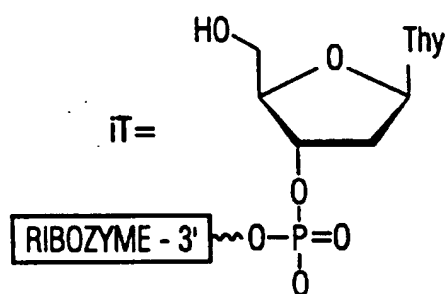
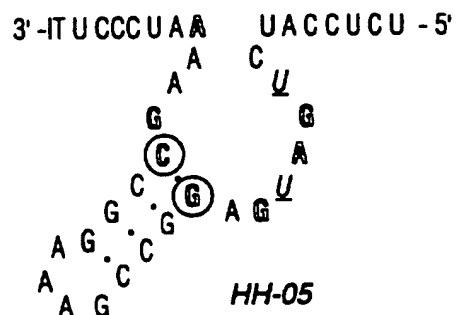
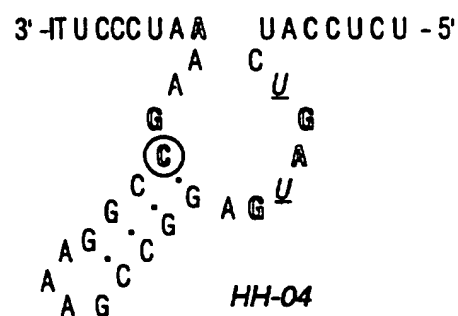
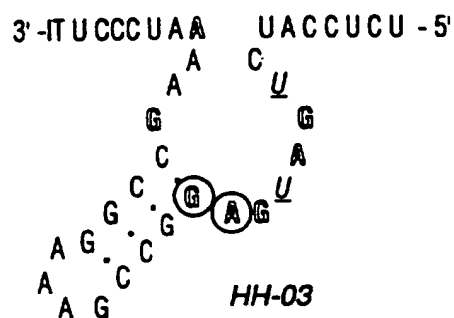
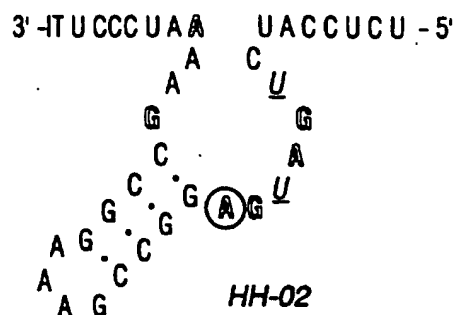
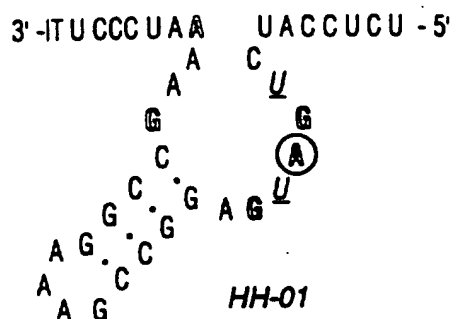


- i) = Ph₃P/DEAD/p-NO₂PhCOOH
 ii) = OH⁺, TBDPSI-Cl
 iii) = H⁺
 iv) = Bz-Cl/Pyr
 v) = AcOH/Ac₂O/H⁺
 vi) = B^{TMS}/CF₃SO₃SiMe₃
 vii) = TBAF
 viii) = DMT-Cl/AgNO₃
 ix) = OH⁻
 x) = TBDMSI-Cl
 xi) = P(OCE)(N-IP₂)Cl

FIG. 77.

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FIG. 78.



N=2'-O-Me	N=RIBO
U=2'-NH ₂ U	(N)=TALO

WHERE THE ALPHABET "N" REPRESENTS A NUCLEOTIDE, A, U, G, OR C
SUBSTITUTE SHEET (RULE 26)

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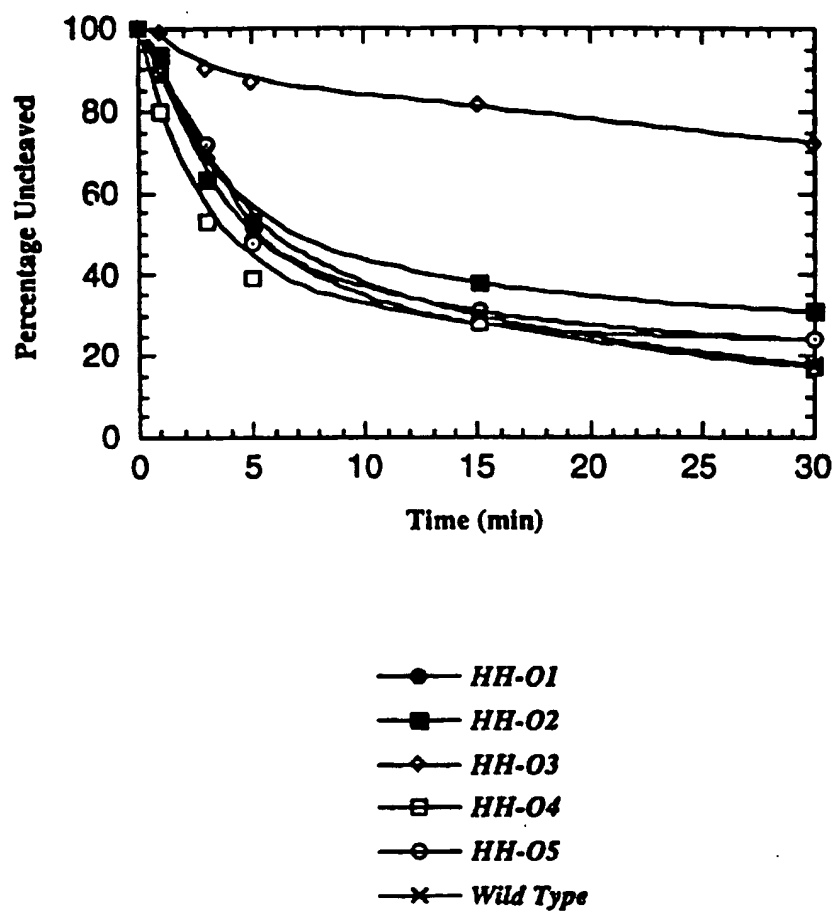


FIG. 79.

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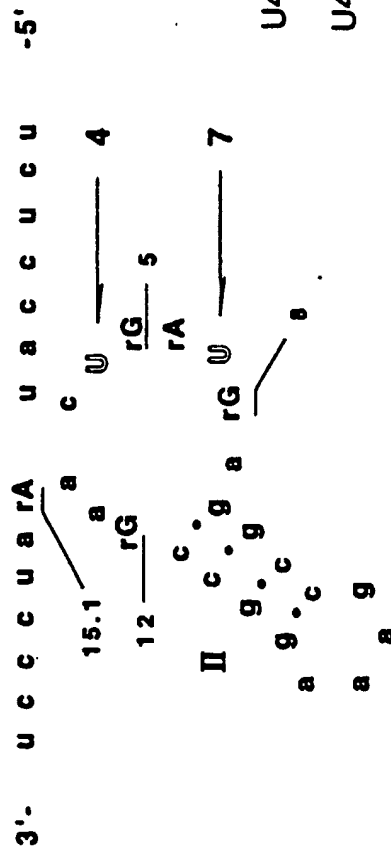
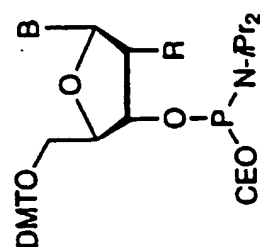


Table 1 Entries

U4 & U7 = 2'-C-Allyl-U	12-14
U4 & U7 = 2'-F-ribo-U	9-11
U4 & U7 = 2'=CH ₂ -U	3-5
U4 & U7 = 2'=CF ₂ -U	6-8
U4 & U7 = 2'-dU	21-22
U4 & U7 = 2'-F-ara-U	15-17
U4 & U7 = 2'-NH ₂ -U	18-20
U4 & U7 = 2'-O-Me-ribo-U	2

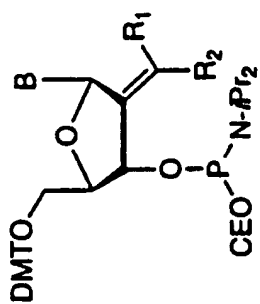
Lower case = 2'-O-Me
rN = ribonucleotide

FIG. 80.



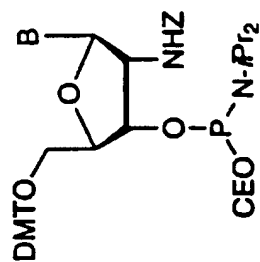
1

FIG. 8Ia.



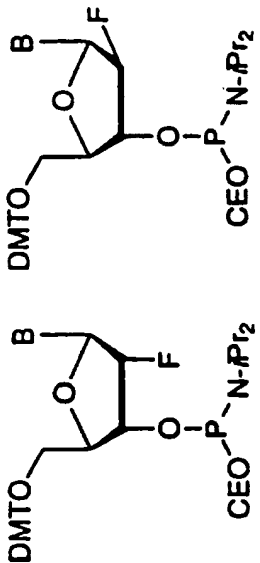
2

FIG. 8Ib.



3

FIG. 8Ic.

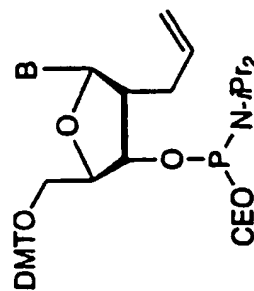


4

FIG. 8Id.

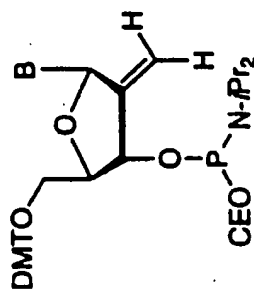
5

FIG. 8Ie.



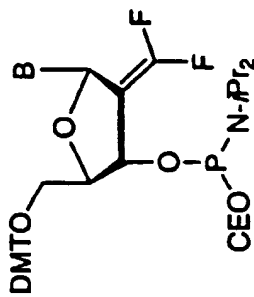
10 & 12

FIG. 8If.



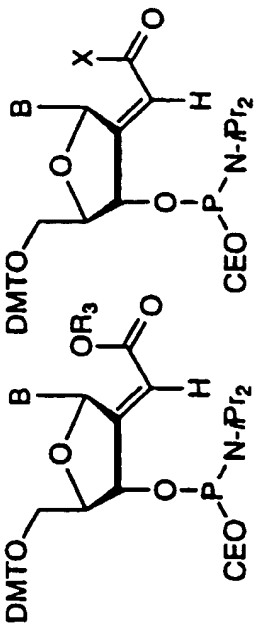
17, 22 & 31

FIG. 8Ig.



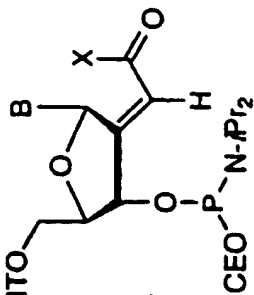
18, 26 & 32

FIG. 8Ih.



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FIG. 8Ii.



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FIG. 8Ij.

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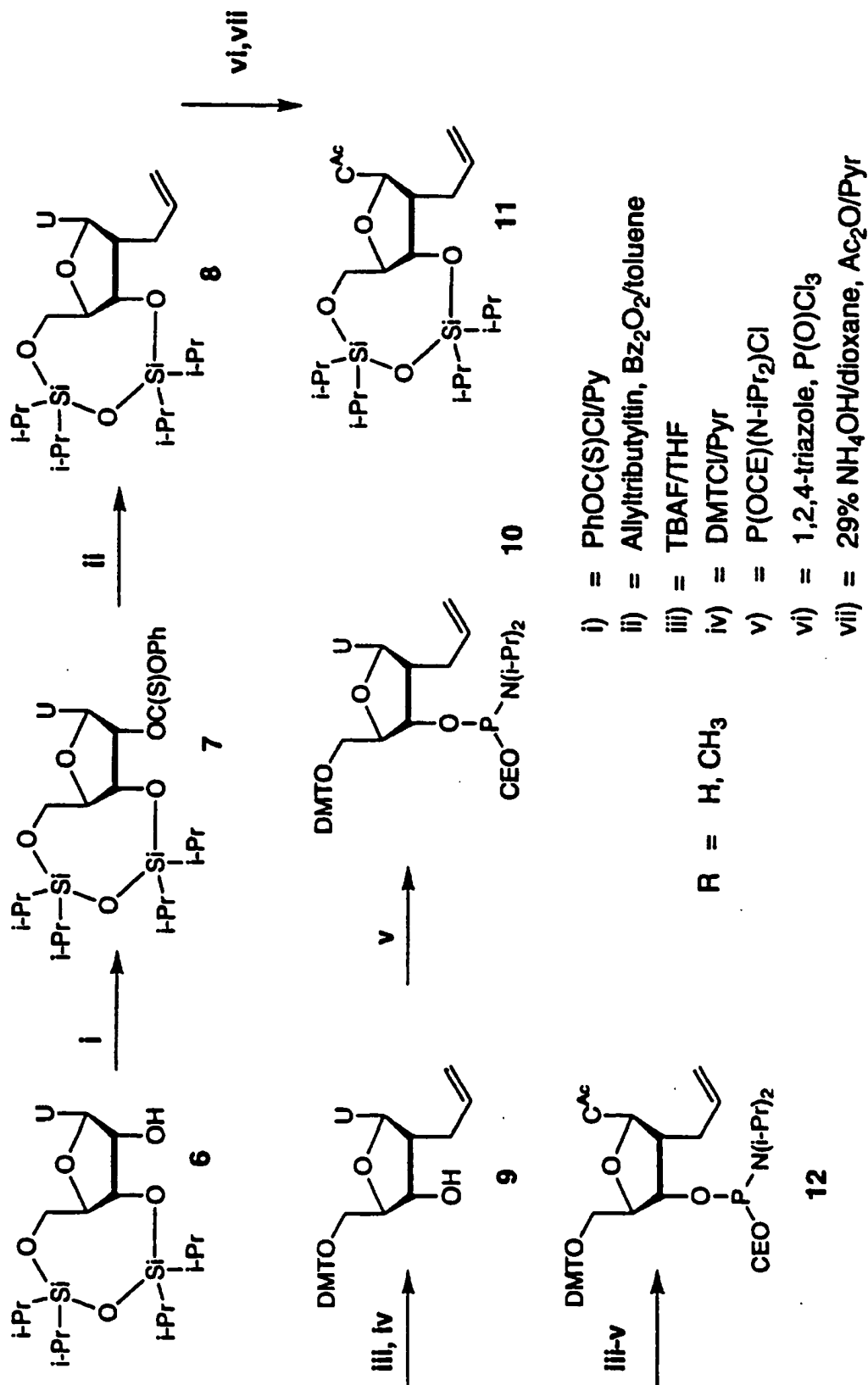
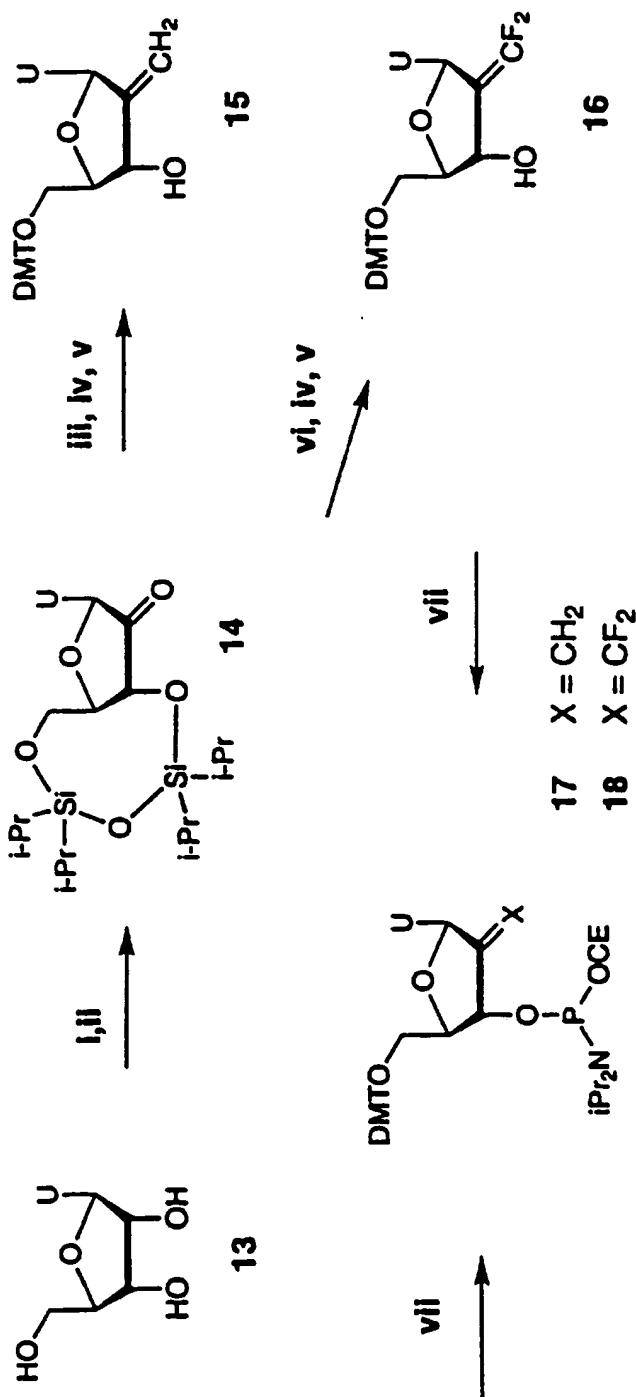


FIG. 82.

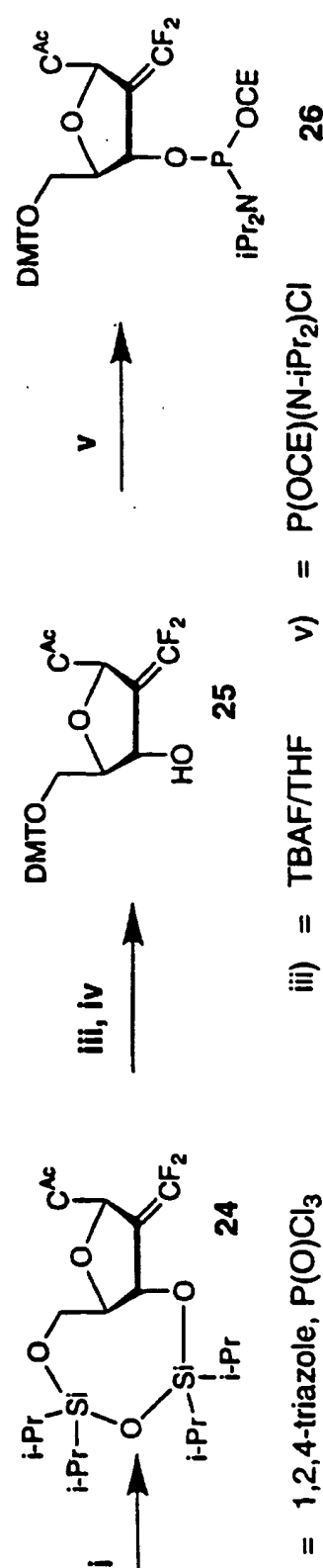
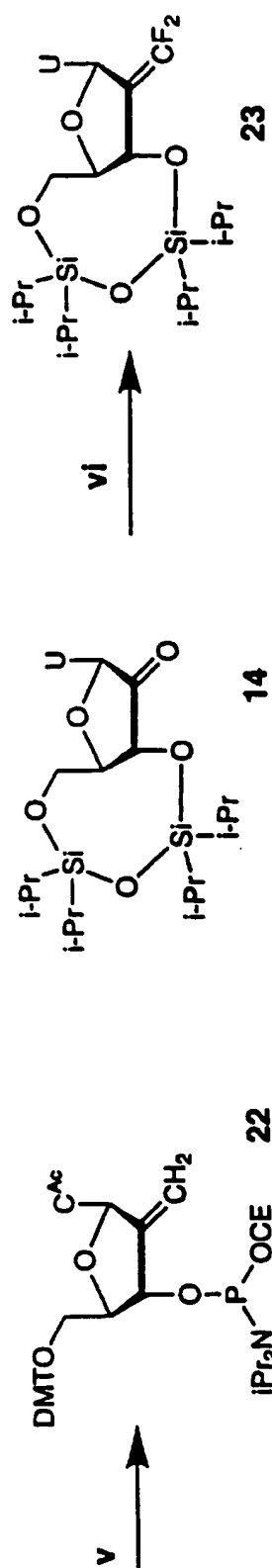
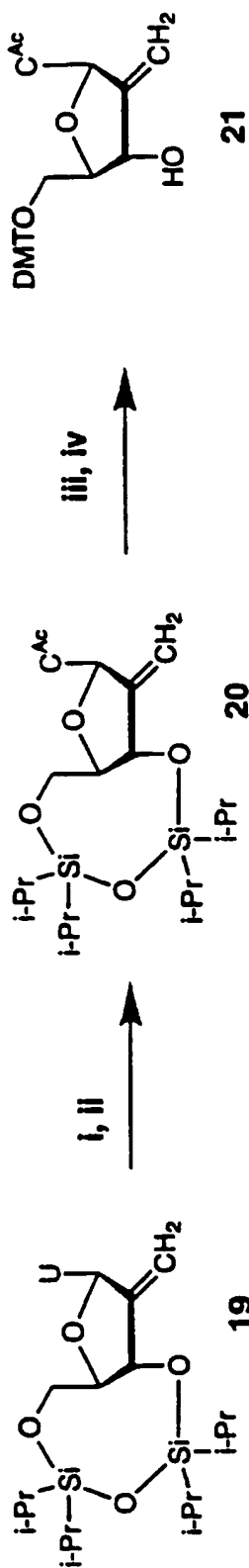
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FIG. 83.



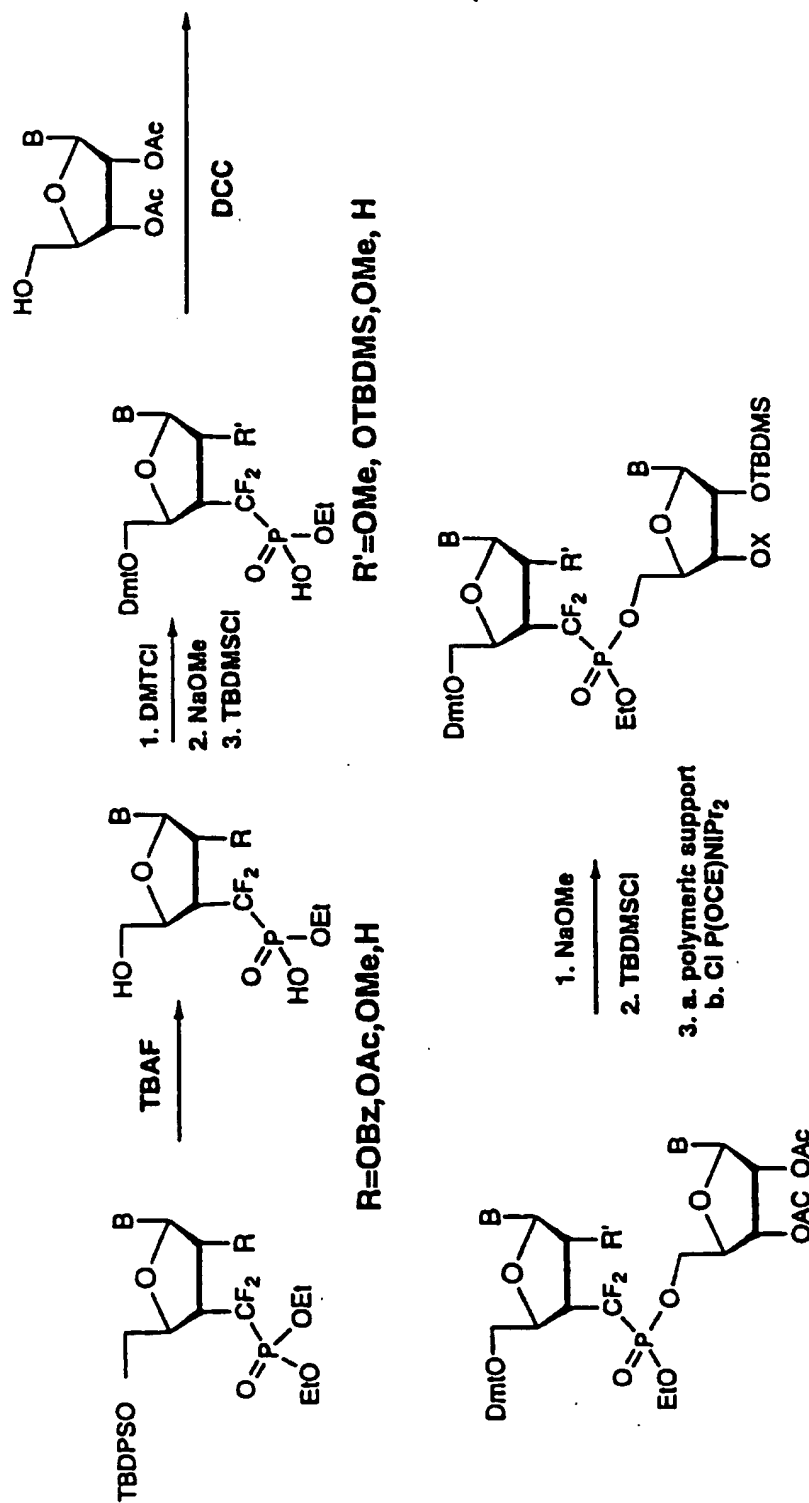
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FIG. 84.



i) = 1,2,4-triazole, P(O)Cl₃
 ii) = 29% NH₄OH/dioxane, Ac₂O/Pyr
 iii) = TBAF/THF
 iv) = DMTC/Pyr
 v) = P(OCE)(N-iPr₂)Cl
 vi) = Ph₃P, ClCF₂COONa

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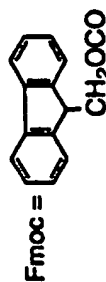


$\text{R' = OMe, OTBDMS, H}$
 $\text{X = polymeric support}$
 X = P(OCE)NIPr_2

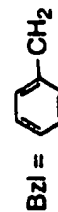
FIG. 91.



EEDQ = N-ethoxycarbonyl-2-ethoxy-1,2-dihydroquinoline



$R = \text{CH}_3$, $\text{CH}_2\text{-}$  (phe), $(\text{CH}_2)_4\text{NH-Fmoc}$, $(\text{CH}_2)_4\text{NH-Cbz}$, CH_2COOBzl (asp), $(\text{CH}_2)_4\text{NH-Fmoc}$, $(\text{CH}_2)_4\text{NH-Cbz}$, CH_2COOBzl (asp)



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FIG. 93a.

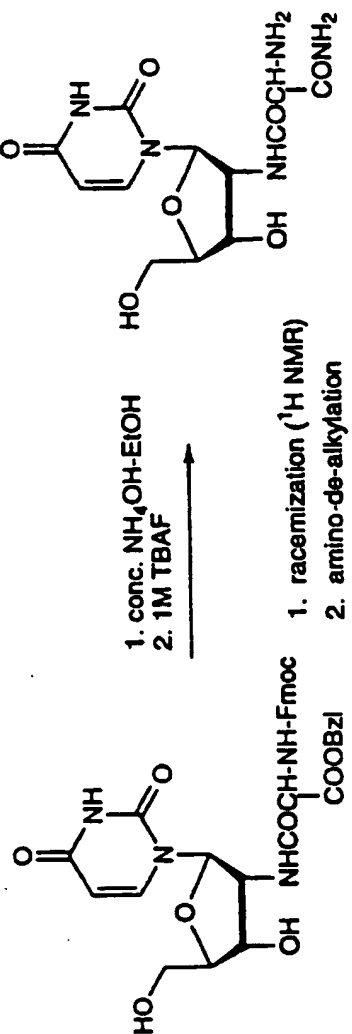
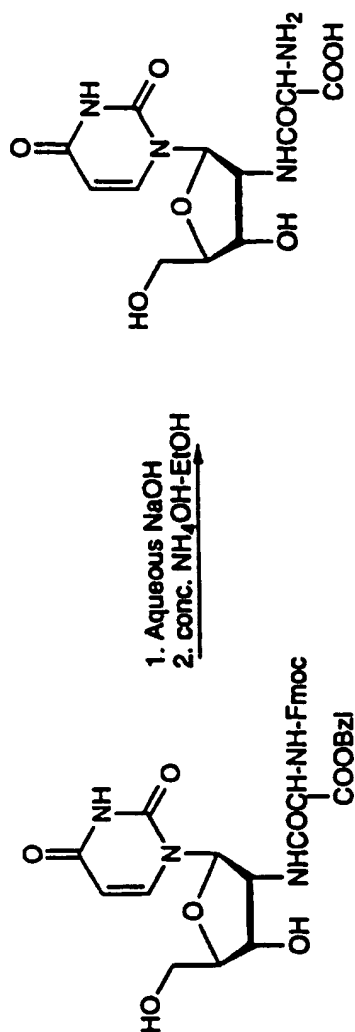


FIG. 93b.



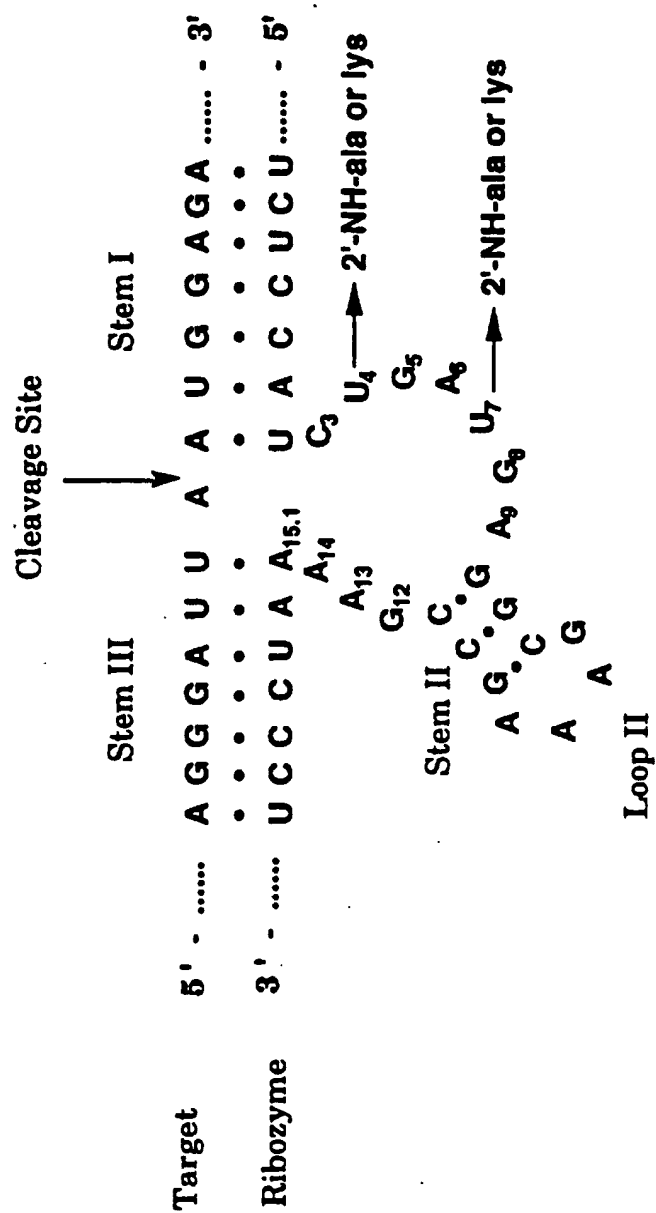
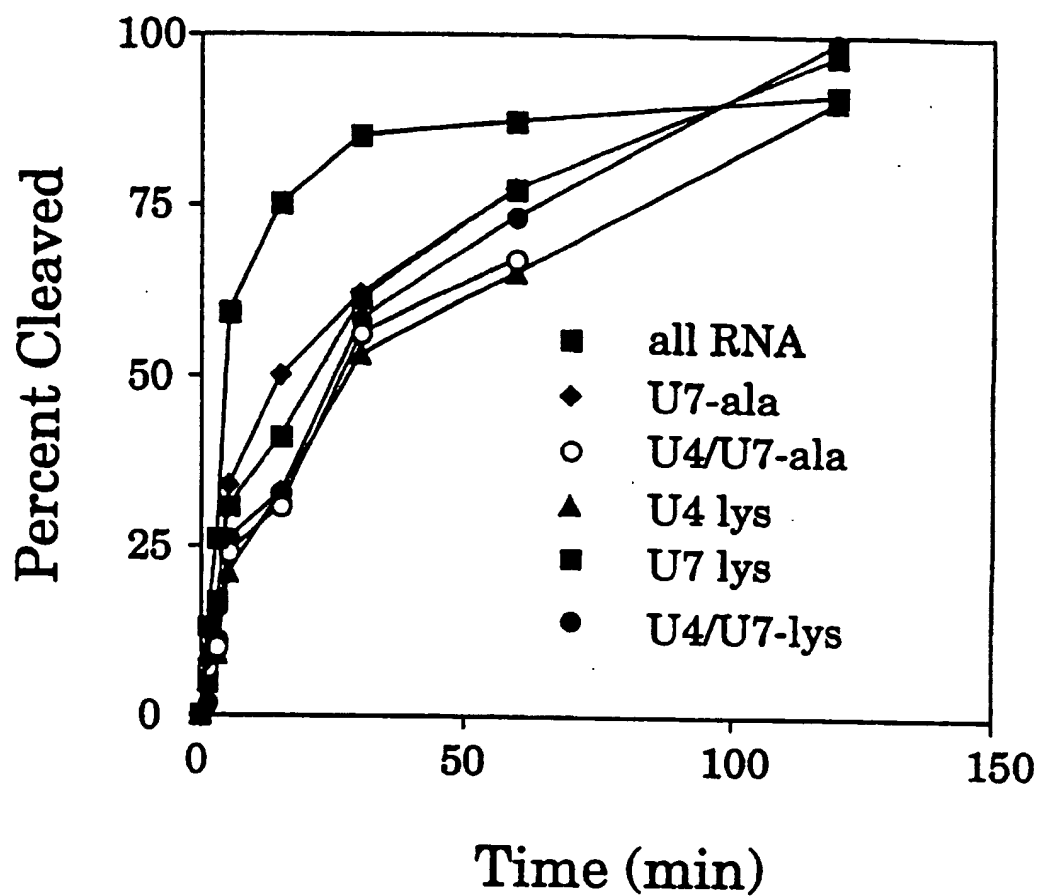


FIG. 94.

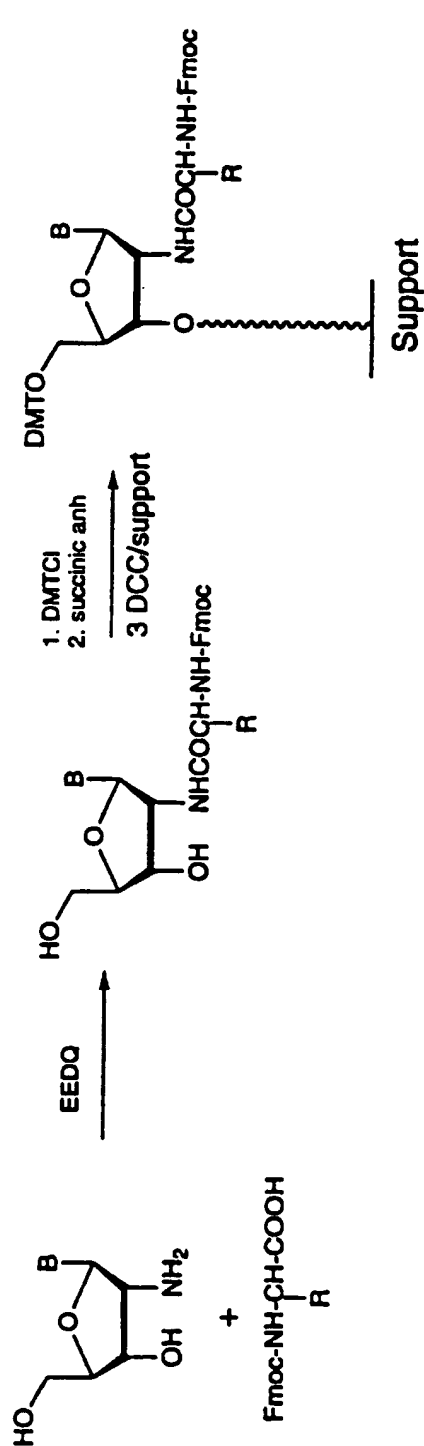
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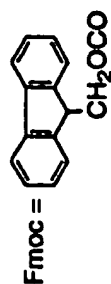
[Ribozyme] = 40 nM [Substrate] = ~1nM

FIG. 95.

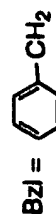
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EEDQ = N-ethoxycarbonyl-2-ethoxy-1,2-dihydroquinoline



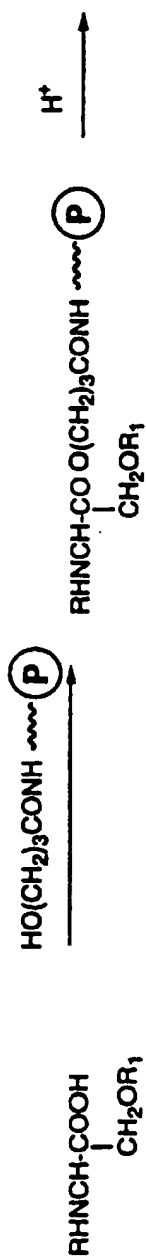
R = CH₃, CH₂-(phe), (CH₂)₄NH-Fmoc, (CH₂)₄NH-CBZ, CH₂COOBzl
(ala) (lys) (asp)



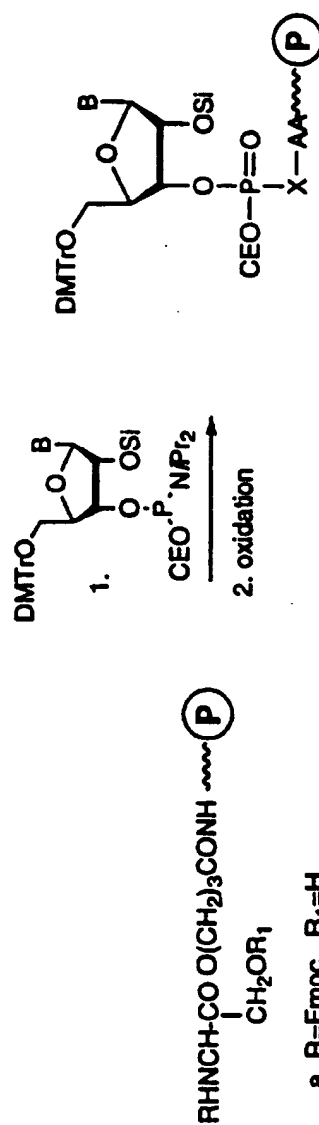
B = Ura, Cyt^{bz}, Ade^{bz}, Gua^{ibu}, mod. base, H

FIG. 96.

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a R=Fmoc, R₁=DMTr
 b R=MMTr, R₁=Bz

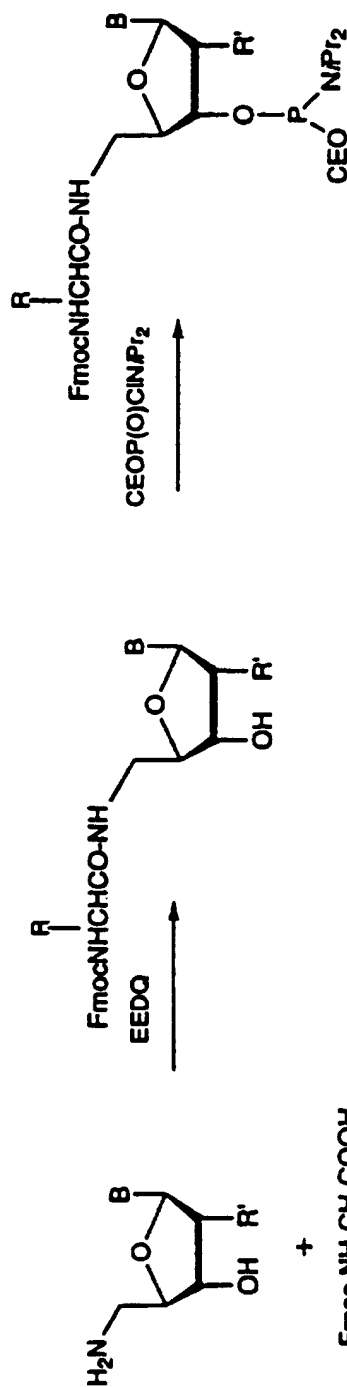


a X=O, AA=CH₂CH(NHFmoc)CO
 b X=NH, AA=CH(CH₂OBz)CO

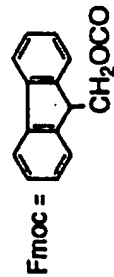
B= Ura, Cyt^{bz}, Ade^{bz}, Gua^{ibu}, mod. base, H

FIG. 97.

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EEDQ = N-ethoxycarbonyl-2-ethoxy-1,2-dihydroquinoline



R = CH₃, CH₂- (phe), (CH₂)₄NH-Fmoc, (CH₂)₄NH-CBZ, CH₂COOBzl (asp)

CBZ = -CH₂OCOBzl = -CH₂

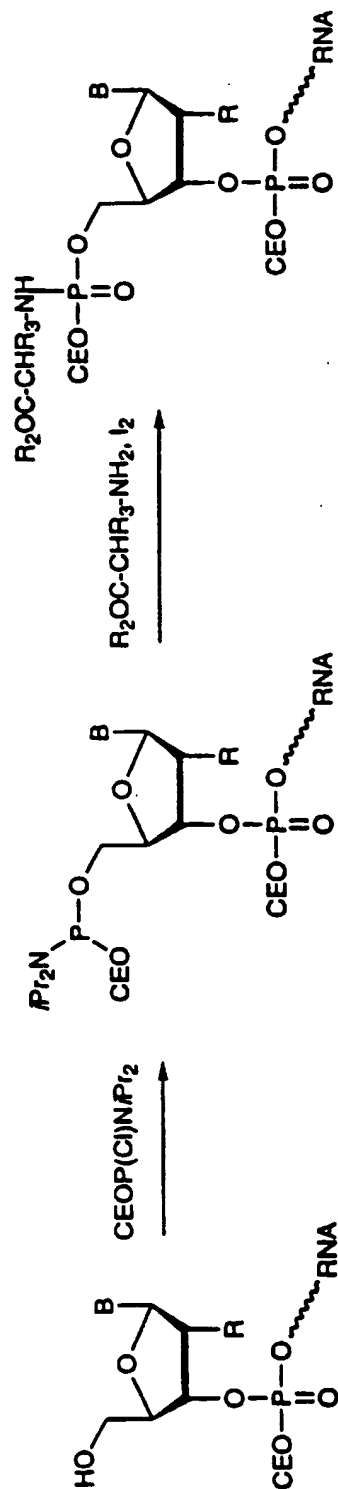
R' = H, OMe, OTBDMSi

B = Ura, Cyt^{bz}, Ade^{bz}, Gua^{ibu}, mod. base, H

FIG. 98.

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FIG. 99.



B = Ura, Cyt^{bz}, Ade^{bz}, Gua^{bu}, mod. base, H
 R = H, OCH₃, OTBDMS, Hal, NHR₁
 R₂ = OBzl, peptidyl

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FIG. 100.

Reversion of mutant RNA

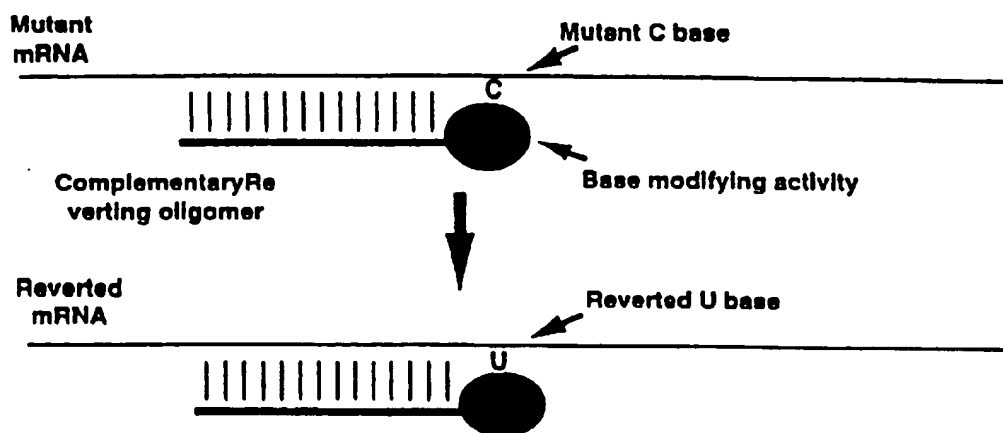
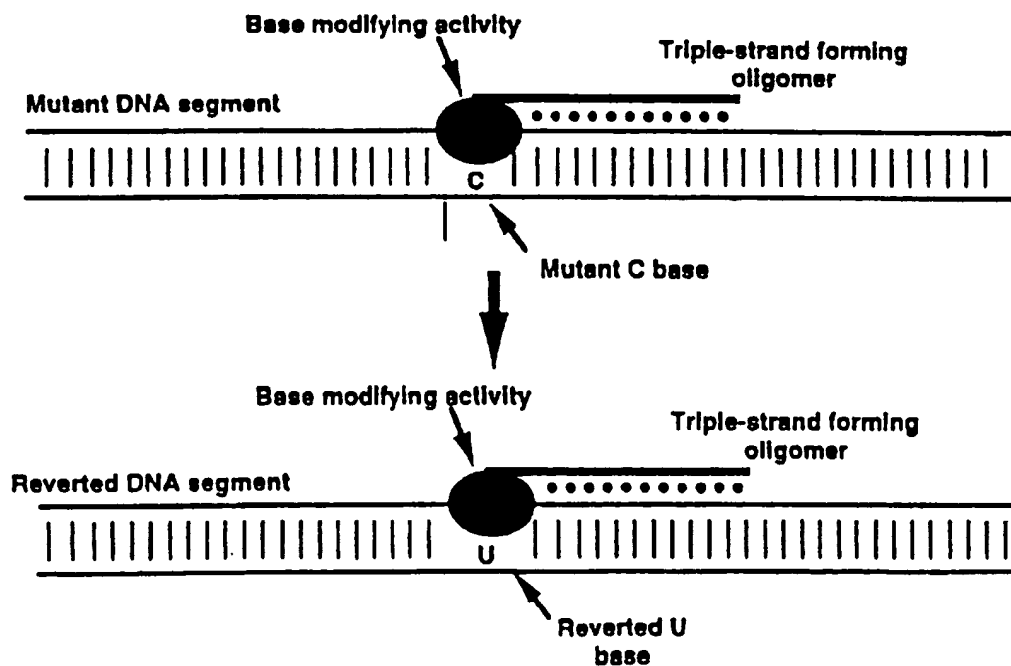
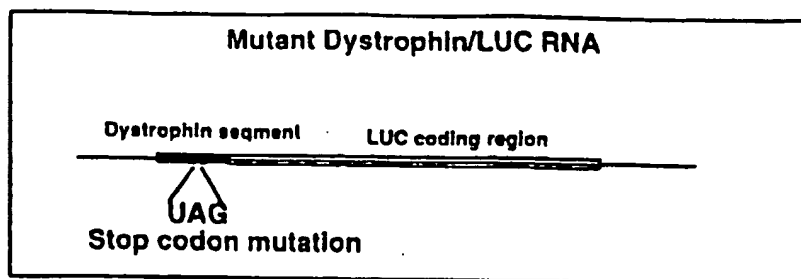
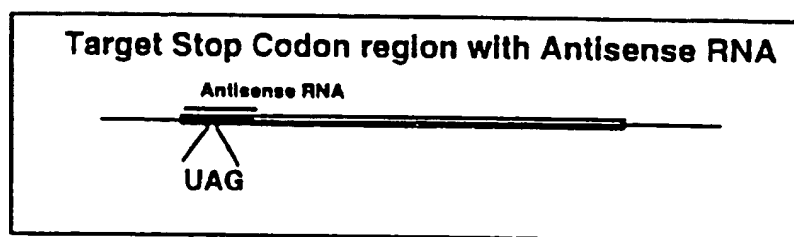
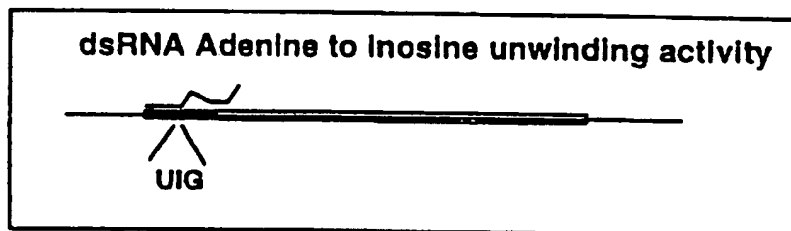
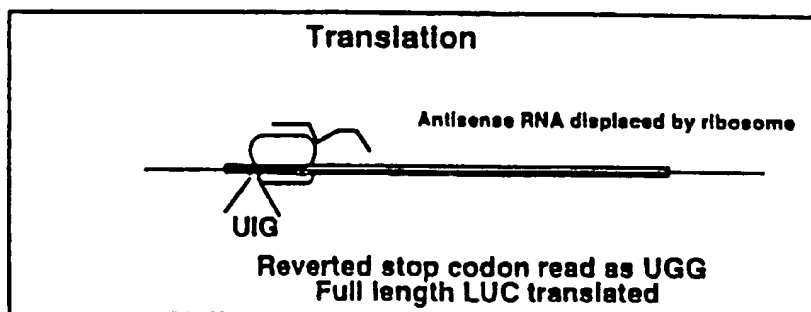


FIG. 101.

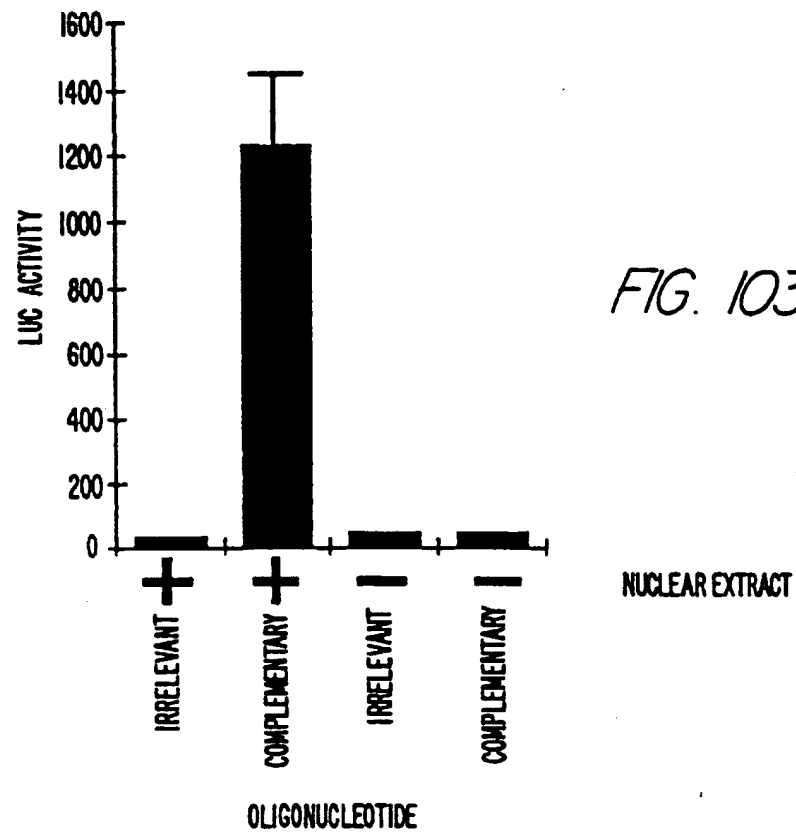
Reversion of mutant DNA



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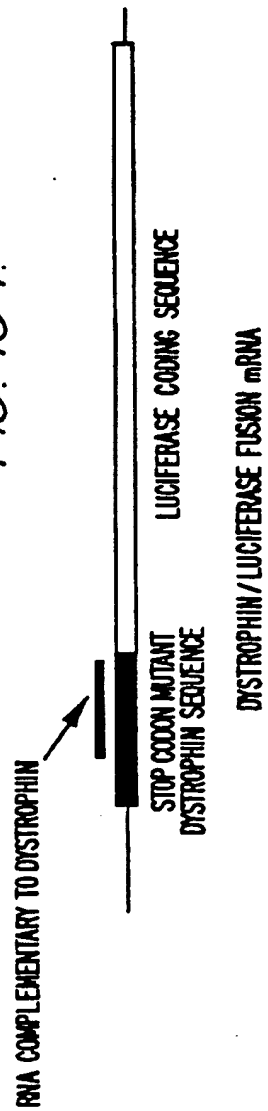
*FIG. 102a.**FIG. 102b.**FIG. 102c.**FIG. 102d.*

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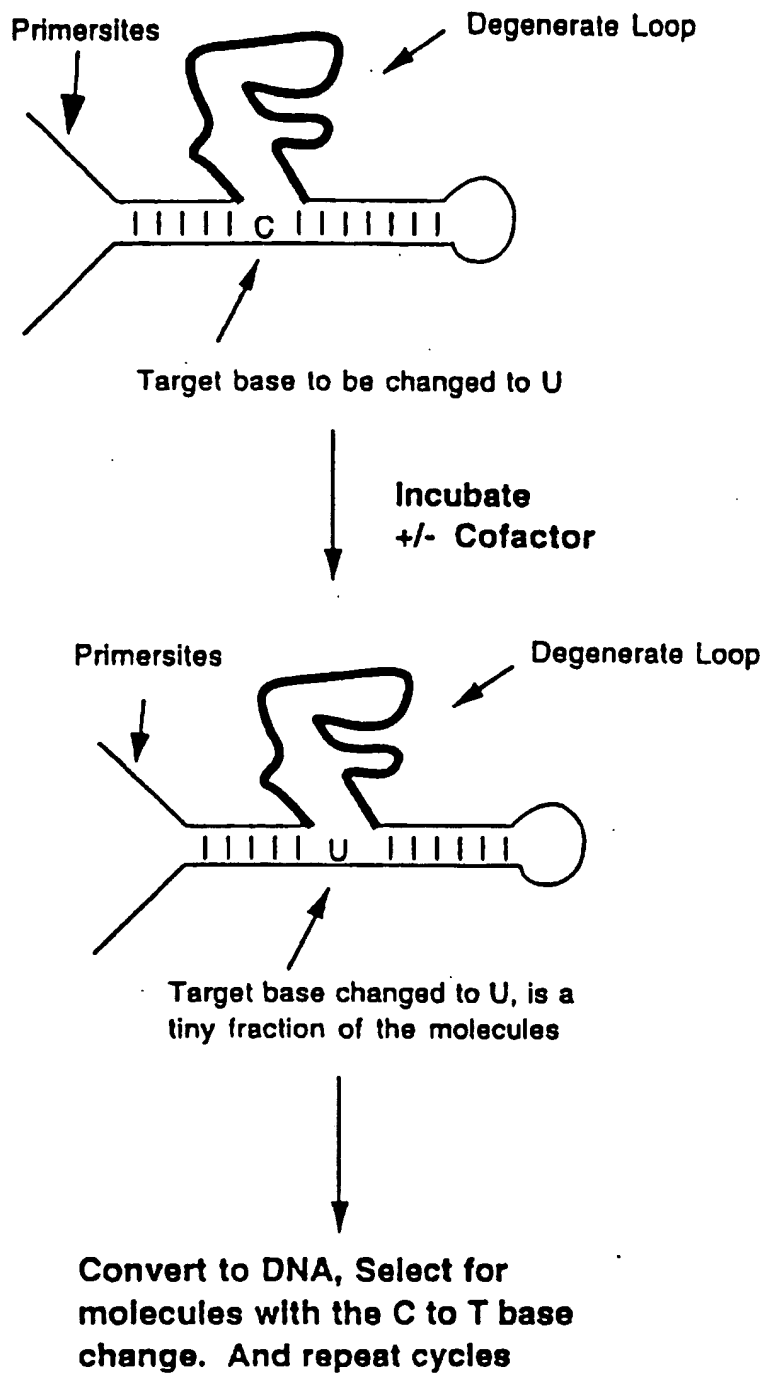
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FIG. 104.

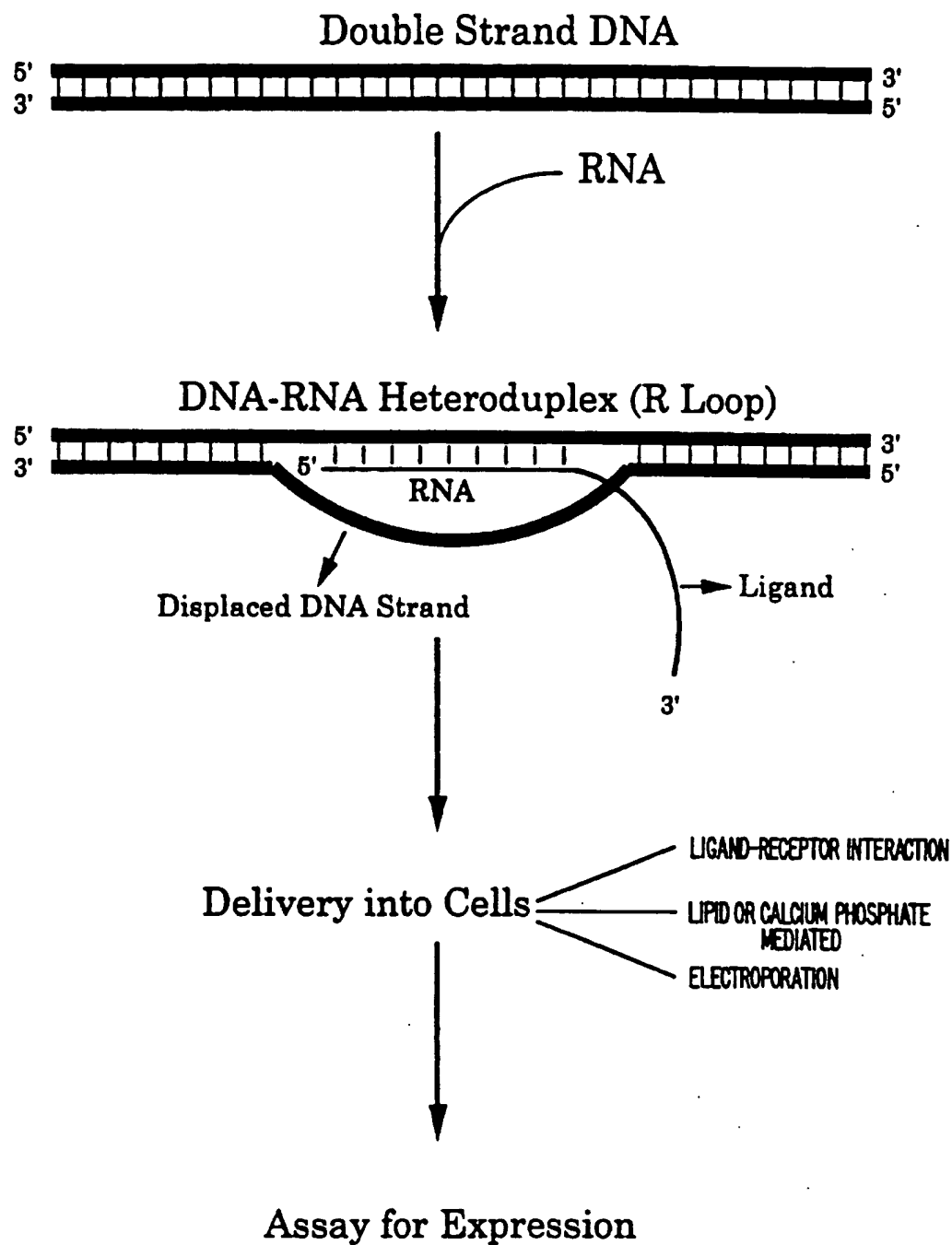


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FIG. 105.



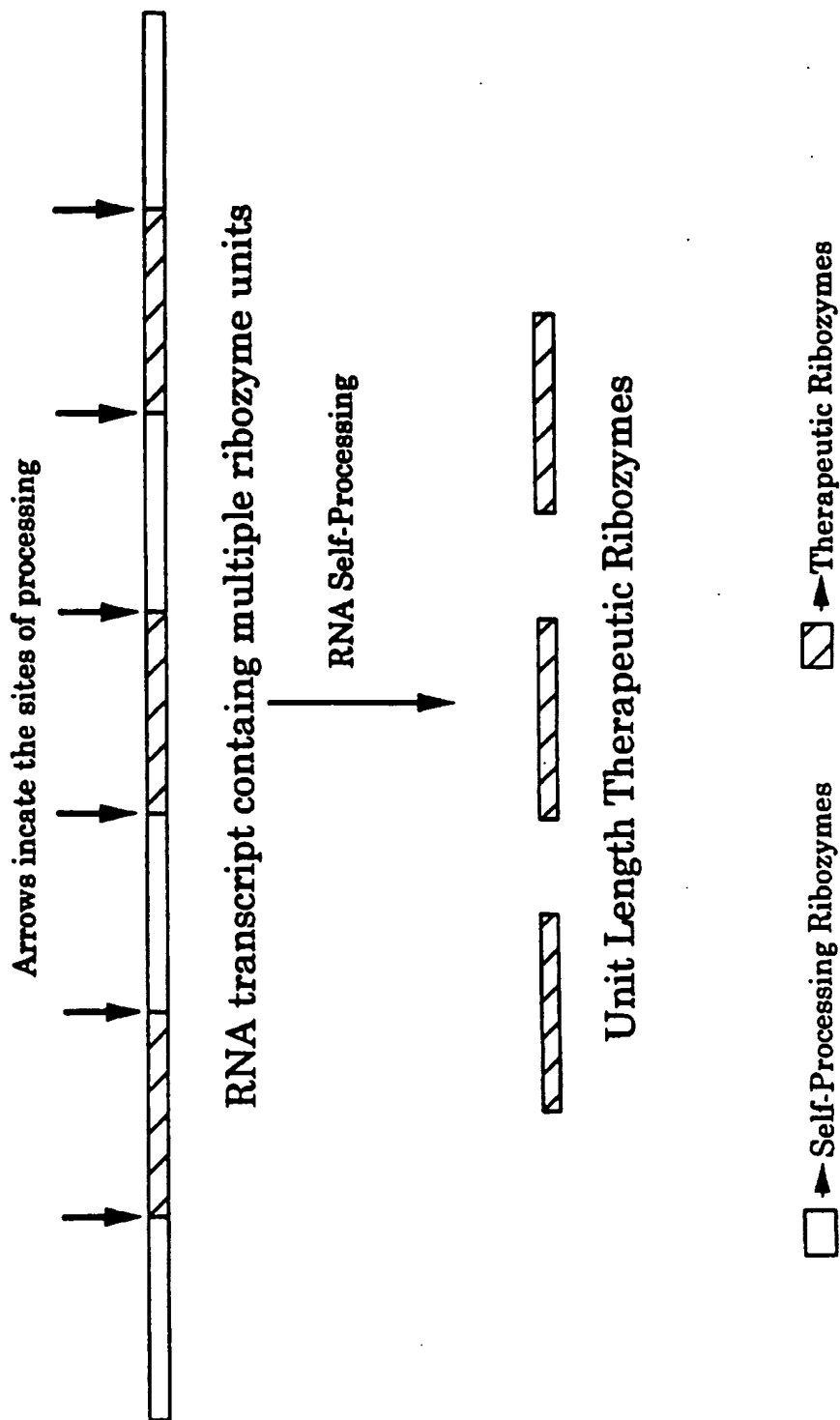
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*FIG. 106.*

SUBSTITUTE SHEET (RULE 26)

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FIG. 107.



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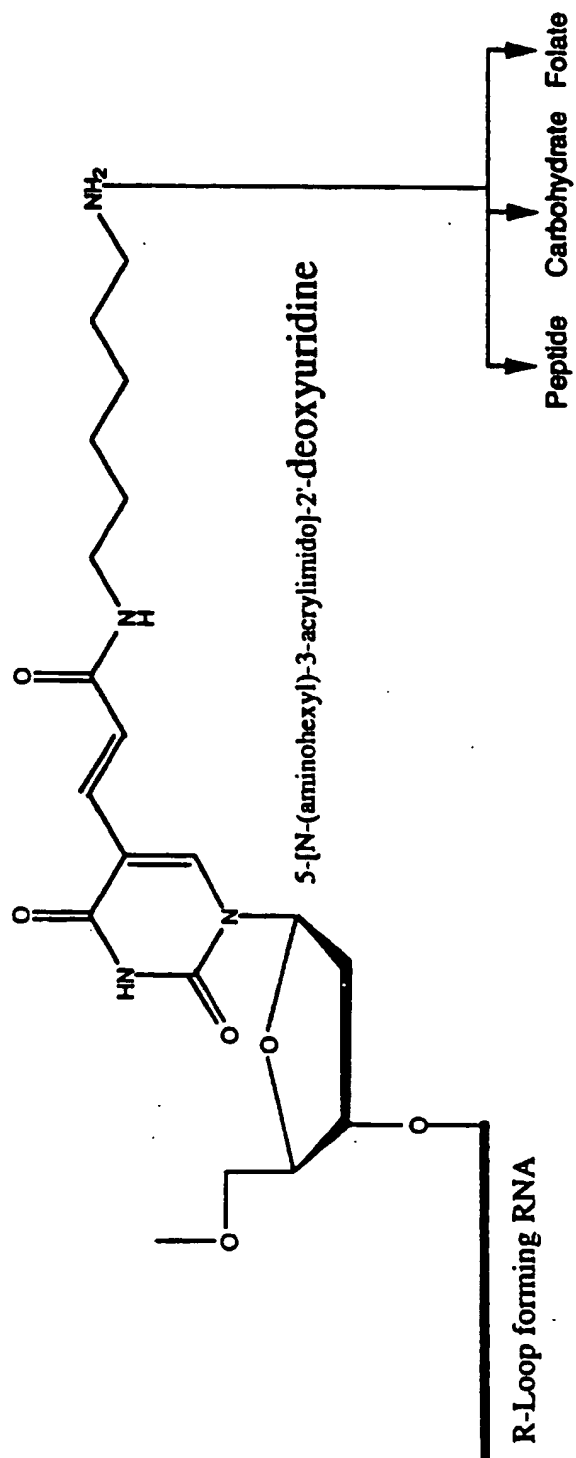


FIG. 108.

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